



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 01:26 AM UTC

PDB ID : 6VBV / pdb_00006vbv
EMDB ID : EMD-21145
Title : Structure of the bovine BBSome:ARL6:GTP complex
Authors : Singh, S.K.; Gui, M.; Koh, F.; Yip, M.C.J.; Brown, A.
Deposited on : 2019-12-19
Resolution : 3.50 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:

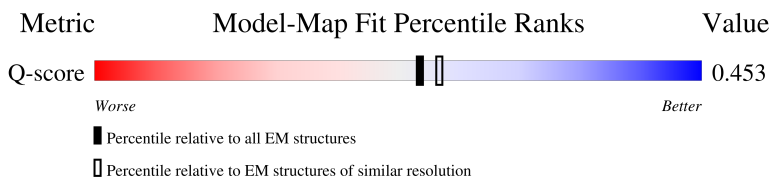
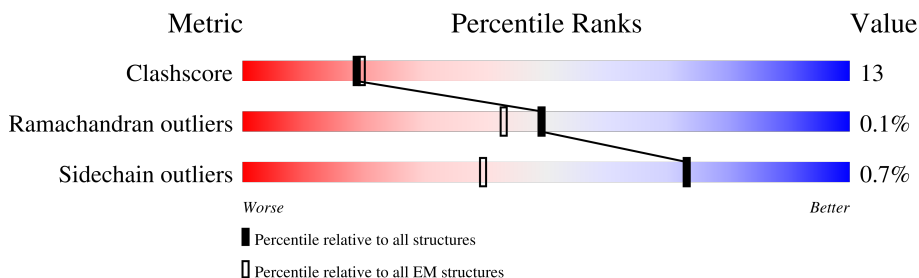
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	0	69	
2	1	592	
3	2	721	
4	4	519	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	5	341	
6	7	715	
7	8	501	
8	9	887	
9	3	186	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
11	GTP	3	201	-	-	X	-

2 Entry composition i

There are 11 unique types of molecules in this entry. The entry contains 31676 atoms, of which 0 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 Bardet-Biedl syndrome 18 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	52	421	270	70	77	4	0	0

- Molecule 2 is a protein called BBS1 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	486	3767	2418	657	673	19	0	0

- Molecule 3 is a protein called Bardet-Biedl syndrome 2 protein homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	659	5145	3245	896	977	27	0	0

- Molecule 4 is a protein called Bardet-Biedl syndrome 4 protein homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	4	391	3156	2047	518	571	20	0	0

- Molecule 5 is a protein called Bardet-Biedl syndrome 5 protein homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	5	300	2411	1533	422	450	6	0	0

- Molecule 6 is a protein called Bardet-Biedl syndrome 7 protein homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	7	706	5575	3532	942	1079	22	0	0

- Molecule 7 is a protein called Tetratricopeptide repeat domain 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	8	475	3797	2417	655	705	20	0	0

- Molecule 8 is a protein called Bardet-Biedl syndrome 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	9	764	6034	3857	1018	1128	31	0	0

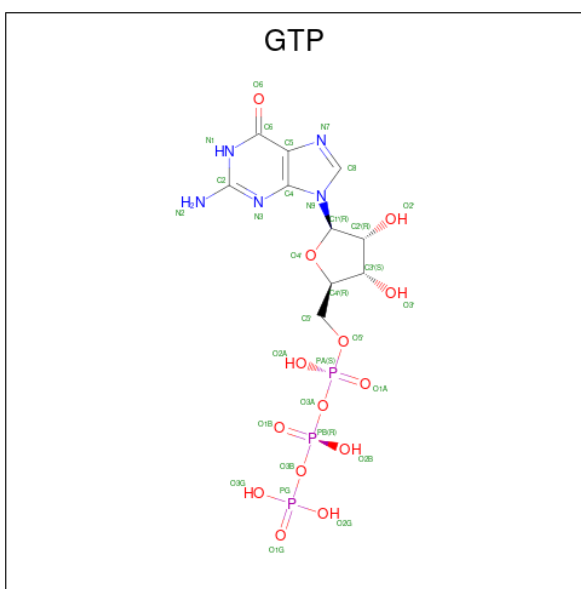
- Molecule 9 is a protein called ADP-ribosylation factor-like protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	3	167	1336	850	231	249	6	0	0

