



Full wwPDB EM Validation Report ⓘ

Oct 12, 2024 – 06:31 PM EDT

PDB ID : 6DQN
EMDB ID : EMD-7981
Title : Class 1 IP3-bound human type 3 1,4,5-inositol trisphosphate receptor
Authors : Hite, R.K.; Paknejad, N.
Deposited on : 2018-06-11
Resolution : 3.33 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

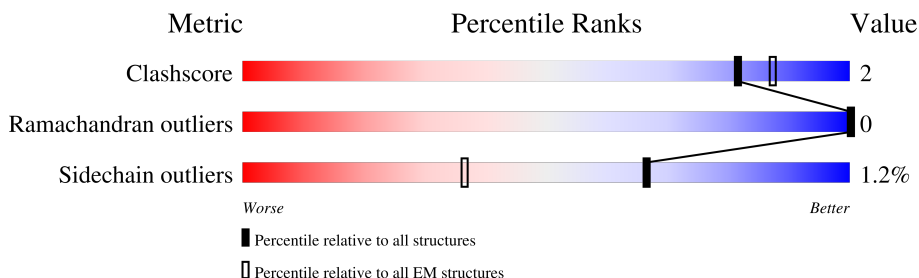
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.33 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2671	<div> <div>29%</div> <div>76%</div> <div>6%</div> <div>18%</div> </div>
1	B	2671	<div> <div>29%</div> <div>76%</div> <div>6%</div> <div>18%</div> </div>
1	C	2671	<div> <div>29%</div> <div>76%</div> <div>6%</div> <div>18%</div> </div>
1	D	2671	<div> <div>29%</div> <div>76%</div> <div>6%</div> <div>18%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 138912 atoms, of which 69432 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

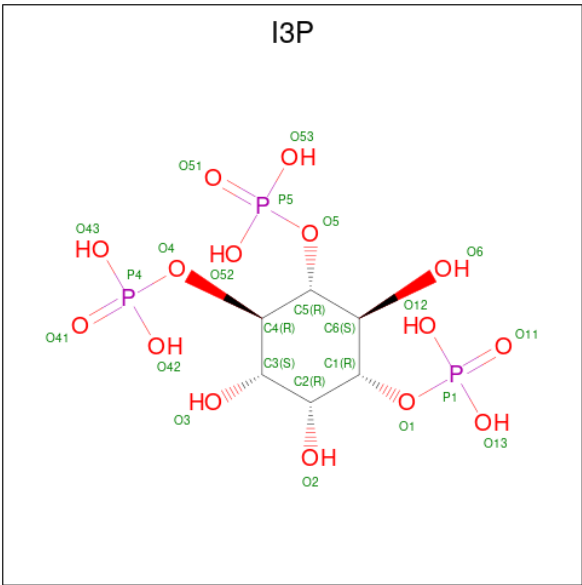
- Molecule 1 is a protein called Inositol 1,4,5-trisphosphate receptor type 3.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	2186	Total	C	H	N	O	S	0	0
			34694	11058	17349	2985	3199	103		
1	B	2186	Total	C	H	N	O	S	0	0
			34694	11058	17349	2985	3199	103		
1	C	2186	Total	C	H	N	O	S	0	0
			34694	11058	17349	2985	3199	103		
1	D	2186	Total	C	H	N	O	S	0	0
			34694	11058	17349	2985	3199	103		

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total	Zn	0
			1	1	
2	B	1	Total	Zn	0
			1	1	
2	C	1	Total	Zn	0
			1	1	
2	D	1	Total	Zn	0
			1	1	

- Molecule 3 is D-MYO-INOSITOL-1,4,5-TRIPHOSPHATE (three-letter code: I3P) (formula: C₆H₁₅O₁₅P₃).

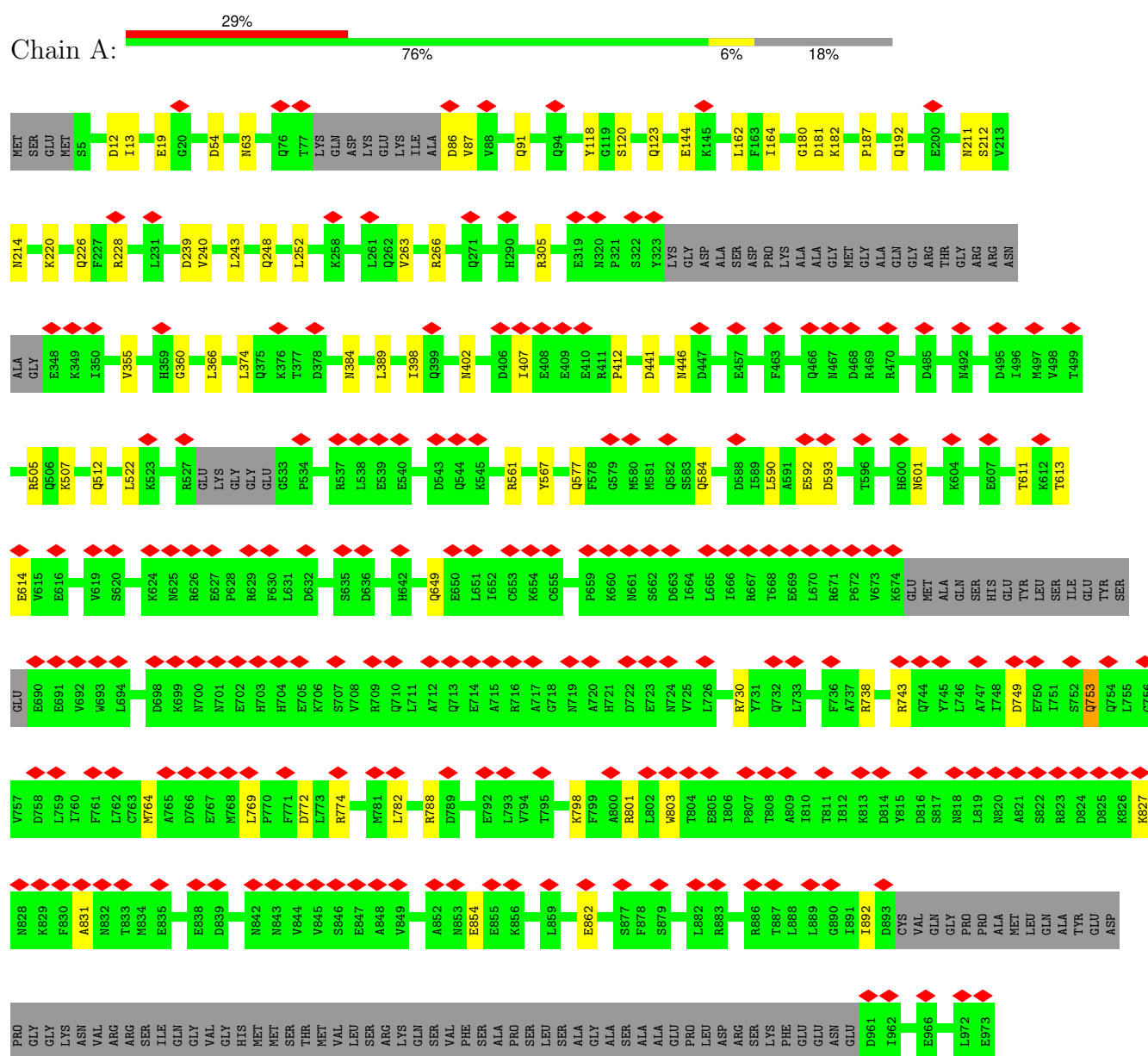


Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	H	O	P	0
			33	6	9	15	3	
3	B	1	Total	C	H	O	P	0
			33	6	9	15	3	
3	C	1	Total	C	H	O	P	0
			33	6	9	15	3	
3	D	1	Total	C	H	O	P	0
			33	6	9	15	3	

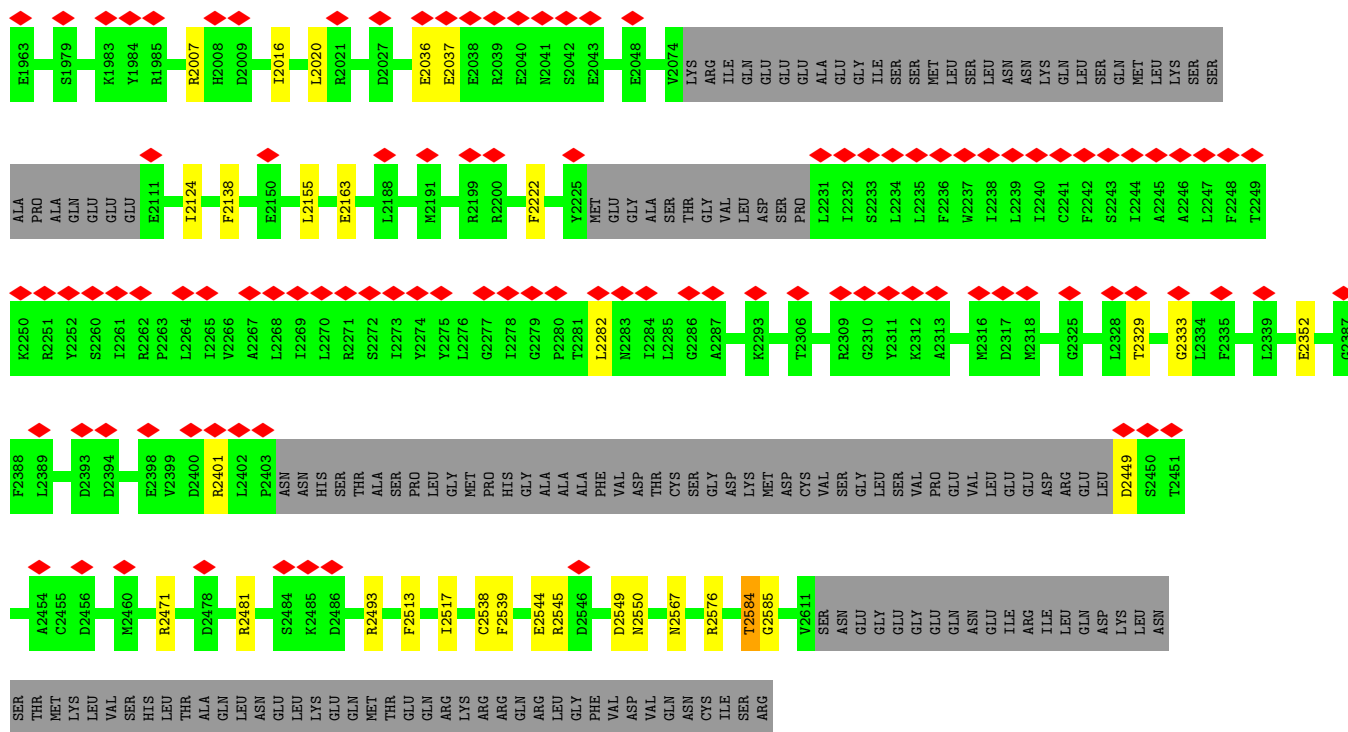
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

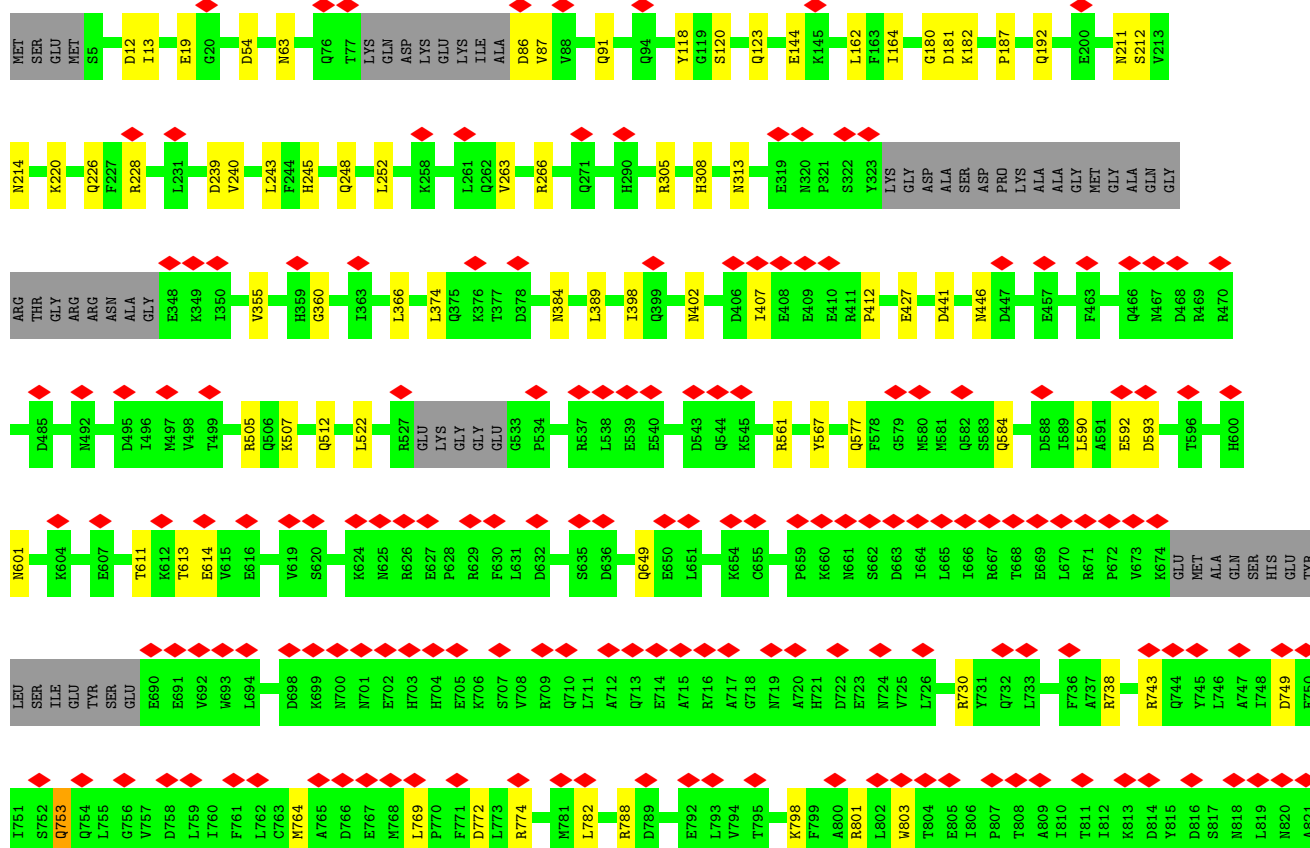
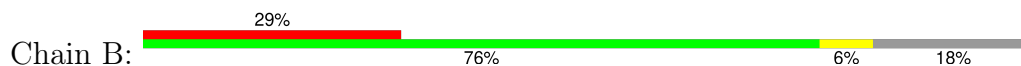
- Molecule 1: Inositol 1,4,5-trisphosphate receptor type 3





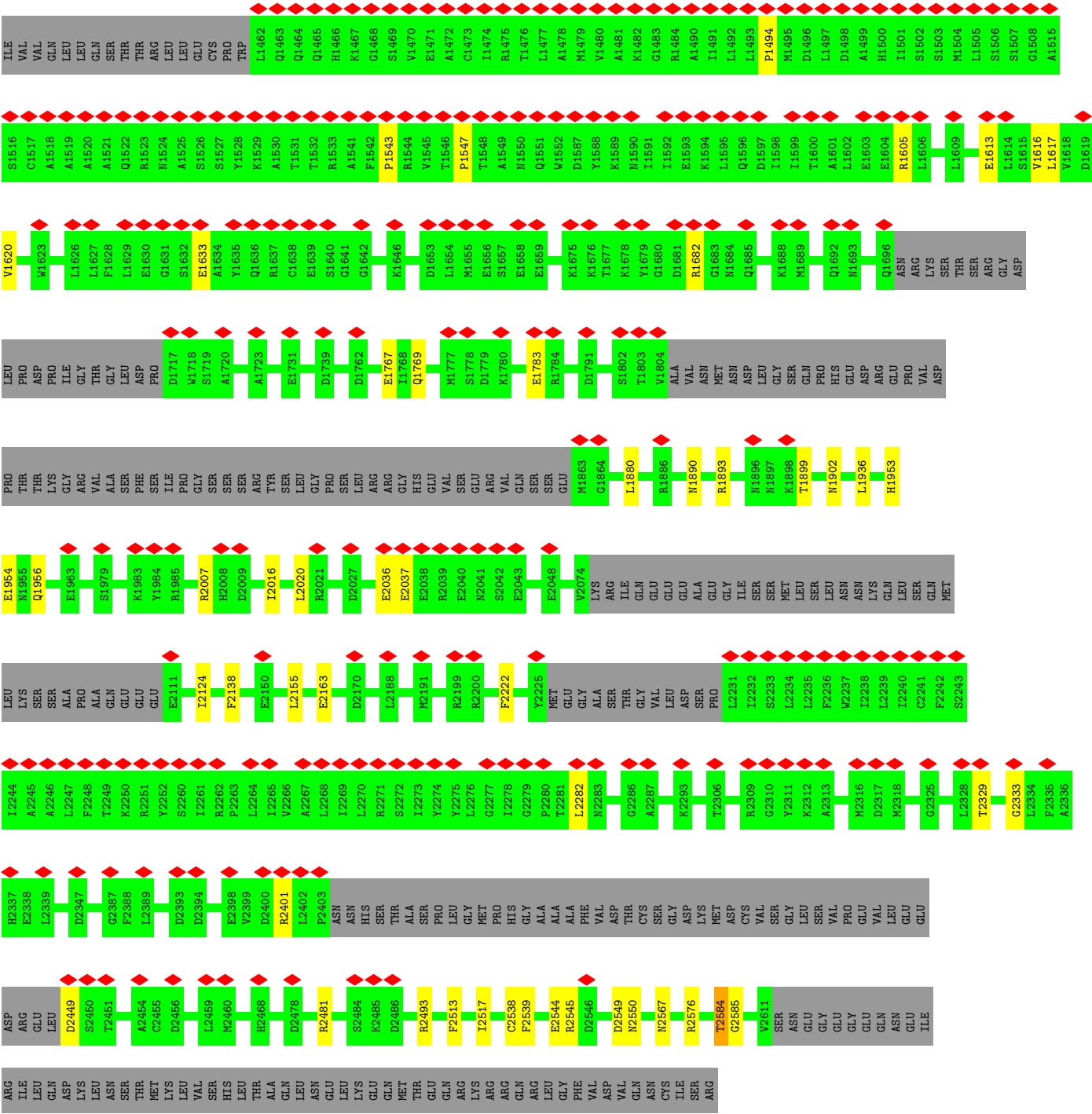


• Molecule 1: Inositol 1,4,5-trisphosphate receptor type 3

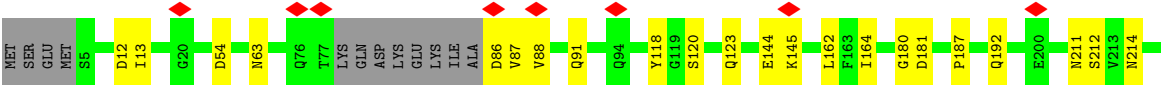
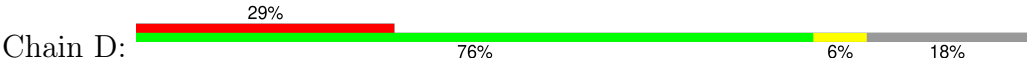


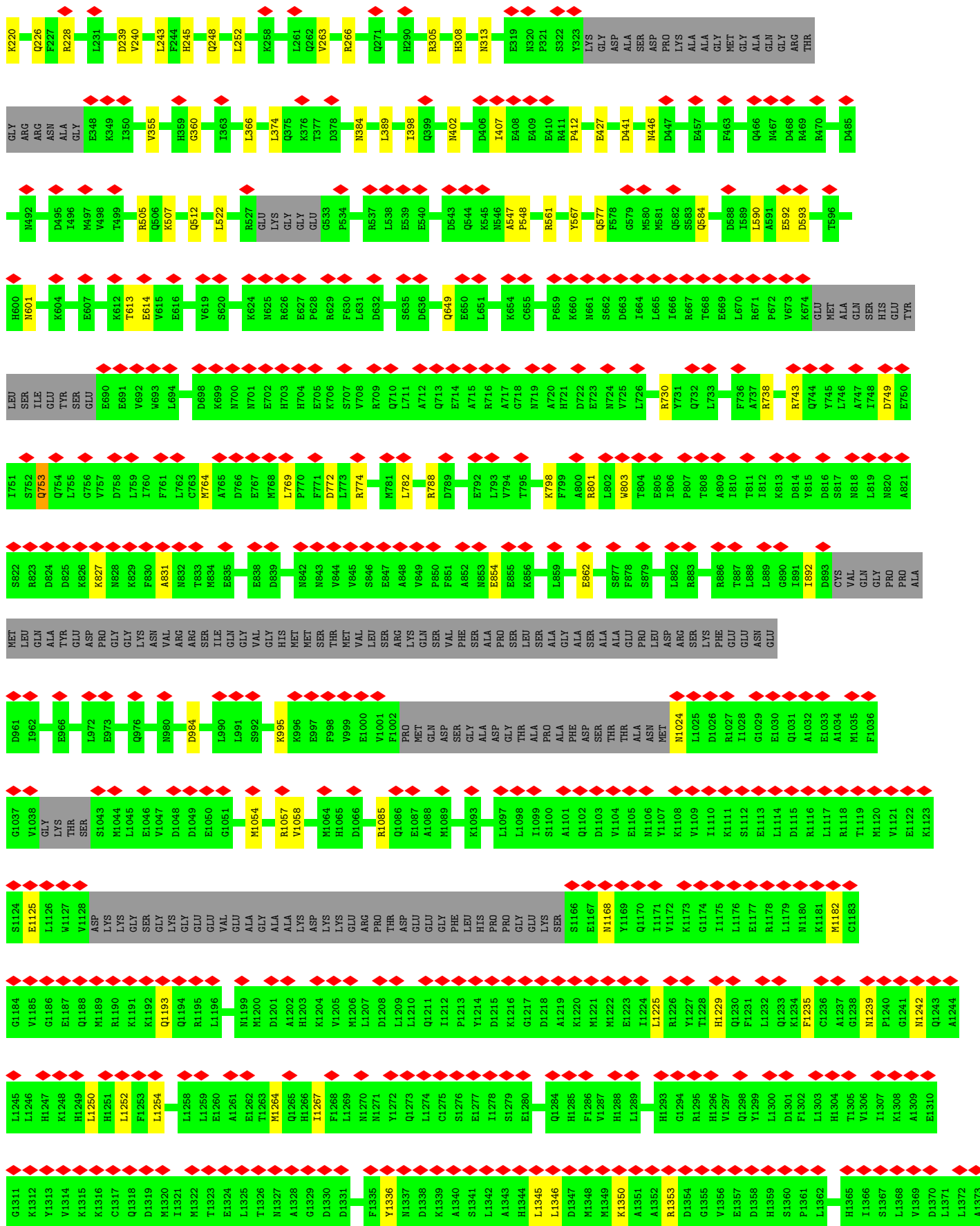
L1617	V1618	D1619	V1620	V1623	L1626	L1627	F1628	L1629	E1633	A1634	Y1635	Q1636	R1637	C1638	E1639	S1640	G1641	G1642	K1646	D1653	L1654	M1655	E1656	S1657	E1658	E1659	K1675	K1676	L1677	K1678	Y1679	G1680	D1681	R1682	G1683	M1684	Q1685	K1688	M1689	Q1692	M1693	Q1696	ASN	ARG	LYS	SER	THR	SER														
S1507	Q1508	A1515	S1516	C1517	A1518	A1519	A1520	A1521	Q1522	R1523	A1524	A1525	S1526	S1527	Y1528	K1529	A1530	T1531	T1532	R1533	A1541	F1542	P1543	R1544	V1545	T1546	P1547	T1548	A1549	N1550	Q1551	W1552	V1587	Y1588	K1589	N1590	I1591	I1592	E1593	K1594	L1595	Q1596	D1597	I1598	I1599	T1600	A1601	L1602	M1603	Q1606	R1605	L1606	L1609	E1613	L1614	S1615	V1616					
HIS	GLN	THR	ILE	VAL	VAL	GLN	LEU	LEU	GLN	SER	THR	THR	ARG	ASP	MET	ARG	VAL	CYS	PRO	TRP	L1462	Q1463	Q1464	Q1465	H1466	K1467	G1468	S1469	V1470	E1471	A1472	C1473	I1474	R1475	T1476	L1477	A1478	M1479	V1480	A1481	K1482	G1483	R1484	A1490	I1491	L1492	L1493	P1494	M1495	D1496	L1497	D1498	A1499	H1500	T1501	S1502	S1503	M1504	L1505	S1506		
SER	ASN	HIS	TRP	THR	LEU	PHE	GLU	ASN	PHE	THR	LEU	ASP	MET	ARG	CYS	SER	LYS	ARG	LYS	ARG	VAL	A1434	D1435	P1436	T1437	L1438	E1439	K1440	Y1441	V1442	L1443	S1444	V1445	V1446	L1447	D1448	T1449	I1450	N1451	A1452	F1453	F1454	SER	SER	PRO	PHE	SER	GLU	ASN	SER	THR	SER	LEU	GLN	THR	GLU	VAL	MET	LYS	GLU	ILE	THR
A1374	C1375	A1376	E1377	G1378	K1379	N1380	V1381	Y1382	T1383	D1384	E1385	T1386	K1387	T1388	S1389	L1390	L1391	P1392	L1393	E1394	D1395	V1396	V1397	S1398	V1399	V1400	T1401	H1402	E1403	D1404	C1405	I1406	T1407	E1408	V1409	K1410	M1411	A1412	Y1413	V1414	N1415	F1416	V1417	N1418	H1419	C1420	V1421	V1422	D1423	THR	GLU	VAL	GLU	MET	LYS	GLU	ILE	THR				
G1311	K1312	Y1313	V1314	K1315	K1316	C1317	Q1318	D1319	M1320	I1321	M1322	T1323	E1324	L1325	T1326	N1327	A1328	G1329	D1330	D1331	F1335	Y1336	N1337	D1338	K1339	A1340	S1341	L1342	A1343	H1344	L1345	L1346	D1347	M1348	M1349	K1350	A1351	A1352	R1353	D1354	G1355	V1356	E1357	D1358	K1359	S1360	P1361	L1362	H1365	I1366	S1367	L1368	V1369	D1370	L1371	L1372	A1373					
L1245	L1246	H1247	K1248	H1249	L1250	H1251	L1252	F1253	L1254	L1258	L1259	E1260	A1261	E1262	T1263	M1264	Q1265	H1266	I1267	F1268	N1270	N1271	Y1272	Q1273	L1274	C1275	S1276	E1277	L1278	S1279	E1280	Q1284	H1285	F1286	V1287	H1288	L1289	H1293	G1294	R1295	H1296	V1297	Q1298	L1299	L1300	D1301	F1302	L1303	H1304	T1305	V1306	I1307	K1308	A1309	E1310							
G1184	V1185	G1186	E1187	K1188	M1189	R1190	K1191	L1192	Q1193	Q1194	R1195	L1196	N1199	M1200	D1201	A1202	H1203	K1204	V1205	M1206	L1207	D1208	L1209	L1210	Q1211	I1212	P1213	Y1214	D1215	K1216	G1217	D1218	A1219	K1220	M1221	M1222	E1223	I1224	L1225	R1226	Y1227	T1228	H1229	Q1230	F1231	L1232	Q1233	K1234	F1235	G1236	A1237	G1238	N1239	P1240	G1241	N1242	Q1243	A1244				
S1124	E1125	L1126	W1127	V1128	ASP	LYS	LYS	GLY	SER	GLY	LYS	GLU	VAL	ALA	ALA	LYS	ASP	LYS	LYS	GLU	ARG	PRO	THR	ASP	GLU	Q1211	GLY	PHE	LEU	HIS	PRO	GLY	LYS	SER	S1166	E1167	N1168	Y1169	Q1170	I1171	K1173	G1174	I1175	L1176	E1177	R1178	L1179	N1180	K1181	M1182	C1183											
G1037	V1038	GLY	THR	SER	S1043	M1044	L1045	E1046	V1047	D1048	D1049	E1050	G1051	M1054	R1057	V1058	M1064	H1065	D1066	R1085	Q1086	E1087	A1088	H1089	K1093	L1097	L1098	I1099	S1100	A1101	Q1102	D1103	V1104	E1105	M1106	Y1107	K1108	V1109	I1110	K1111	S1112	E1113	L1114	D1115	R1116	L1117	R1118	T1119	M1120	V1121	E1122	K1123										
D961	I962	E966	L972	E973	Q976	N980	D984	L990	L991	S992	K996	E997	F998	V999	E1000	V1001	F1002	PRO	MET	GLN	ASP	SER	GLY	ALA	ASP	PRO	THR	ALA	PRO	ALA	PHE	ASP	SER	SER	THR	ALA	ASN	MET	N1024	L1025	D1026	R1027	I1028	G1029	E1030	Q1031	A1032	E1033	A1034	M1035	F1036											
S822	R823	D824	R825	K826	N828	K829	F830	A831	N832	T833	M834	E835	E838	D839	N842	N843	V844	V845	S846	E847	A848	V849	P850	F851	A852	N853	E854	E855	K856	L859	E862	S877	F878	S879	L882	R883	R886	T887	L888	L889	G890	I891	I892	D893	CYS	VAL	GLN	GLY	PRO	ALA												