- Molecule 10 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	AltConf
10	2	2	Total Ca 2 2	0

- Molecule 11 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

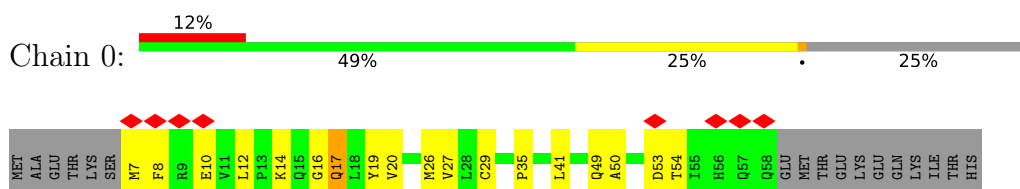


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
11	3	1	32	10	5	14	3	0

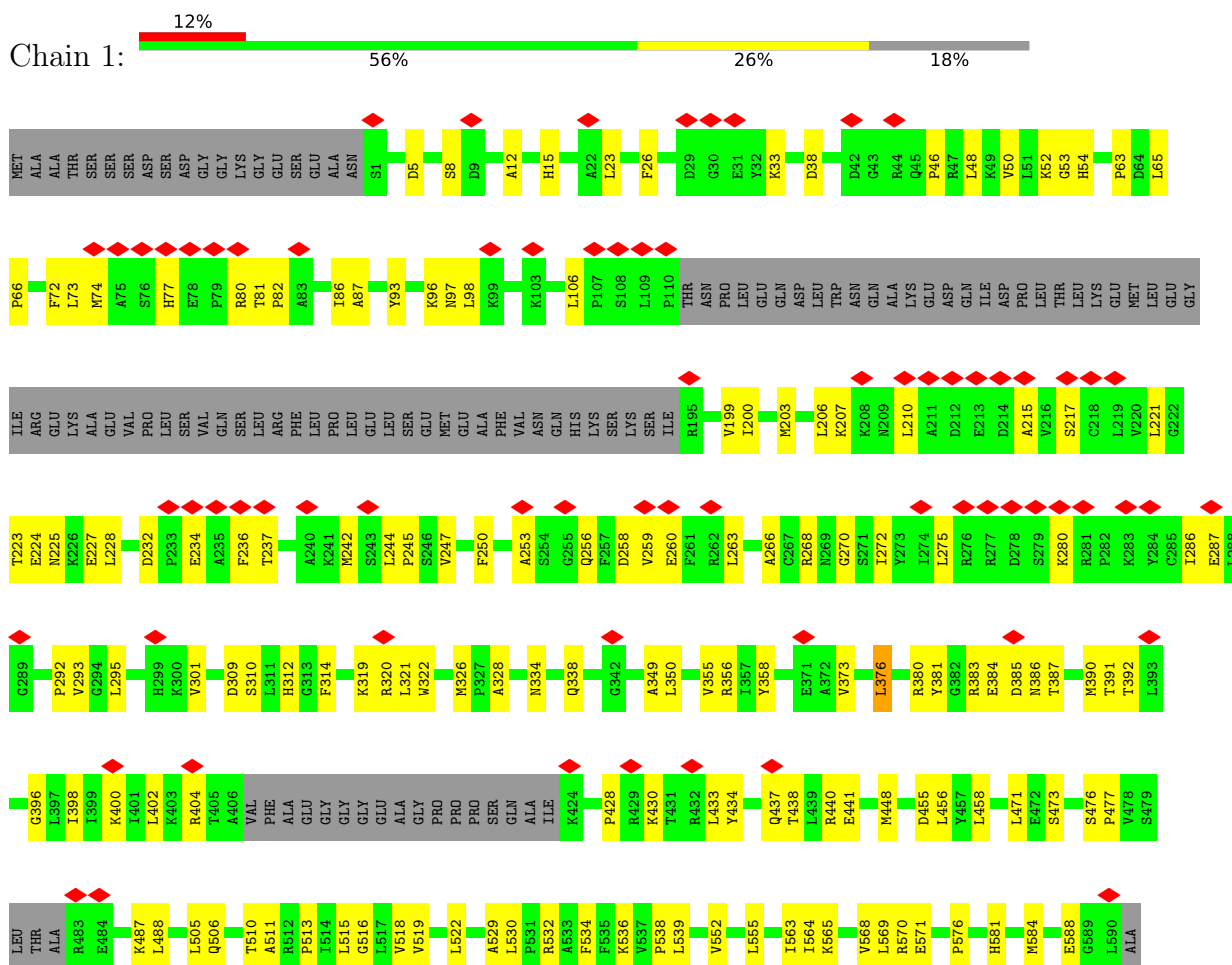
3 Residue-property plots [i](#)