● Molecule 1: Inositol 1,4,5-trisphosphate receptor type 3







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	38777	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	61	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	Not provided	
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	40.044	Depositor
Minimum map value	-27.584	Depositor
Average map value	-0.009	Depositor
Map value standard deviation	1.073	Depositor
Recommended contour level	5.13	Depositor
Map size (Å)	417.79202, 417.79202, 417.79202	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.088, 1.088, 1.088	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, I3P

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.25	0/17650	0.44	4/23851 (0.0%)
1	B	0.25	0/17650	0.44	4/23851 (0.0%)
1	C	0.25	0/17650	0.44	4/23851 (0.0%)
1	D	0.25	0/17650	0.44	4/23851 (0.0%)
All	All	0.25	0/70600	0.44	16/95404 (0.0%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1543	PRO	N-CA-CB	5.65	110.08	103.30
1	B	1543	PRO	N-CA-CB	5.65	110.08	103.30
1	C	1543	PRO	N-CA-CB	5.65	110.08	103.30
1	D	1543	PRO	N-CA-CB	5.65	110.08	103.30
1	A	1547	PRO	N-CA-CB	5.65	110.08	103.30
1	B	1547	PRO	N-CA-CB	5.62	110.04	103.30
1	C	1547	PRO	N-CA-CB	5.62	110.04	103.30
1	D	1547	PRO	N-CA-CB	5.61	110.03	103.30
1	A	1494	PRO	N-CA-CB	5.59	110.01	103.30
1	B	1494	PRO	N-CA-CB	5.58	110.00	103.30
1	C	1494	PRO	N-CA-CB	5.58	110.00	103.30
1	D	1494	PRO	N-CA-CB	5.58	110.00	103.30
1	B	1436	PRO	N-CA-CB	5.46	109.86	103.30
1	C	1436	PRO	N-CA-CB	5.46	109.86	103.30
1	D	1436	PRO	N-CA-CB	5.46	109.86	103.30
1	A	1436	PRO	N-CA-CB	5.43	109.82	103.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	17345	17349	17180	83	0
1	B	17345	17349	17180	84	0
1	C	17345	17349	17180	83	0
1	D	17345	17349	17180	86	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	24	9	9	2	0
3	B	24	9	9	2	0
3	C	24	9	9	2	0
3	D	24	9	9	2	0
All	All	69480	69432	68756	329	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (329) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1054:MET:SD	1:B:1057:ARG:NH2	2.65	0.70
1:D:1182:MET:O	1:D:1193:GLN:NE2	2.25	0.70
1:A:1054:MET:SD	1:A:1057:ARG:NH2	2.65	0.69
1:C:1054:MET:SD	1:C:1057:ARG:NH2	2.65	0.69
1:C:1182:MET:O	1:C:1193:GLN:NE2	2.25	0.69
1:D:803:TRP:O	1:D:995:LYS:NZ	2.25	0.69
1:B:803:TRP:O	1:B:995:LYS:NZ	2.25	0.69
1:B:2481:ARG:O	1:B:2493:ARG:NH2	2.26	0.69
1:C:798:LYS:O	1:C:801:ARG:NH1	2.26	0.69
1:D:2481:ARG:O	1:D:2493:ARG:NH2	2.26	0.69
1:B:144:GLU:OE2	1:B:211:ASN:ND2	2.26	0.69
1:B:1085:ARG:NH1	1:B:1613:GLU:OE2	2.26	0.69
1:A:798:LYS:O	1:A:801:ARG:NH1	2.26	0.69
1:C:2481:ARG:O	1:C:2493:ARG:NH2	2.26	0.69
1:A:144:GLU:OE2	1:A:211:ASN:ND2	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1182:MET:O	1:A:1193:GLN:NE2	2.25	0.68
1:A:2481:ARG:O	1:A:2493:ARG:NH2	2.25	0.68
1:B:1182:MET:O	1:B:1193:GLN:NE2	2.25	0.68
1:C:803:TRP:O	1:C:995:LYS:NZ	2.25	0.68
1:D:1054:MET:SD	1:D:1057:ARG:NH2	2.65	0.68
1:C:144:GLU:OE2	1:C:211:ASN:ND2	2.26	0.68
1:D:798:LYS:O	1:D:801:ARG:NH1	2.26	0.68
1:A:764:MET:O	1:A:774:ARG:NH1	2.27	0.68
1:C:1085:ARG:NH1	1:C:1613:GLU:OE2	2.26	0.68
1:A:803:TRP:O	1:A:995:LYS:NZ	2.25	0.68
1:A:1085:ARG:NH1	1:A:1613:GLU:OE2	2.26	0.68
1:B:798:LYS:O	1:B:801:ARG:NH1	2.26	0.68
1:D:144:GLU:OE2	1:D:211:ASN:ND2	2.26	0.68
1:D:1085:ARG:NH1	1:D:1613:GLU:OE2	2.26	0.68
1:A:2163:GLU:O	1:B:2545:ARG:NH1	2.27	0.67
1:C:764:MET:O	1:C:774:ARG:NH1	2.27	0.67
1:D:764:MET:O	1:D:774:ARG:NH1	2.27	0.67
1:B:764:MET:O	1:B:774:ARG:NH1	2.27	0.67
1:A:2401:ARG:NH2	1:A:2449:ASP:OD2	2.29	0.66
1:B:2401:ARG:NH2	1:B:2449:ASP:OD2	2.29	0.66
1:A:2545:ARG:NH1	1:D:2163:GLU:O	2.29	0.66
1:C:2163:GLU:O	1:D:2545:ARG:NH1	2.29	0.65
1:D:2401:ARG:NH2	1:D:2449:ASP:OD2	2.29	0.65
1:C:2401:ARG:NH2	1:C:2449:ASP:OD2	2.29	0.65
1:C:743:ARG:NH1	1:C:788:ARG:O	2.30	0.65
1:B:2163:GLU:O	1:C:2545:ARG:NH1	2.29	0.65
1:D:743:ARG:NH1	1:D:788:ARG:O	2.30	0.64
1:A:743:ARG:NH1	1:A:788:ARG:O	2.30	0.63
1:B:743:ARG:NH1	1:B:788:ARG:O	2.30	0.63
1:A:730:ARG:NH2	1:A:772:ASP:OD2	2.33	0.62
1:A:561:ARG:NH1	1:A:593:ASP:O	2.33	0.62
1:B:561:ARG:NH1	1:B:593:ASP:O	2.33	0.62
1:D:561:ARG:NH1	1:D:593:ASP:O	2.33	0.62
1:C:730:ARG:NH2	1:C:772:ASP:OD2	2.33	0.61
1:C:561:ARG:NH1	1:C:593:ASP:O	2.33	0.61
1:B:730:ARG:NH2	1:B:772:ASP:OD2	2.33	0.61
1:D:730:ARG:NH2	1:D:772:ASP:OD2	2.33	0.61
1:D:226:GLN:OE1	1:D:228:ARG:NH1	2.36	0.58
1:B:226:GLN:OE1	1:B:228:ARG:NH1	2.36	0.58
1:C:2329:THR:O	1:C:2333:GLY:N	2.37	0.58
1:A:226:GLN:OE1	1:A:228:ARG:NH1	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2329:THR:O	1:D:2333:GLY:N	2.37	0.58
1:C:226:GLN:OE1	1:C:228:ARG:NH1	2.36	0.58
1:A:2329:THR:O	1:A:2333:GLY:N	2.37	0.57
1:A:192:GLN:NE2	1:A:214:ASN:OD1	2.38	0.57
1:B:19:GLU:OE1	1:B:182:LYS:NZ	2.30	0.57
1:B:2329:THR:O	1:B:2333:GLY:N	2.37	0.57
1:C:192:GLN:NE2	1:C:214:ASN:OD1	2.38	0.57
1:C:192:GLN:O	1:C:212:SER:OG	2.23	0.56
1:D:192:GLN:NE2	1:D:214:ASN:OD1	2.38	0.56
1:D:1954:GLU:N	1:D:1954:GLU:OE1	2.38	0.56
1:B:892:ILE:HG21	1:B:1058:VAL:HG13	1.88	0.56
1:C:892:ILE:HG21	1:C:1058:VAL:HG13	1.88	0.56
1:D:192:GLN:O	1:D:212:SER:OG	2.23	0.56
1:D:649:GLN:NE2	1:D:738:ARG:O	2.38	0.56
1:A:1954:GLU:N	1:A:1954:GLU:OE1	2.38	0.56
1:C:649:GLN:NE2	1:C:738:ARG:O	2.38	0.56
1:B:192:GLN:NE2	1:B:214:ASN:OD1	2.38	0.56
1:A:649:GLN:NE2	1:A:738:ARG:O	2.38	0.56
1:B:1605:ARG:O	1:B:1682:ARG:NH2	2.39	0.56
1:A:118:TYR:OH	1:A:181:ASP:OD2	2.24	0.56
1:A:892:ILE:HG21	1:A:1058:VAL:HG13	1.88	0.56
1:B:1954:GLU:N	1:B:1954:GLU:OE1	2.39	0.56
1:D:892:ILE:HG21	1:D:1058:VAL:HG13	1.88	0.55
1:A:1605:ARG:O	1:A:1682:ARG:NH2	2.39	0.55
1:C:1605:ARG:O	1:C:1682:ARG:NH2	2.39	0.55
1:A:192:GLN:O	1:A:212:SER:OG	2.23	0.55
1:C:118:TYR:OH	1:C:181:ASP:OD2	2.24	0.55
1:C:1954:GLU:OE1	1:C:1954:GLU:N	2.39	0.55
1:B:118:TYR:OH	1:B:181:ASP:OD2	2.24	0.55
1:D:1605:ARG:O	1:D:1682:ARG:NH2	2.39	0.55
1:B:192:GLN:O	1:B:212:SER:OG	2.23	0.55
1:B:649:GLN:NE2	1:B:738:ARG:O	2.38	0.54
1:A:446:ASN:ND2	1:A:512:GLN:OE1	2.40	0.54
1:D:118:TYR:OH	1:D:181:ASP:OD2	2.24	0.54
1:D:446:ASN:ND2	1:D:512:GLN:OE1	2.40	0.54
1:C:446:ASN:ND2	1:C:512:GLN:OE1	2.40	0.54
1:A:614:GLU:N	1:A:614:GLU:OE1	2.41	0.54
1:B:446:ASN:ND2	1:B:512:GLN:OE1	2.40	0.54
1:D:614:GLU:OE1	1:D:614:GLU:N	2.41	0.53
1:A:1350:LYS:O	1:A:1353:ARG:NH1	2.42	0.53
1:C:407:ILE:HG22	1:C:412:PRO:HG3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1350:LYS:O	1:C:1353:ARG:NH1	2.42	0.53
1:D:1350:LYS:O	1:D:1353:ARG:NH1	2.42	0.53
1:B:266:ARG:NH2	3:B:3002:I3P:O42	2.42	0.53
1:A:407:ILE:HG22	1:A:412:PRO:HG3	1.90	0.53
1:B:1350:LYS:O	1:B:1353:ARG:NH1	2.42	0.53
1:C:801:ARG:NH2	1:C:984:ASP:OD1	2.42	0.52
1:D:266:ARG:NH2	3:D:3002:I3P:O42	2.42	0.52
1:A:266:ARG:NH2	3:A:3002:I3P:O42	2.42	0.52
1:C:614:GLU:N	1:C:614:GLU:OE1	2.41	0.52
1:A:801:ARG:NH2	1:A:984:ASP:OD1	2.42	0.52
1:B:407:ILE:HG22	1:B:412:PRO:HG3	1.90	0.52
1:D:801:ARG:NH2	1:D:984:ASP:OD1	2.42	0.52
1:D:407:ILE:HG22	1:D:412:PRO:HG3	1.90	0.52
1:B:801:ARG:NH2	1:B:984:ASP:OD1	2.42	0.52
1:C:266:ARG:NH2	3:C:3002:I3P:O42	2.42	0.52
1:B:86:ASP:OD1	1:B:87:VAL:N	2.44	0.51
1:D:1235:PHE:O	1:D:1242:ASN:ND2	2.43	0.51
1:B:577:GLN:N	1:B:577:GLN:OE1	2.44	0.51
1:C:86:ASP:OD1	1:C:87:VAL:N	2.44	0.51
1:D:86:ASP:OD1	1:D:87:VAL:N	2.44	0.51
1:A:86:ASP:OD1	1:A:87:VAL:N	2.44	0.51
1:A:577:GLN:N	1:A:577:GLN:OE1	2.44	0.51
1:B:614:GLU:OE1	1:B:614:GLU:N	2.41	0.51
1:D:577:GLN:OE1	1:D:577:GLN:N	2.44	0.51
1:D:1125:GLU:N	1:D:1125:GLU:OE1	2.44	0.51
1:C:180:GLY:O	1:C:220:LYS:NZ	2.44	0.51
1:C:577:GLN:N	1:C:577:GLN:OE1	2.44	0.51
1:A:180:GLY:O	1:A:220:LYS:NZ	2.44	0.50
1:A:441:ASP:OD2	1:A:505:ARG:NE	2.45	0.50
1:A:1235:PHE:O	1:A:1242:ASN:ND2	2.43	0.50
1:B:180:GLY:O	1:B:220:LYS:NZ	2.44	0.50
1:A:1125:GLU:N	1:A:1125:GLU:OE1	2.44	0.50
1:B:1125:GLU:N	1:B:1125:GLU:OE1	2.44	0.50
1:C:441:ASP:OD2	1:C:505:ARG:NE	2.45	0.50
1:C:592:GLU:OE1	1:C:592:GLU:N	2.45	0.50
1:C:1125:GLU:OE1	1:C:1125:GLU:N	2.44	0.50
1:C:1235:PHE:O	1:C:1242:ASN:ND2	2.43	0.50
1:D:441:ASP:OD2	1:D:505:ARG:NE	2.45	0.50
1:C:2155:LEU:HD13	1:C:2155:LEU:O	2.12	0.49
1:B:592:GLU:N	1:B:592:GLU:OE1	2.45	0.49
1:B:2155:LEU:HD13	1:B:2155:LEU:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:180:GLY:O	1:D:220:LYS:NZ	2.44	0.49
1:B:441:ASP:OD2	1:B:505:ARG:NE	2.45	0.49
1:A:613:THR:OG1	1:A:614:GLU:OE1	2.31	0.49
1:A:1767:GLU:N	1:A:1767:GLU:OE1	2.46	0.49
1:A:2155:LEU:HD13	1:A:2155:LEU:O	2.12	0.49
1:D:2155:LEU:O	1:D:2155:LEU:HD13	2.12	0.49
1:D:613:THR:OG1	1:D:614:GLU:OE1	2.31	0.49
1:A:248:GLN:NE2	1:A:402:ASN:OD1	2.46	0.49
1:C:248:GLN:NE2	1:C:402:ASN:OD1	2.46	0.49
1:C:2538:CYS:SG	1:C:2539:PHE:N	2.86	0.49
1:D:592:GLU:N	1:D:592:GLU:OE1	2.45	0.49
1:B:248:GLN:NE2	1:B:402:ASN:OD1	2.46	0.49
1:B:1235:PHE:O	1:B:1242:ASN:ND2	2.43	0.49
1:D:12:ASP:OD1	1:D:13:ILE:N	2.46	0.49
1:D:2036:GLU:OE1	1:D:2036:GLU:N	2.46	0.48
1:B:2538:CYS:SG	1:B:2539:PHE:N	2.86	0.48
1:C:1767:GLU:N	1:C:1767:GLU:OE1	2.46	0.48
1:C:2544:GLU:OE1	1:C:2544:GLU:N	2.47	0.48
1:D:2538:CYS:SG	1:D:2539:PHE:N	2.86	0.48
1:A:854:GLU:N	1:A:854:GLU:OE1	2.46	0.48
1:A:2538:CYS:SG	1:A:2539:PHE:N	2.86	0.48
1:C:854:GLU:OE1	1:C:854:GLU:N	2.46	0.48
1:B:613:THR:OG1	1:B:614:GLU:OE1	2.31	0.48
1:A:1394:GLU:OE1	1:A:1394:GLU:N	2.47	0.48
1:A:2513:PHE:CE2	1:A:2517:ILE:HD11	2.49	0.48
1:C:613:THR:OG1	1:C:614:GLU:OE1	2.31	0.48
1:D:248:GLN:NE2	1:D:402:ASN:OD1	2.46	0.48
1:B:1767:GLU:N	1:B:1767:GLU:OE1	2.46	0.48
1:D:1767:GLU:OE1	1:D:1767:GLU:N	2.46	0.48
1:A:12:ASP:OD1	1:A:13:ILE:N	2.46	0.48
1:A:2037:GLU:N	1:A:2037:GLU:OE1	2.46	0.48
1:C:2036:GLU:OE1	1:C:2036:GLU:N	2.46	0.48
1:D:120:SER:O	1:D:164:ILE:HG22	2.14	0.48
1:A:592:GLU:N	1:A:592:GLU:OE1	2.45	0.48
1:B:12:ASP:OD1	1:B:13:ILE:N	2.46	0.48
1:B:2513:PHE:CE2	1:B:2517:ILE:HD11	2.49	0.48
1:C:2513:PHE:CE2	1:C:2517:ILE:HD11	2.49	0.48
1:C:12:ASP:OD1	1:C:13:ILE:N	2.46	0.47
1:D:854:GLU:N	1:D:854:GLU:OE1	2.46	0.47
1:C:120:SER:O	1:C:164:ILE:HG22	2.14	0.47
1:D:389:LEU:HD12	1:D:398:ILE:HD12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:854:GLU:N	1:B:854:GLU:OE1	2.46	0.47
1:B:1394:GLU:N	1:B:1394:GLU:OE1	2.47	0.47
1:B:2037:GLU:OE1	1:B:2037:GLU:N	2.46	0.47
1:A:2036:GLU:OE1	1:A:2036:GLU:N	2.46	0.47
1:C:2037:GLU:OE1	1:C:2037:GLU:N	2.46	0.47
1:D:1956:GLN:OE1	1:D:2007:ARG:NE	2.47	0.47
1:A:120:SER:O	1:A:164:ILE:HG22	2.14	0.47
1:A:389:LEU:HD12	1:A:398:ILE:HD12	1.96	0.47
1:C:1394:GLU:N	1:C:1394:GLU:OE1	2.47	0.47
1:D:2513:PHE:CE2	1:D:2517:ILE:HD11	2.49	0.47
1:B:2544:GLU:OE1	1:B:2544:GLU:N	2.47	0.47
1:A:827:LYS:O	1:A:831:ALA:N	2.48	0.47
1:B:1953:HIS:O	1:B:2007:ARG:NH2	2.48	0.47
1:C:389:LEU:HD12	1:C:398:ILE:HD12	1.96	0.47
1:C:862:GLU:OE1	1:C:862:GLU:N	2.48	0.47
1:C:1953:HIS:O	1:C:2007:ARG:NH2	2.48	0.47
1:D:2037:GLU:OE1	1:D:2037:GLU:N	2.46	0.47
1:A:862:GLU:N	1:A:862:GLU:OE1	2.48	0.46
1:A:1239:ASN:OD1	1:A:1242:ASN:N	2.46	0.46
1:C:827:LYS:O	1:C:831:ALA:N	2.48	0.46
1:D:1769:GLN:NE2	1:D:1880:LEU:O	2.49	0.46
1:A:1617:LEU:O	1:A:1617:LEU:HD23	2.16	0.46
1:A:1953:HIS:O	1:A:2007:ARG:NH2	2.48	0.46
1:B:120:SER:O	1:B:164:ILE:HG22	2.14	0.46
1:B:1617:LEU:HD23	1:B:1617:LEU:O	2.16	0.46
1:C:1956:GLN:OE1	1:C:2007:ARG:NE	2.47	0.46
1:A:1633:GLU:OE1	1:A:1633:GLU:N	2.48	0.46
1:B:862:GLU:N	1:B:862:GLU:OE1	2.48	0.46
1:C:1769:GLN:NE2	1:C:1880:LEU:O	2.49	0.46
1:D:522:LEU:O	1:D:584:GLN:NE2	2.46	0.46
1:D:1394:GLU:OE1	1:D:1394:GLU:N	2.47	0.46
1:B:239:ASP:OD1	1:B:240:VAL:N	2.49	0.46
1:B:2124:ILE:HD12	1:B:2138:PHE:HE1	1.81	0.46
1:C:2124:ILE:HD12	1:C:2138:PHE:HE1	1.81	0.46
1:D:1633:GLU:OE1	1:D:1633:GLU:N	2.48	0.46
1:D:384:ASN:ND2	1:D:384:ASN:O	2.49	0.46
1:A:239:ASP:OD1	1:A:240:VAL:N	2.49	0.46
1:A:2124:ILE:HD12	1:A:2138:PHE:HE1	1.81	0.46
1:B:827:LYS:O	1:B:831:ALA:N	2.48	0.46
1:C:239:ASP:OD1	1:C:240:VAL:N	2.49	0.46
1:D:1953:HIS:O	1:D:2007:ARG:NH2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1769:GLN:NE2	1:B:1880:LEU:O	2.49	0.46
1:D:862:GLU:N	1:D:862:GLU:OE1	2.48	0.46
1:C:1617:LEU:O	1:C:1617:LEU:HD23	2.16	0.46
1:B:389:LEU:HD12	1:B:398:ILE:HD12	1.96	0.46
1:C:749:ASP:O	1:C:753:GLN:NE2	2.49	0.46
1:C:1633:GLU:N	1:C:1633:GLU:OE1	2.48	0.46
1:D:827:LYS:O	1:D:831:ALA:N	2.48	0.46
1:A:1769:GLN:NE2	1:A:1880:LEU:O	2.49	0.45
1:B:384:ASN:ND2	1:B:384:ASN:O	2.49	0.45
1:B:522:LEU:O	1:B:584:GLN:NE2	2.46	0.45
1:C:522:LEU:O	1:C:584:GLN:NE2	2.46	0.45
1:D:2124:ILE:HD12	1:D:2138:PHE:HE1	1.81	0.45
1:D:239:ASP:OD1	1:D:240:VAL:N	2.49	0.45
1:A:384:ASN:O	1:A:384:ASN:ND2	2.49	0.45
1:A:1616:VAL:O	1:A:1620:VAL:HG23	2.17	0.45
1:D:1239:ASN:OD1	1:D:1242:ASN:N	2.46	0.45
1:C:1616:VAL:O	1:C:1620:VAL:HG23	2.17	0.45
1:D:749:ASP:O	1:D:753:GLN:NE2	2.49	0.45
1:B:749:ASP:O	1:B:753:GLN:NE2	2.49	0.45
1:D:1616:VAL:O	1:D:1620:VAL:HG23	2.17	0.45
1:A:749:ASP:O	1:A:753:GLN:NE2	2.49	0.45
1:D:1617:LEU:HD23	1:D:1617:LEU:O	2.16	0.45
1:B:1616:VAL:O	1:B:1620:VAL:HG23	2.17	0.44
1:B:1633:GLU:N	1:B:1633:GLU:OE1	2.48	0.44
1:C:384:ASN:O	1:C:384:ASN:ND2	2.49	0.44
1:C:1239:ASN:OD1	1:C:1242:ASN:N	2.46	0.44
1:D:2544:GLU:N	1:D:2544:GLU:OE1	2.47	0.44
1:B:1239:ASN:OD1	1:B:1242:ASN:N	2.46	0.44
1:B:2549:ASP:OD1	1:B:2550:ASN:N	2.50	0.44
1:D:2549:ASP:OD1	1:D:2550:ASN:N	2.50	0.44
1:B:2016:ILE:HG22	1:B:2020:LEU:HD12	1.99	0.44
1:B:2036:GLU:OE1	1:B:2036:GLU:N	2.46	0.44
1:C:2016:ILE:HG22	1:C:2020:LEU:HD12	1.99	0.44
1:A:2544:GLU:OE1	1:A:2544:GLU:N	2.47	0.44
1:A:2352:GLU:OE2	1:D:2367:ARG:NE	2.47	0.43
1:A:252:LEU:HD11	1:A:263:VAL:HG22	2.00	0.43
1:B:611:THR:OG1	1:B:614:GLU:OE1	2.35	0.43
1:A:19:GLU:OE1	1:A:182:LYS:NZ	2.30	0.43
1:C:1783:GLU:OE1	1:C:1899:THR:OG1	2.37	0.43
1:D:1783:GLU:OE1	1:D:1899:THR:OG1	2.37	0.43
1:B:305:ARG:NH2	1:B:360:GLY:O	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2016:ILE:HG22	1:D:2020:LEU:HD12	1.99	0.43
1:A:305:ARG:NH2	1:A:360:GLY:O	2.52	0.43
1:D:243:LEU:HD12	1:D:252:LEU:HD23	2.00	0.43
1:D:252:LEU:HD11	1:D:263:VAL:HG22	2.00	0.43
1:A:1956:GLN:OE1	1:A:2007:ARG:NE	2.47	0.43
1:B:162:LEU:HD23	1:B:187:PRO:HA	2.00	0.43
1:C:243:LEU:HD12	1:C:252:LEU:HD23	2.00	0.43
1:C:1890:ASN:OD1	1:C:1893:ARG:NH2	2.51	0.43
1:D:1890:ASN:OD1	1:D:1893:ARG:NH2	2.51	0.43
1:A:2584:THR:HG22	1:A:2585:GLY:H	1.84	0.43
1:B:2584:THR:HG22	1:B:2585:GLY:H	1.84	0.43
1:D:245:HIS:NE2	1:D:427:GLU:OE1	2.50	0.43
1:A:2016:ILE:HG22	1:A:2020:LEU:HD12	1.99	0.43
1:B:1783:GLU:OE1	1:B:1899:THR:OG1	2.37	0.43
1:C:2584:THR:HG22	1:C:2585:GLY:H	1.84	0.43
1:D:305:ARG:NH2	1:D:360:GLY:O	2.51	0.43
1:B:1103:ASP:O	1:B:1107:TYR:N	2.51	0.42
1:C:305:ARG:NH2	1:C:360:GLY:O	2.51	0.42
1:A:522:LEU:O	1:A:584:GLN:NE2	2.46	0.42
1:A:1783:GLU:OE1	1:A:1899:THR:OG1	2.37	0.42
1:B:243:LEU:HD12	1:B:252:LEU:HD23	2.00	0.42
1:C:611:THR:OG1	1:C:614:GLU:OE1	2.35	0.42
1:D:507:LYS:NZ	3:D:3002:I3P:O53	2.49	0.42
1:D:1264:MET:HA	1:D:1267:ILE:HD12	2.01	0.42
1:B:252:LEU:HD11	1:B:263:VAL:HG22	2.00	0.42
1:B:2124:ILE:HD11	1:B:2567:ASN:O	2.20	0.42
1:C:162:LEU:HD23	1:C:187:PRO:HA	2.00	0.42
1:D:162:LEU:HD23	1:D:187:PRO:HA	2.00	0.42
1:D:2124:ILE:HD11	1:D:2567:ASN:O	2.20	0.42
1:A:1890:ASN:OD1	1:A:1893:ARG:NH2	2.51	0.42
1:A:2124:ILE:HD11	1:A:2567:ASN:O	2.20	0.42
1:B:507:LYS:NZ	3:B:3002:I3P:O53	2.49	0.42
1:C:308:HIS:N	1:C:313:ASN:O	2.49	0.42
1:C:2124:ILE:HD11	1:C:2567:ASN:O	2.20	0.42
1:A:63:ASN:N	1:A:123:GLN:OE1	2.52	0.42
1:A:162:LEU:HD23	1:A:187:PRO:HA	2.00	0.42
1:B:1890:ASN:OD1	1:B:1893:ARG:NH2	2.51	0.42
1:C:63:ASN:N	1:C:123:GLN:OE1	2.52	0.42
1:D:2584:THR:HG22	1:D:2585:GLY:H	1.84	0.42
1:B:245:HIS:NE2	1:B:427:GLU:OE1	2.50	0.42
1:C:252:LEU:HD11	1:C:263:VAL:HG22	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:243:LEU:HD12	1:A:252:LEU:HD23	2.00	0.42
1:B:63:ASN:N	1:B:123:GLN:OE1	2.52	0.42
1:A:2471:ARG:NH2	1:D:2478:ASP:OD1	2.49	0.42
1:A:1264:MET:HA	1:A:1267:ILE:HD12	2.01	0.41
1:D:63:ASN:N	1:D:123:GLN:OE1	2.52	0.41
1:A:1336:TYR:HB2	1:A:1345:LEU:HD22	2.02	0.41
1:C:1336:TYR:HB2	1:C:1345:LEU:HD22	2.02	0.41
1:A:2549:ASP:OD1	1:A:2550:ASN:N	2.50	0.41
1:B:2319:GLU:O	1:B:2323:HIS:ND1	2.52	0.41
1:C:507:LYS:NZ	3:C:3002:I3P:O53	2.49	0.41
1:D:1336:TYR:HB2	1:D:1345:LEU:HD22	2.02	0.41
1:B:1264:MET:HA	1:B:1267:ILE:HD12	2.01	0.41
1:B:1336:TYR:HB2	1:B:1345:LEU:HD22	2.02	0.41
1:C:2549:ASP:OD1	1:C:2550:ASN:N	2.50	0.41
1:A:611:THR:OG1	1:A:614:GLU:OE1	2.35	0.41
1:A:1331:ASP:OD2	1:D:145:LYS:NZ	2.36	0.41
1:D:308:HIS:N	1:D:313:ASN:O	2.49	0.41
1:A:507:LYS:NZ	3:A:3002:I3P:O53	2.49	0.41
1:B:308:HIS:N	1:B:313:ASN:O	2.49	0.41
1:B:1956:GLN:OE1	1:B:2007:ARG:NE	2.47	0.41
1:C:547:ALA:HB3	1:C:548:PRO:HD3	2.04	0.40
1:C:815:TYR:OH	1:C:984:ASP:OD2	2.39	0.40
1:C:1264:MET:HA	1:C:1267:ILE:HD12	2.01	0.40
1:D:547:ALA:HB3	1:D:548:PRO:HD3	2.04	0.40
1:C:1103:ASP:O	1:C:1107:TYR:N	2.51	0.40
1:D:86:ASP:OD1	1:D:88:VAL:N	2.53	0.40
1:D:1225:LEU:O	1:D:1229:HIS:ND1	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	2144/2671 (80%)	2070 (96%)	74 (4%)	0	100	100
1	B	2144/2671 (80%)	2070 (96%)	74 (4%)	0	100	100
1	C	2144/2671 (80%)	2070 (96%)	74 (4%)	0	100	100
1	D	2144/2671 (80%)	2070 (96%)	74 (4%)	0	100	100
All	All	8576/10684 (80%)	8280 (96%)	296 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1879/2385 (79%)	1856 (99%)	23 (1%)	67	80
1	B	1879/2385 (79%)	1856 (99%)	23 (1%)	67	80
1	C	1879/2385 (79%)	1856 (99%)	23 (1%)	67	80
1	D	1879/2385 (79%)	1856 (99%)	23 (1%)	67	80
All	All	7516/9540 (79%)	7424 (99%)	92 (1%)	66	80