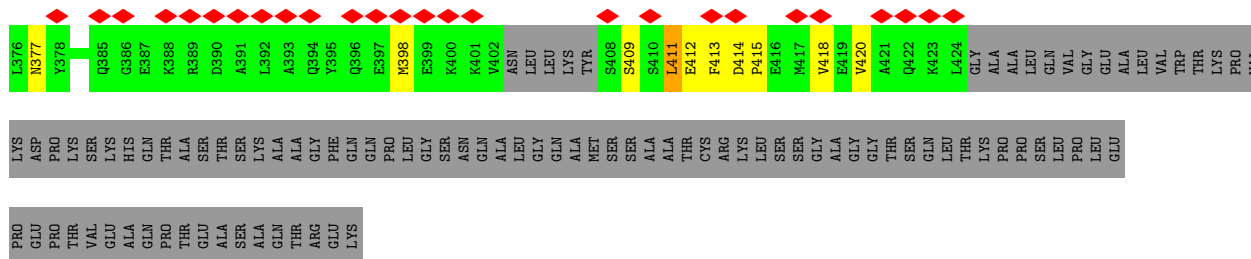
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Bardet-Biedl syndrome 18 protein

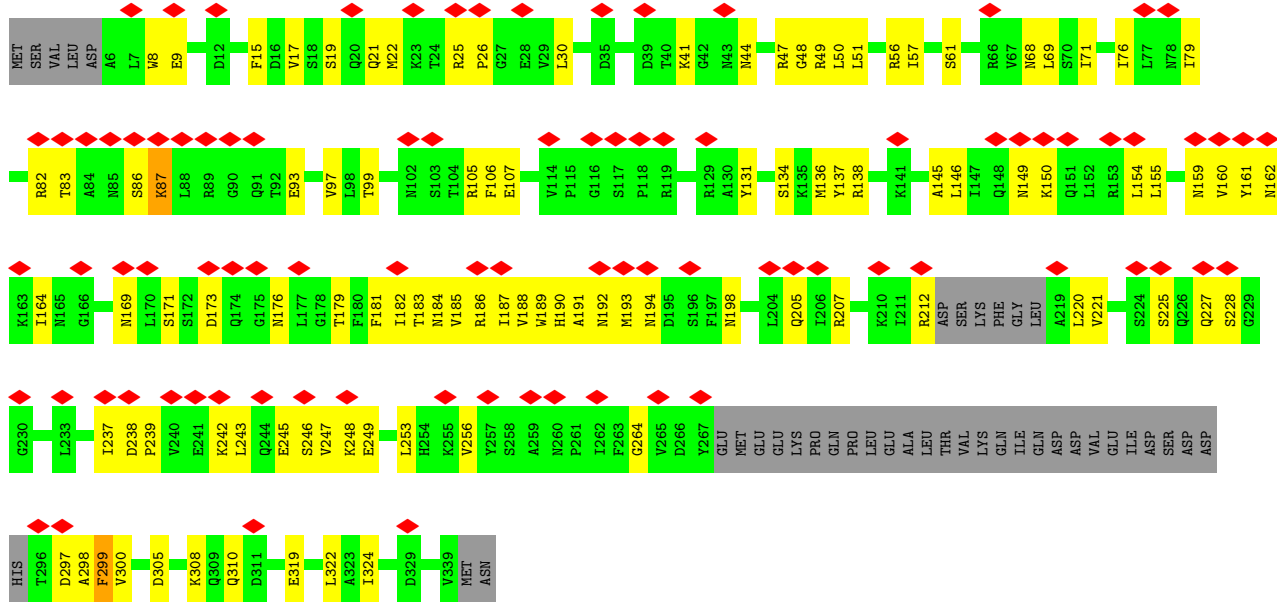


- Molecule 2: BBS1 domain-containing protein

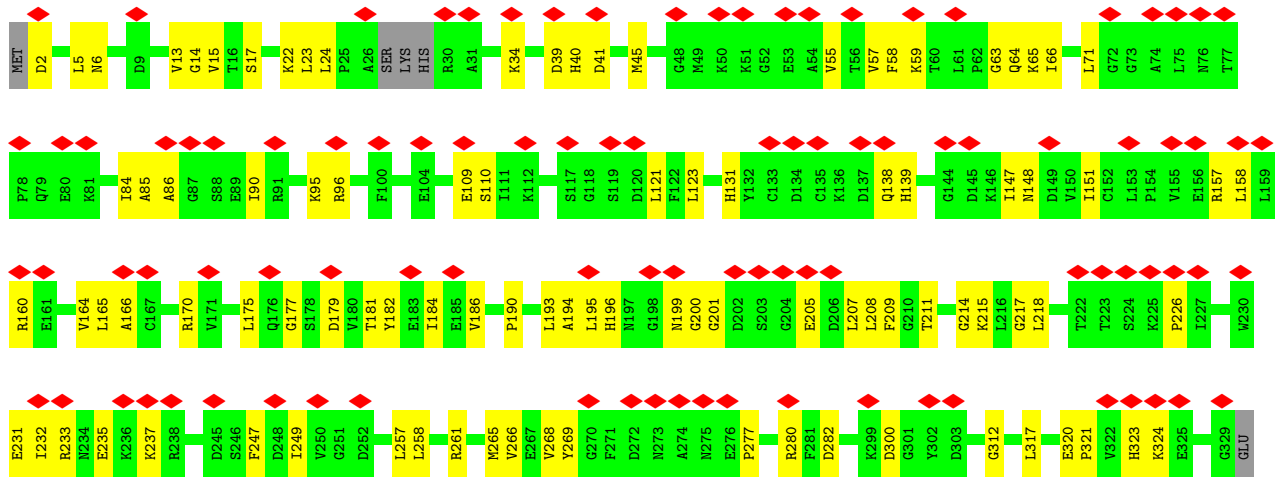




• Molecule 5: Bardet-Biedl syndrome 5 protein homolog



• Molecule 6: Bardet-Biedl syndrome 7 protein homolog



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	75201	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 ($e^-/\text{\AA}^2$)	56	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.128	Depositor
Minimum map value	-0.090	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	339.19998, 339.19998, 339.19998	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0	0.50	0/426	0.59	0/572
2	1	0.23	0/3840	0.45	0/5205
3	2	0.30	0/5237	0.56	4/7092 (0.1%)
4	4	0.21	0/3223	0.38	0/4357
5	5	0.19	0/2456	0.43	0/3324
6	7	0.22	1/5676 (0.0%)	0.41	0/7674
7	8	0.24	1/3883 (0.0%)	0.42	4/5262 (0.1%)
8	9	0.19	0/6153	0.39	1/8325 (0.0%)
9	3	0.12	0/1361	0.30	0/1835
All	All	0.23	2/32255 (0.0%)	0.44	9/43646 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	7	428	SER	CA-CB	-10.00	1.45	1.53
7	8	20	ALA	C-O	-5.08	1.18	1.24