All (92) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	ASP
1	A	91	GLN
1	A	355	VAL
1	A	366	LEU
1	A	374	LEU
1	A	567	TYR
1	A	590	LEU
1	A	601	ASN
1	A	753	GLN
1	A	769	LEU
1	A	782	LEU
1	A	1024	ASN
1	A	1168	ASN

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Mol	Chain	Res	Type
1	A	1250	LEU
1	A	1252	LEU
1	A	1254	LEU
1	A	1346	LEU
1	A	1902	ASN
1	A	1936	LEU
1	A	2222	PHE
1	A	2282	LEU
1	A	2576	ARG
1	A	2584	THR
1	B	54	ASP
1	B	91	GLN
1	B	355	VAL
1	B	366	LEU
1	B	374	LEU
1	B	567	TYR
1	B	590	LEU
1	B	601	ASN
1	B	753	GLN
1	B	769	LEU
1	B	782	LEU
1	B	1024	ASN
1	B	1168	ASN
1	B	1250	LEU
1	B	1252	LEU
1	B	1254	LEU
1	B	1346	LEU
1	B	1902	ASN
1	B	1936	LEU
1	B	2222	PHE
1	B	2282	LEU
1	B	2576	ARG
1	B	2584	THR
1	C	54	ASP
1	C	91	GLN
1	C	355	VAL
1	C	366	LEU
1	C	374	LEU
1	C	567	TYR
1	C	590	LEU
1	C	601	ASN
1	C	753	GLN

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Mol	Chain	Res	Type
1	C	769	LEU
1	C	782	LEU
1	C	1024	ASN
1	C	1168	ASN
1	C	1250	LEU
1	C	1252	LEU
1	C	1254	LEU
1	C	1346	LEU
1	C	1902	ASN
1	C	1936	LEU
1	C	2222	PHE
1	C	2282	LEU
1	C	2576	ARG
1	C	2584	THR
1	D	54	ASP
1	D	91	GLN
1	D	355	VAL
1	D	366	LEU
1	D	374	LEU
1	D	567	TYR
1	D	590	LEU
1	D	601	ASN
1	D	753	GLN
1	D	769	LEU
1	D	782	LEU
1	D	1024	ASN
1	D	1168	ASN
1	D	1250	LEU
1	D	1252	LEU
1	D	1254	LEU
1	D	1346	LEU
1	D	1902	ASN
1	D	1936	LEU
1	D	2222	PHE
1	D	2282	LEU
1	D	2576	ARG
1	D	2584	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	I3P	B	3002	-	24,24,24	1.34	3 (12%)	39,39,39	0.84	1 (2%)
3	I3P	A	3002	-	24,24,24	1.33	3 (12%)	39,39,39	0.84	1 (2%)
3	I3P	C	3002	-	24,24,24	1.34	3 (12%)	39,39,39	0.84	1 (2%)
3	I3P	D	3002	-	24,24,24	1.34	3 (12%)	39,39,39	0.84	1 (2%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	I3P	B	3002	-	-	2/15/39/39	0/1/1/1
3	I3P	A	3002	-	-	2/15/39/39	0/1/1/1
3	I3P	C	3002	-	-	2/15/39/39	0/1/1/1
3	I3P	D	3002	-	-	2/15/39/39	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	3002	I3P	P4-O4	3.28	1.65	1.59
3	B	3002	I3P	P4-O4	3.25	1.65	1.59
3	C	3002	I3P	P4-O4	3.25	1.65	1.59
3	D	3002	I3P	P4-O4	3.25	1.65	1.59
3	B	3002	I3P	P1-O1	3.24	1.65	1.59
3	C	3002	I3P	P1-O1	3.24	1.65	1.59
3	D	3002	I3P	P1-O1	3.24	1.65	1.59
3	B	3002	I3P	P5-O5	3.22	1.65	1.59
3	C	3002	I3P	P5-O5	3.22	1.65	1.59
3	D	3002	I3P	P5-O5	3.22	1.65	1.59
3	A	3002	I3P	P1-O1	3.21	1.65	1.59
3	A	3002	I3P	P5-O5	3.18	1.65	1.59

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	3002	I3P	C5-C6-C1	2.28	113.72	109.11
3	C	3002	I3P	C5-C6-C1	2.28	113.72	109.11
3	A	3002	I3P	C5-C6-C1	2.27	113.70	109.11
3	D	3002	I3P	C5-C6-C1	2.25	113.67	109.11

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	3002	I3P	C5-O5-P5-O51
3	B	3002	I3P	C5-O5-P5-O51
3	C	3002	I3P	C5-O5-P5-O51
3	D	3002	I3P	C5-O5-P5-O51
3	A	3002	I3P	C4-O4-P4-O43
3	B	3002	I3P	C4-O4-P4-O43
3	C	3002	I3P	C4-O4-P4-O43
3	D	3002	I3P	C4-O4-P4-O43

There are no ring outliers.

4 monomers are involved in 8 short contacts:

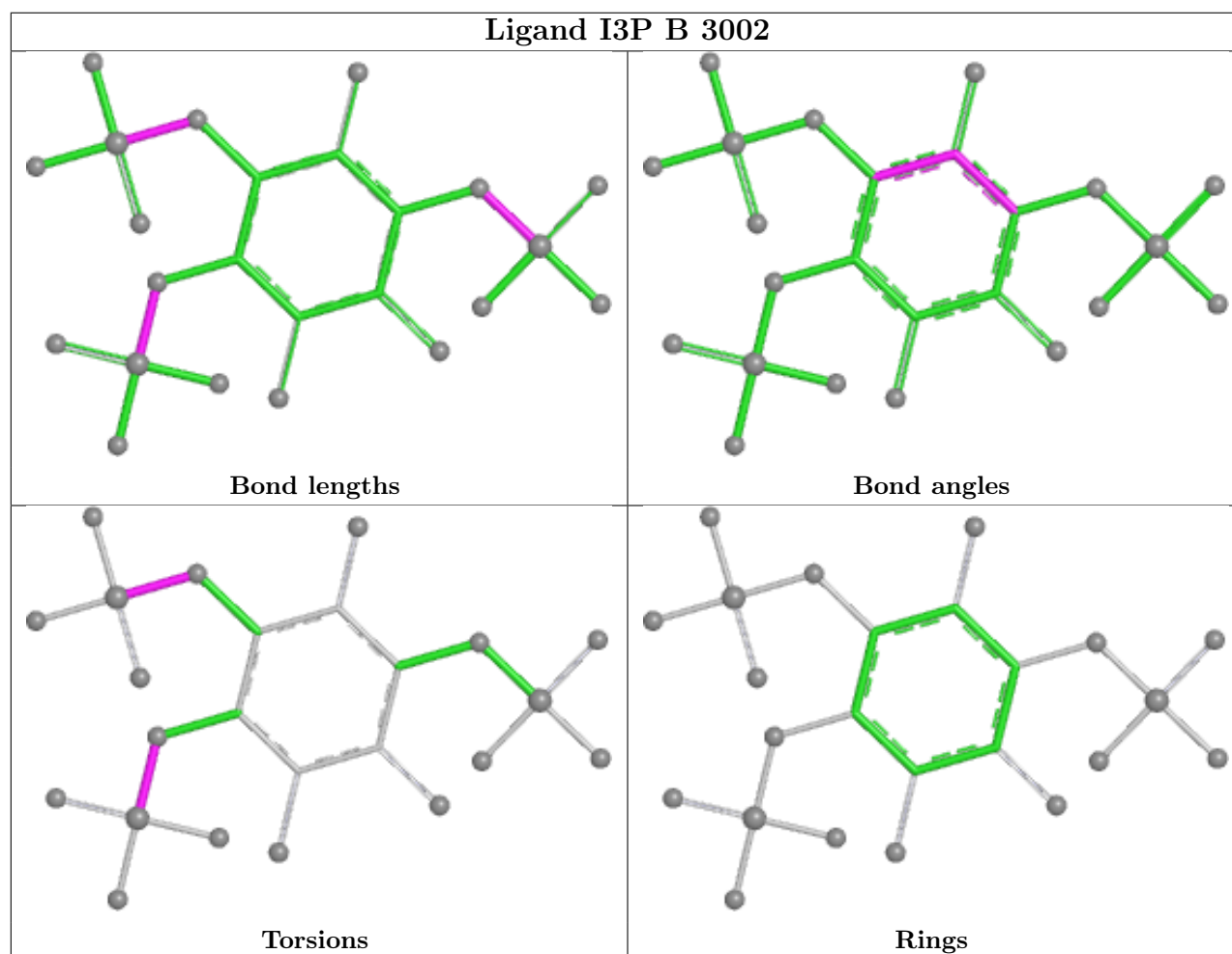
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	3002	I3P	2	0
3	A	3002	I3P	2	0

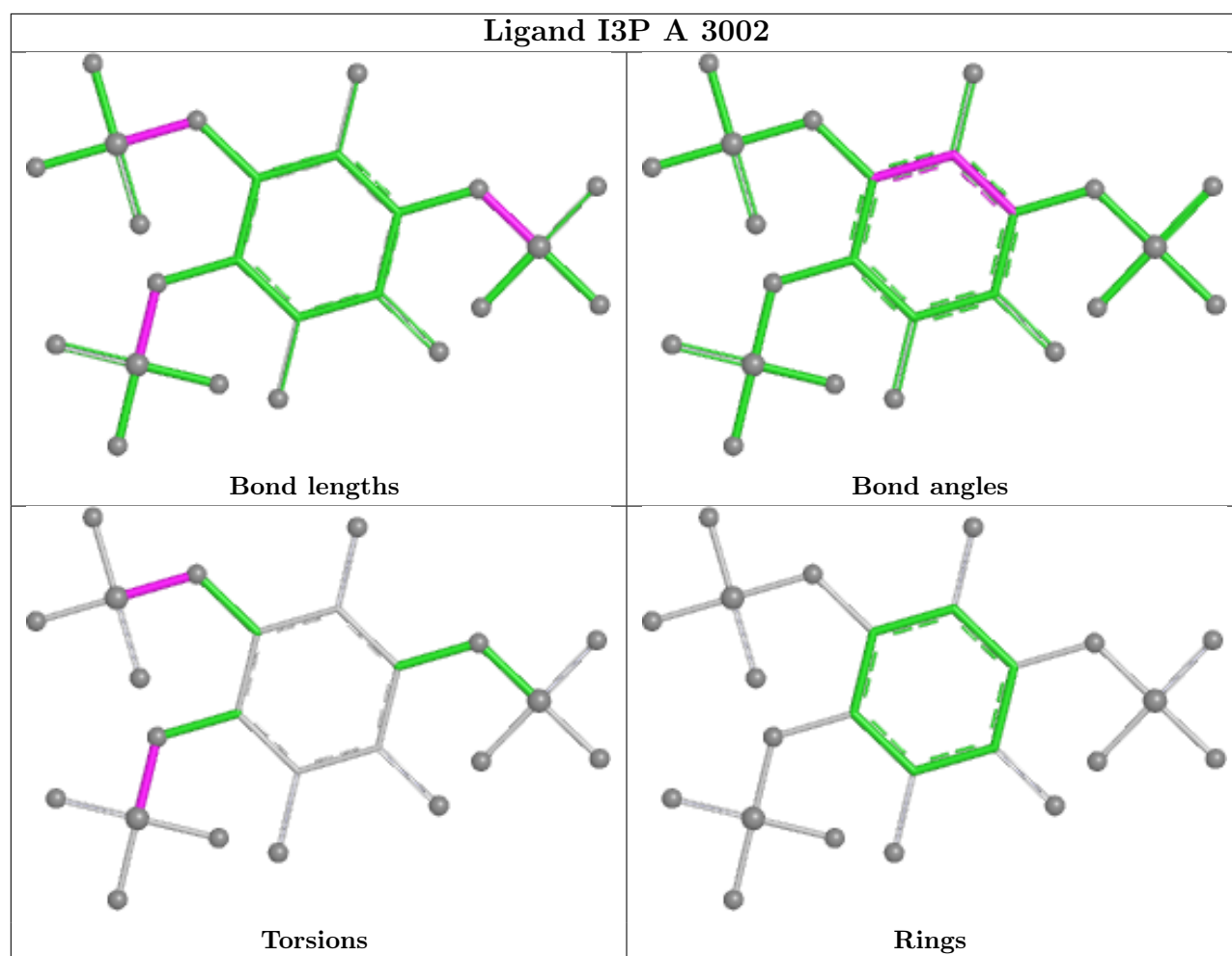
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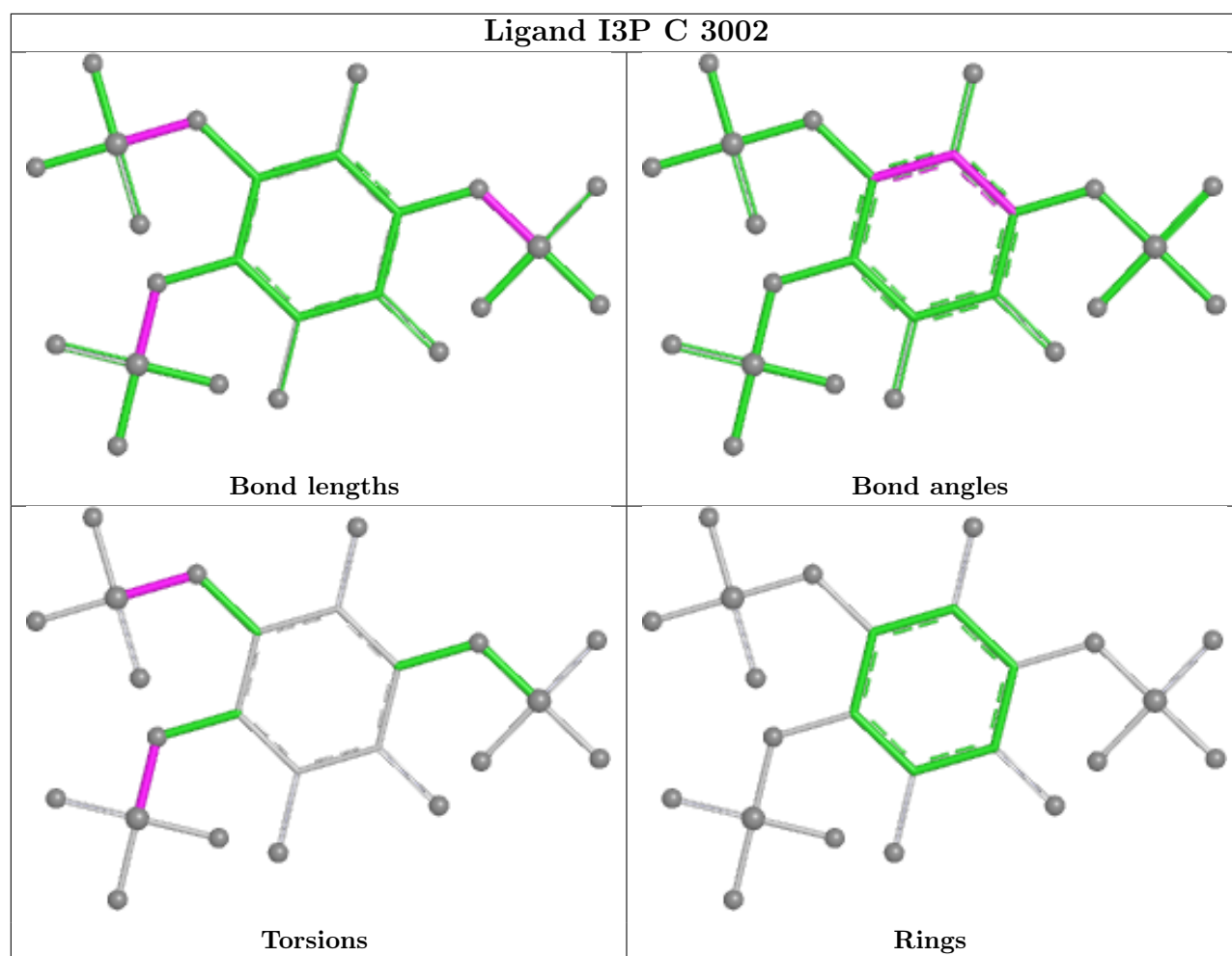
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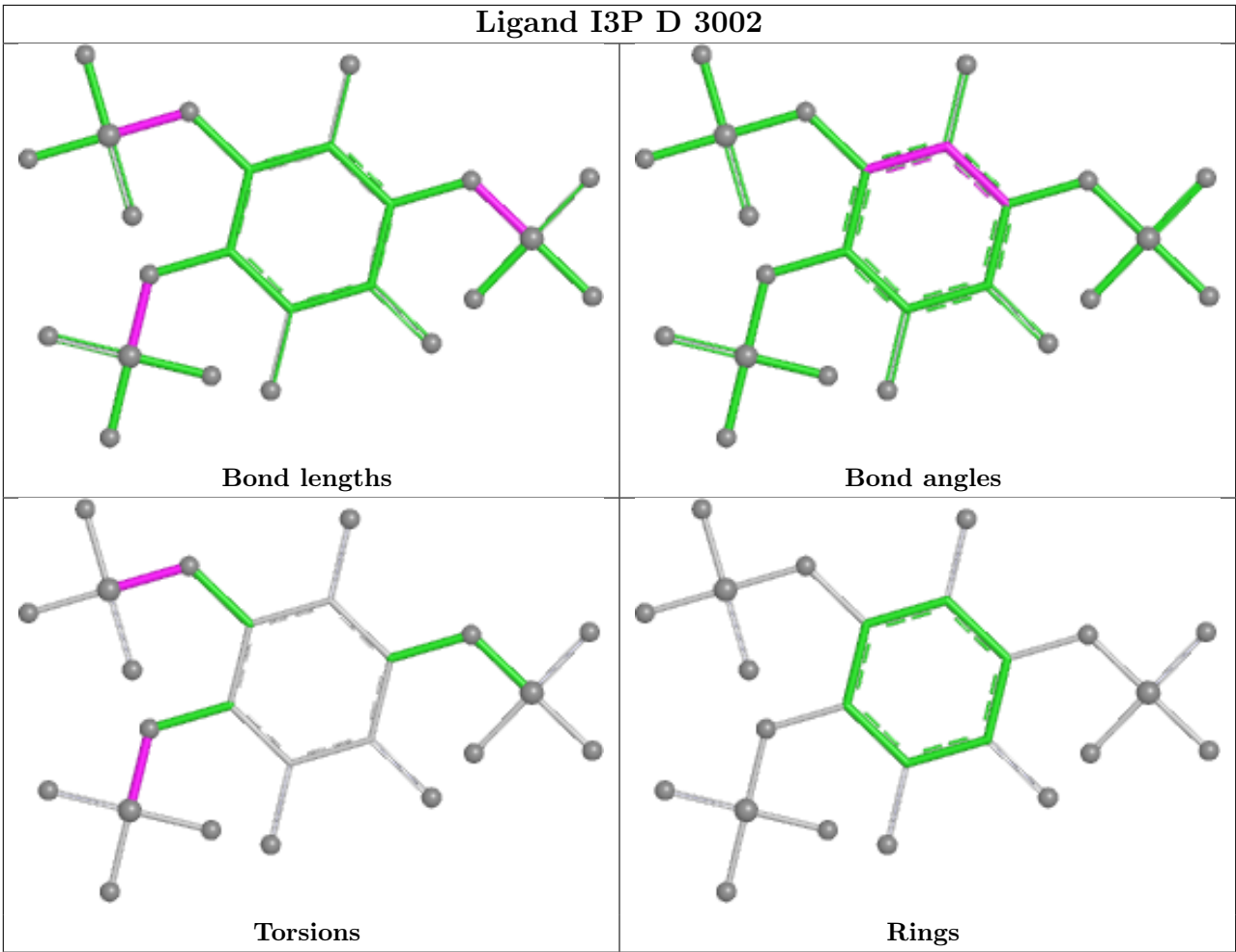
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	3002	I3P	2	0
3	D	3002	I3P	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	5
1	B	5
1	C	5
1	D	5

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1552:TRP	C	1587:ASP	N	47.85

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	1552:TRP	C	1587:ASP	N	47.85
1	C	1552:TRP	C	1587:ASP	N	47.85
1	D	1552:TRP	C	1587:ASP	N	47.85
1	B	1484:ARG	C	1490:ALA	N	16.56
1	C	1484:ARG	C	1490:ALA	N	16.56
1	D	1484:ARG	C	1490:ALA	N	16.56
1	A	1484:ARG	C	1490:ALA	N	16.55
1	A	1533:ARG	C	1541:ALA	N	14.33
1	B	1533:ARG	C	1541:ALA	N	14.33
1	C	1533:ARG	C	1541:ALA	N	14.33
1	D	1533:ARG	C	1541:ALA	N	14.33
1	A	1508:GLY	C	1515:ALA	N	7.89
1	B	1508:GLY	C	1515:ALA	N	7.89
1	C	1508:GLY	C	1515:ALA	N	7.89
1	D	1508:GLY	C	1515:ALA	N	7.89
1	A	2252:TYR	C	2260:SER	N	6.10
1	B	2252:TYR	C	2260:SER	N	6.10
1	C	2252:TYR	C	2260:SER	N	6.10
1	D	2252:TYR	C	2260:SER	N	6.10

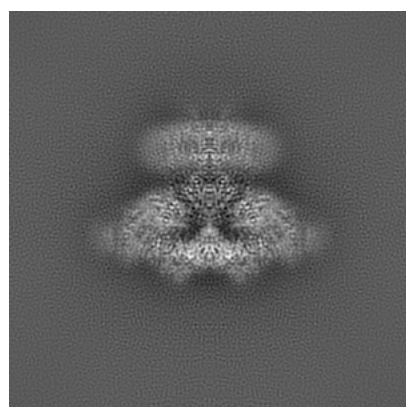
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7981. These allow visual inspection of the internal detail of the map and identification of artifacts.