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	2	172	ASP	CB-CA-C	8.40	118.15	109.83
3	2	251	ASP	CB-CA-C	-5.79	103.13	111.70
7	8	20	ALA	N-CA-C	-5.61	105.16	111.28
8	9	362	ASP	CB-CA-C	-5.53	102.25	110.71
7	8	25	GLN	N-CA-C	-5.52	104.95	110.97
7	8	17	GLN	N-CA-C	-5.50	105.68	112.72
7	8	24	THR	N-CA-C	-5.50	105.19	111.07
3	2	431	HIS	CA-C-N	5.33	125.26	119.78
3	2	431	HIS	C-N-CA	5.33	125.26	119.78

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	0	421	0	450	25	0
2	1	3767	0	3926	124	0
3	2	5145	0	5109	168	0
4	4	3156	0	3179	59	0
5	5	2411	0	2412	75	0
6	7	5575	0	5576	160	0
7	8	3797	0	3740	76	0
8	9	6034	0	6068	157	0
9	3	1336	0	1352	55	0
10	2	2	0	0	0	0
11	3	32	0	12	14	0
All	All	31676	0	31824	821	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 13.

All (821) 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)
11:3:201:GTP:H5'	11:3:201:GTP:C8	1.65	1.32
11:3:201:GTP:H8	11:3:201:GTP:C5'	1.73	1.00
2:1:349:ALA:HB2	2:1:376:LEU:HD21	1.44	0.96
3:2:429:VAL:HG11	6:7:408:LEU:HD21	1.48	0.93
3:2:651:ASN:HD21	8:9:677:GLN:HE22	1.17	0.91
11:3:201:GTP:C8	11:3:201:GTP:C5'	2.52	0.89
1:0:16:GLY:HA3	4:4:278:MET:HE2	1.52	0.89
11:3:201:GTP:H5'	11:3:201:GTP:H8	0.78	0.85
5:5:324:ILE:HG13	8:9:359:LEU:HB2	1.60	0.84
9:3:61:SER:HB3	9:3:178:GLN:HE22	1.42	0.83
9:3:26:ASP:OD2	9:3:73:GLN:HG2	1.79	0.82
3:2:545:TYR:HB2	3:2:557:ASN:HB2	1.61	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:270:GLY:HA2	2:1:292:PRO:HD3	1.64	0.80
6:7:131:HIS:HB3	6:7:139:HIS:HB2	1.64	0.78
9:3:35:ASN:HD21	9:3:44:SER:HB3	1.49	0.77
3:2:377:ILE:HD11	3:2:462:GLY:HA2	1.68	0.76
6:7:321:PRO:HB3	9:3:139:THR:HG22	1.70	0.74
2:1:72:PHE:HB2	2:1:217:SER:HB2	1.70	0.74
5:5:17:VAL:HB	5:5:68:ASN:HD21	1.52	0.73
5:5:79:ILE:HG22	5:5:97:VAL:HG12	1.70	0.72
9:3:26:ASP:OD2	9:3:73:GLN:CG	2.37	0.72
2:1:437:GLN:NE2	7:8:359:ALA:O	2.22	0.72
8:9:456:LYS:NZ	8:9:458:SER:OG	2.23	0.71
8:9:245:ALA:HA	8:9:264:GLY:HA2	1.72	0.71
2:1:349:ALA:HB1	2:1:373:VAL:HG13	1.73	0.70
6:7:449:ALA:O	6:7:475:ARG:NH1	2.23	0.70