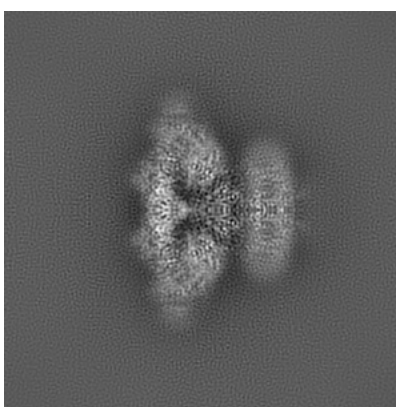
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

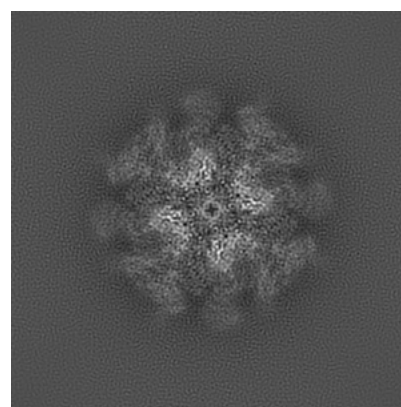
6.1.1 Primary map



X



Y

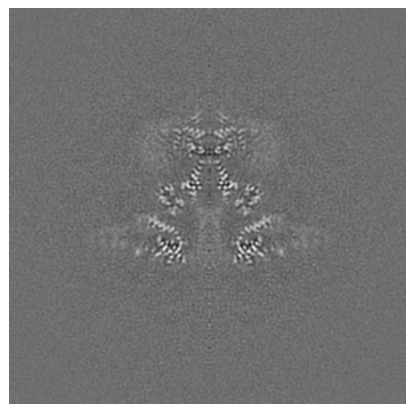


Z

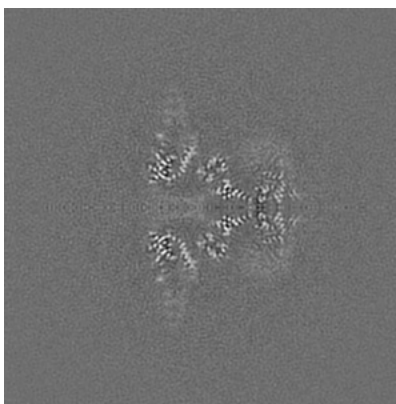
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

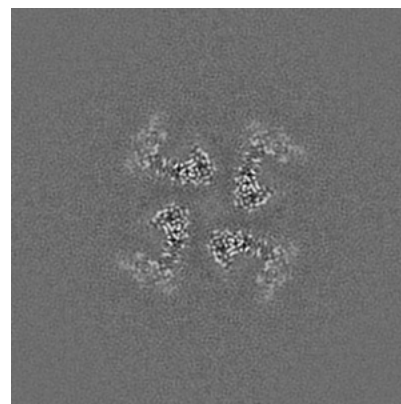
6.2.1 Primary map



X Index: 192



Y Index: 192

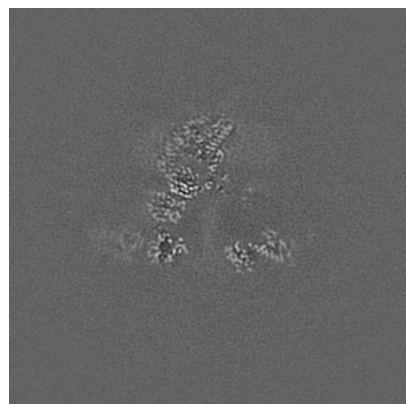


Z Index: 192

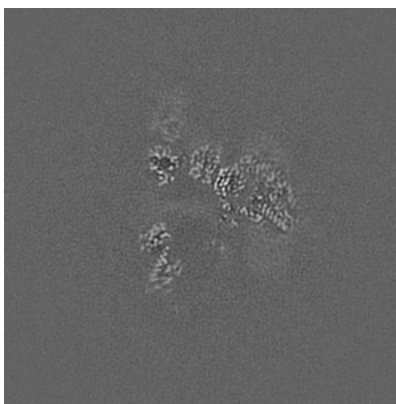
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

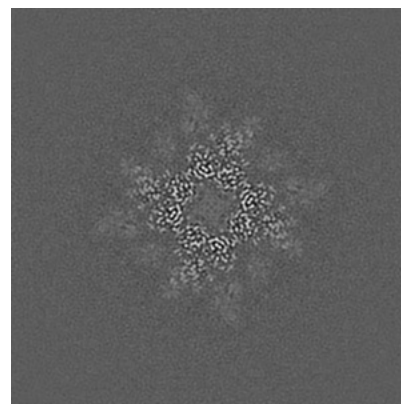
6.3.1 Primary map



X Index: 202



Y Index: 202

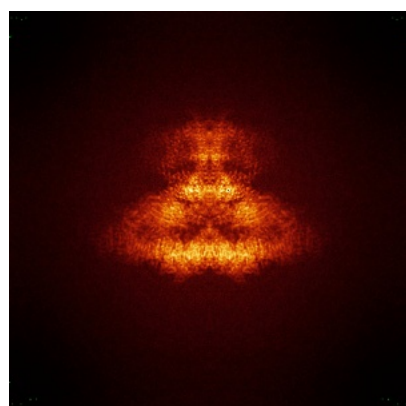


Z Index: 149

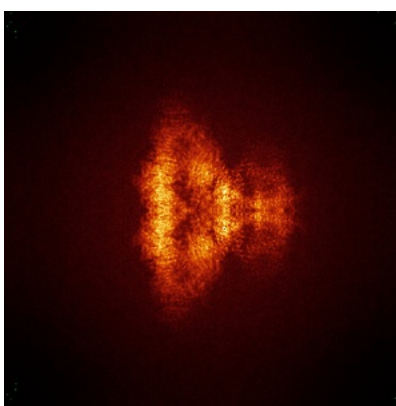
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

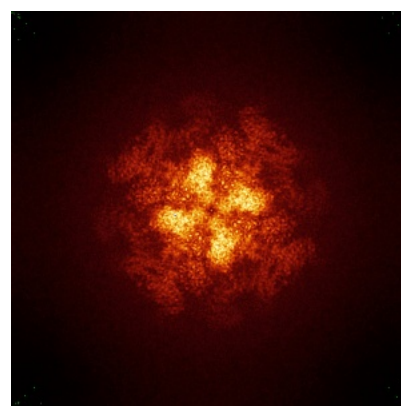
6.4.1 Primary map



X



Y

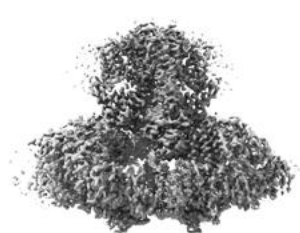


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

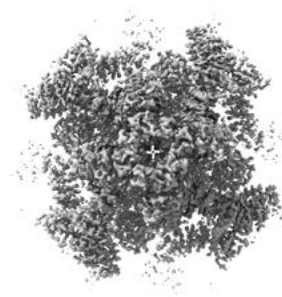
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 5.13. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

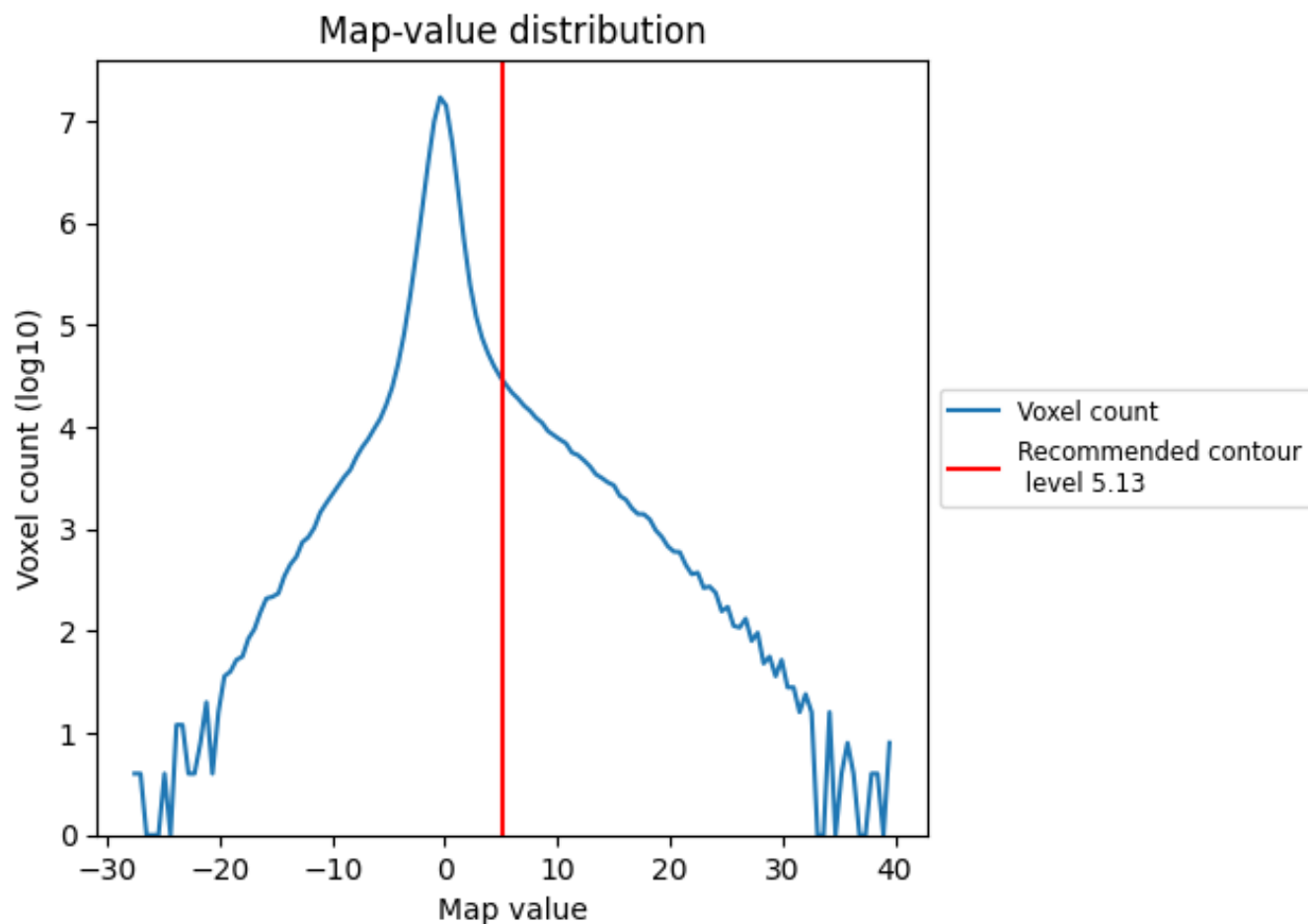
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

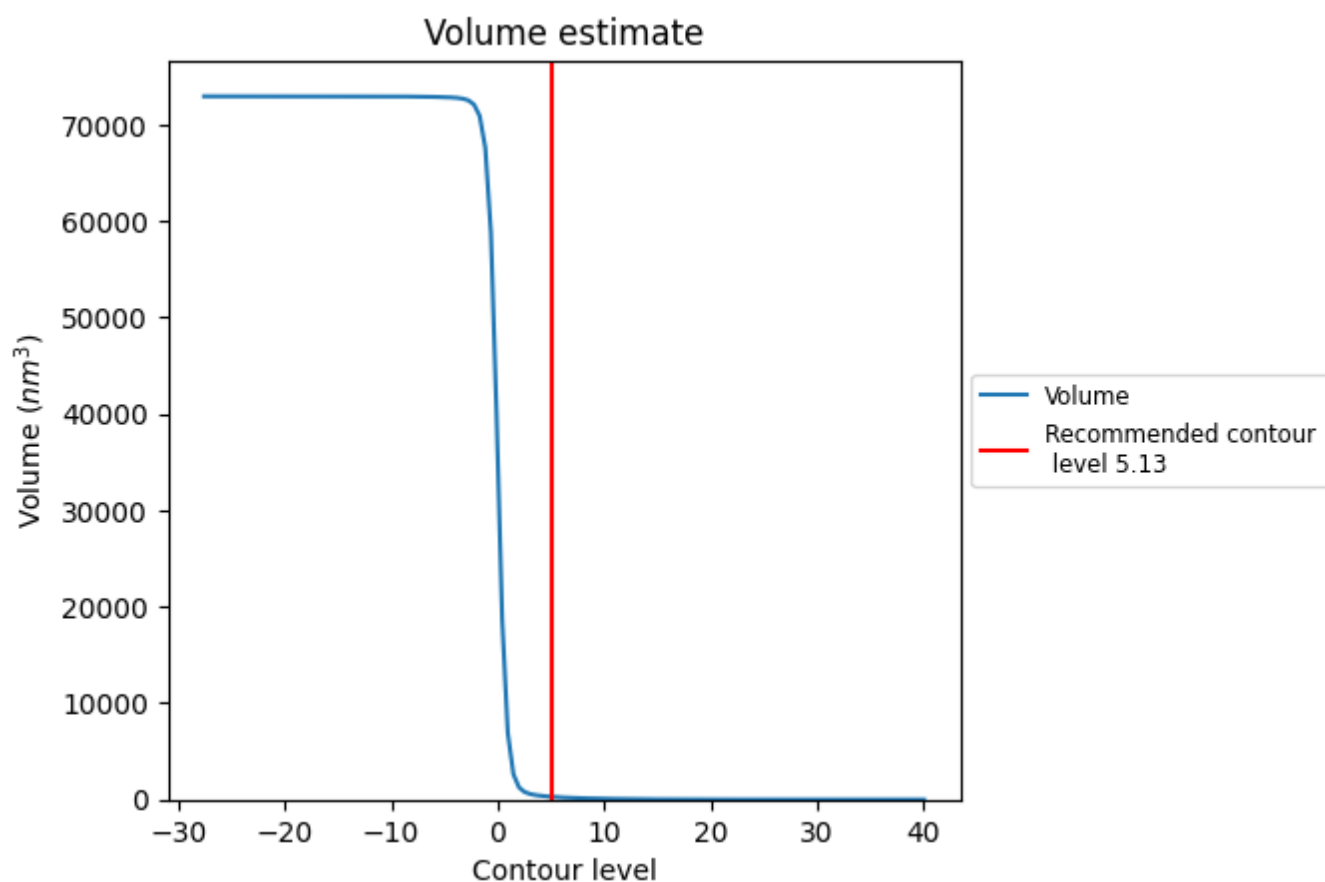
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