3:2:460:PHE:HB3	3:2:469:PHE:HE2	1.55	0.70
8:9:41:ILE:HG21	8:9:95:LEU:HD11	1.73	0.70
7:8:18:LEU:H	7:8:18:LEU:CD2	2.04	0.70
7:8:80:LEU:HG	7:8:260:PRO:HG3	1.74	0.69
7:8:340:GLN:O	8:9:325:GLN:NE2	2.25	0.69
7:8:18:LEU:CD2	7:8:18:LEU:N	2.55	0.69
2:1:386:ASN:HB3	2:1:402:LEU:HB3	1.73	0.69
3:2:415:VAL:HB	3:2:430:VAL:HG12	1.75	0.69
3:2:296:ASP:HA	3:2:304:GLN:HG3	1.75	0.69
6:7:523:TRP:HE1	6:7:587:ARG:HD2	1.58	0.69
2:1:80:ARG:HG2	2:1:81:THR:H	1.58	0.69
5:5:82:ARG:HE	7:8:375:LEU:HD13	1.58	0.68
6:7:148:ASN:ND2	6:7:190:PRO:O	2.21	0.68
3:2:385:THR:HG22	3:2:404:ILE:HG12	1.76	0.68
3:2:417:ILE:CD1	3:2:443:ILE:HG21	2.24	0.68
2:1:519:VAL:HG22	2:1:568:VAL:HG22	1.75	0.67
3:2:39:LYS:NZ	3:2:72:ASN:OD1	2.27	0.67
3:2:558:THR:HG21	3:2:563:LEU:HD22	1.77	0.67
4:4:247:GLN:NE2	4:4:279:CYS:SG	2.63	0.67
7:8:1:MET:HB2	8:9:77:PRO:HG2	1.76	0.67
2:1:199:VAL:O	2:1:224:GLU:N	2.27	0.67
4:4:414:ASP:HB2	4:4:415:PRO:HD3	1.75	0.67
5:5:105:ARG:HH11	8:9:7:ARG:HH22	1.42	0.67
5:5:169:ASN:O	5:5:176:ASN:ND2	2.26	0.67
7:8:18:LEU:N	7:8:18:LEU:HD22	2.10	0.66
8:9:314:ILE:HD12	8:9:322:TRP:HB3	1.76	0.66
8:9:448:ASN:ND2	8:9:477:MET:SD	2.68	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:301:VAL:HG23	2:1:321:LEU:HD21	1.77	0.66
3:2:39:LYS:HE3	6:7:635:HIS:HE1	1.60	0.66
2:1:390:MET:HG2	2:1:398:ILE:O	1.95	0.66
4:4:74:ALA:HB2	4:4:89:LEU:HB2	1.78	0.66
8:9:183:PRO:HB2	8:9:248:ILE:HG22	1.78	0.66
7:8:57:GLU:OE2	7:8:135:ARG:NH1	2.29	0.65
8:9:102:LYS:NZ	8:9:104:CYS:SG	2.61	0.65
8:9:365:LEU:HD12	8:9:365:LEU:H	1.61	0.65
5:5:194:ASN:OD1	8:9:124:LYS:NZ	2.28	0.65
2:1:390:MET:CG	2:1:398:ILE:HB	2.27	0.65
6:7:428:SER:O	6:7:428:SER:OG	2.07	0.65
2:1:12:ALA:O	2:1:396:GLY:N	2.23	0.65
6:7:549:PHE:O	6:7:612:LYS:NZ	2.29	0.65
8:9:2:SER:HB2	8:9:7:ARG:HH11	1.61	0.65
8:9:68:LEU:HD21	8:9:71:GLU:HB2	1.78	0.65
5:5:297:ASP:O	5:5:300:VAL:HG12	1.97	0.65
8:9:498:PRO:O	8:9:610:TRP:NE1	2.26	0.65
3:2:164:HIS:NE2	3:2:184:GLU:OE2	2.29	0.65
6:7:232:ILE:HD11	6:7:277:PRO:HG2	1.79	0.64