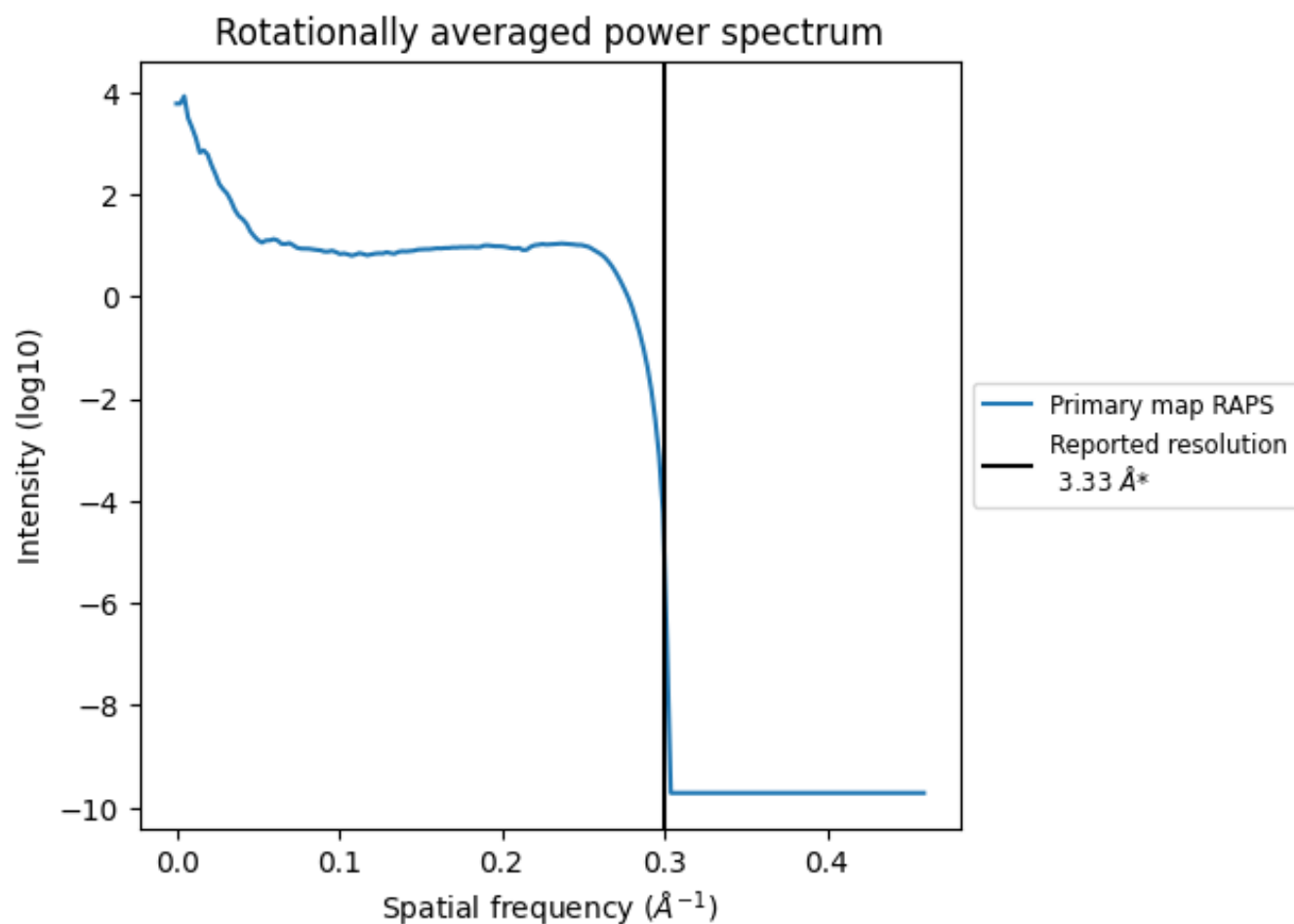
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 280 nm³; this corresponds to an approximate mass of 253 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.300 \AA^{-1}

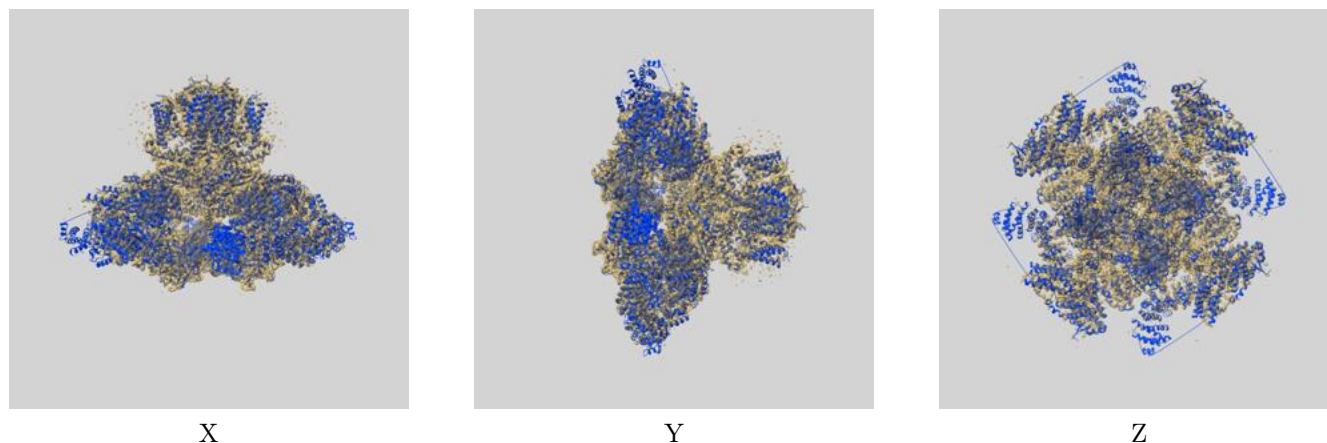
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

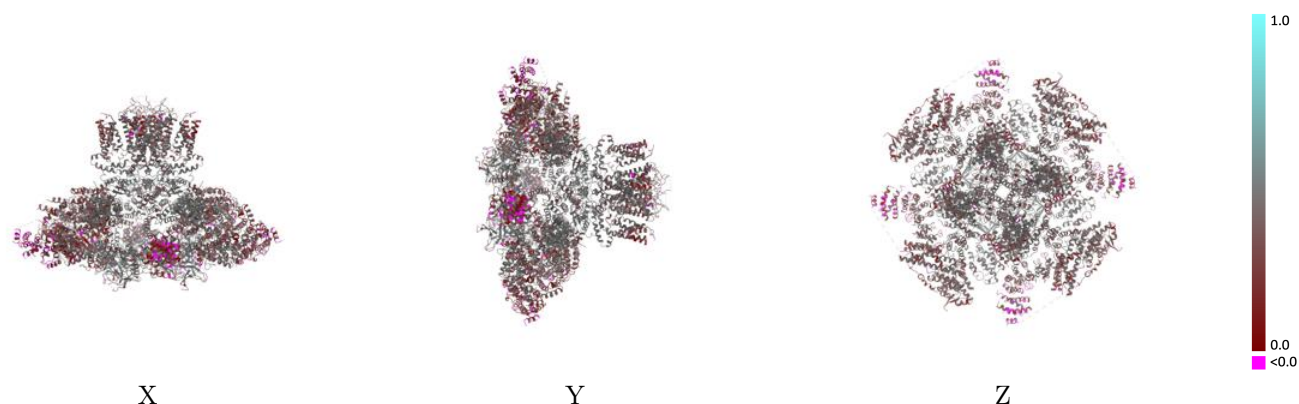
This section contains information regarding the fit between EMDB map EMD-7981 and PDB model 6DQN. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



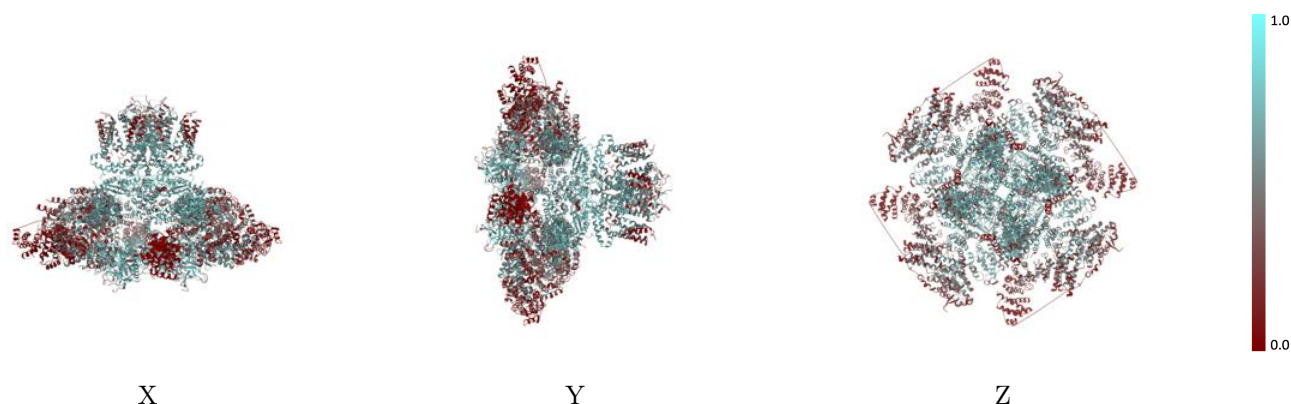
The images above show the 3D surface view of the map at the recommended contour level 5.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



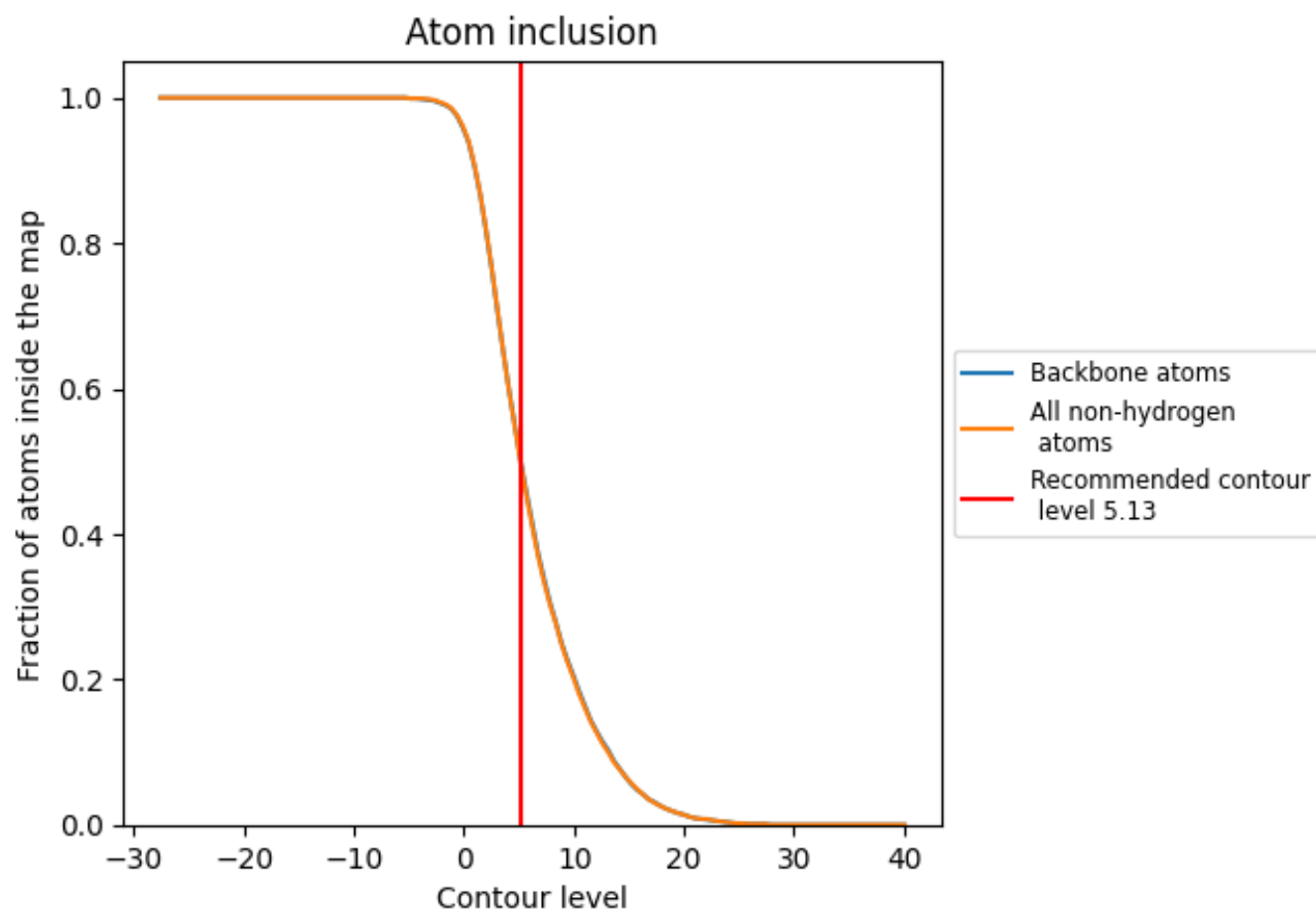
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (5.13).

9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 50% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (5.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.5000	<div></div> 0.3870
A	<div></div> 0.5040	<div></div> 0.3870
B	<div></div> 0.5040	<div></div> 0.3860
C	<div></div> 0.5040	<div></div> 0.3870
D	<div></div> 0.5040	<div></div> 0.3870