2:1:440:ARG:NH1	2:1:448:MET:SD	2.71	0.64
9:3:36:LYS:HD3	9:3:43:GLN:HE22	1.61	0.64
8:9:491:LEU:HD22	8:9:534:VAL:HG23	1.80	0.64
8:9:45:PHE:HA	8:9:78:ILE:H	1.63	0.64
8:9:103:LEU:HB3	8:9:129:HIS:HB2	1.80	0.64
3:2:250:PHE:O	3:2:259:GLU:N	2.27	0.64
6:7:5:LEU:HB3	6:7:317:LEU:HB3	1.77	0.64
3:2:123:ILE:HG22	3:2:138:ILE:HG13	1.78	0.63
3:2:166:LEU:CD2	3:2:181:VAL:HG12	2.28	0.63
8:9:80:GLN:NE2	8:9:138:MET:O	2.26	0.63
2:1:515:LEU:HD23	2:1:539:LEU:HD13	1.80	0.63
3:2:429:VAL:HG11	6:7:408:LEU:CD2	2.26	0.63
9:3:38:LYS:HE3	9:3:43:GLN:HA	1.80	0.63
2:1:530:LEU:HD21	2:1:552:VAL:HG22	1.81	0.63
3:2:190:VAL:HG13	3:2:197:VAL:HB	1.80	0.63
5:5:131:TYR:O	5:5:138:ARG:NH1	2.31	0.63
6:7:195:LEU:HB2	6:7:200:GLY:HA2	1.80	0.62
2:1:349:ALA:CB	2:1:376:LEU:HD21	2.24	0.62
3:2:503:ILE:HB	3:2:554:ILE:HD11	1.81	0.62
7:8:182:PHE:HE2	7:8:216:GLN:HE21	1.48	0.62
8:9:14:LEU:HD11	8:9:52:PHE:HZ	1.65	0.62
8:9:87:VAL:O	8:9:166:GLN:NE2	2.32	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:124:VAL:HG21	3:2:179:LEU:HD11	1.81	0.62
3:2:129:GLY:HA2	3:2:176:LYS:HB3	1.82	0.62
7:8:42:ARG:NH1	8:9:265:GLU:OE2	2.32	0.62
6:7:411:SER:HB3	6:7:441:LEU:HB3	1.82	0.62
8:9:85:LYS:O	8:9:166:GLN:NE2	2.33	0.62
6:7:462:GLU:OE2	6:7:547:ASN:ND2	2.33	0.62
6:7:249:ILE:O	9:3:135:ARG:NH2	2.33	0.61
7:8:18:LEU:H	7:8:18:LEU:HD23	1.66	0.61
6:7:261:ARG:HG3	6:7:265:MET:HB3	1.81	0.61
8:9:162:MET:HB2	8:9:169:TYR:HE1	1.65	0.61
3:2:25:ASP:HB2	3:2:28:HIS:HB2	1.81	0.61
3:2:377:ILE:HD12	3:2:470:HIS:HD2	1.64	0.61
9:3:32:THR:HG21	11:3:201:GTP:C8	2.35	0.61
8:9:77:PRO:O	8:9:99:HIS:ND1	2.31	0.61
6:7:681:LYS:NZ	6:7:712:PHE:O	2.32	0.61
7:8:231:GLU:HB2	7:8:253:VAL:HG11	1.82	0.61
2:1:33:LYS:HE3	2:1:52:LYS:HD3	1.81	0.61
6:7:623:VAL:HG11	6:7:660:TYR:HB2	1.83	0.61
2:1:390:MET:HG2	2:1:398:ILE:HB	1.82	0.61
4:4:412:GLU:C	4:4:415:PRO:HD2	2.25	0.61
2:1:73:LEU:HD22	2:1:82:PRO:HB3	1.83	0.60
6:7:356:VAL:HG23	6:7:360:ARG:HH12	1.65	0.60
6:7:444:THR:HG22	6:7:444:THR:O	2.01	0.60
8:9:589:THR:HB	8:9:602:GLN:HG2	1.83	0.60
3:2:390:SER:O	3:2:398:ALA:N	2.34	0.60
3:2:271:ALA:HB3	3:2:281:PHE:HB3	1.83	0.60
3:2:531:PHE:HB3	3:2:548:ILE:HB	1.83	0.60
2:1:8:SER:HA	2:1:398:ILE:HD13	1.83	0.60
3:2:348:LEU:HD22	6:7:356:VAL:HG21	1.84	0.60
6:7:237:LYS:NZ	6:7:265:MET:SD	2.75	0.60
1:0:17:GLN:HA	1:0:17:GLN:HE21	1.66	0.60
3:2:411:ILE:C	3:2:412:ILE:HD13	2.26	0.60
4:4:213:LEU:HD12	4:4:221:ALA:HB1	1.83	0.60
6:7:109:GLU:N	6:7:109:GLU:OE1	2.35	0.60
8:9:545:SER:HB3	8:9:604:GLU:HA	1.84	0.60
2:1:77:HIS:O	2:1:77:HIS:ND1	2.33	0.59
8:9:80:GLN:OE1	8:9:138:MET:N	2.29	0.59
1:0:10:GLU:HB3	4:4:377:ASN:HD22	1.67	0.59
3:2:247:ILE:HB	3:2:260:LEU:HD21	1.83	0.59
2:1:563:ILE:HD11	2:1:581:HIS:HB3	1.84	0.59
5:5:134:SER:O	5:5:138:ARG:NH2	2.36	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:7:231:GLU:OE2	6:7:233:ARG:NH1	2.34	0.59
5:5:190:HIS:HD2	5:5:192:ASN:H	1.50	0.59
8:9:196:VAL:HG22	8:9:202:VAL:HG22	1.85	0.59
1:0:29:CYS:H	7:8:422:ASN:HD21	1.51	0.59
3:2:341:LEU:HA	3:2:344:LYS:HD2	1.85	0.59
8:9:724:PHE:HE1	8:9:768:TRP:HB2	1.67	0.59
3:2:167:ALA:HB1	3:2:211:PRO:HD3	1.85	0.59
6:7:138:GLN:O	6:7:139:HIS:ND1	2.36	0.58
7:8:16:PHE:HB3	7:8:47:MET:HG2	1.83	0.58
3:2:413:ARG:HH22	3:2:431:HIS:CE1	2.20	0.58
6:7:517:PHE:HB2	6:7:560:LYS:HA	1.84	0.58
7:8:16:PHE:HA	7:8:19:CYS:SG	2.42	0.58
5:5:237:ILE:HG22	5:5:238:ASP:H	1.69	0.58
8:9:189:ARG:HD3	8:9:258:SER:HB2	1.85	0.58
5:5:212:ARG:HD2	5:5:221:VAL:HG21	1.86	0.58
7:8:332:LEU:HD21	7:8:336:ARG:HH21	1.69	0.58
3:2:100:LEU:HD22	3:2:138:ILE:HD12	1.86	0.58
6:7:346:ARG:O	6:7:350:GLU:HG2	2.04	0.58
8:9:554:LYS:HZ2	8:9:632:PHE:HB2	1.68	0.58
9:3:144:SER:HA	9:3:149:LEU:HD13	1.86	0.58
3:2:344:LYS:HA	3:2:347:ASN:HD22	1.69	0.58
7:8:305:LEU:HD21	7:8:315:ILE:HG13	1.85	0.58
8:9:461:VAL:HG23	8:9:462:GLN:H	1.69	0.57
4:4:411:LEU:O	4:4:415:PRO:HD3	2.03	0.57
5:5:308:LYS:NZ	8:9:362:ASP:OD1	2.37	0.57
6:7:620:ALA:HB2	6:7:663:GLN:HE22	1.69	0.57
4:4:140:ASN:HA	4:4:143:VAL:HG12	1.86	0.57
8:9:748:GLN:HE22	8:9:824:ARG:HD2	1.69	0.57
3:2:31:LEU:HB2	3:2:297:TYR:OH	2.04	0.57
3:2:417:ILE:HD12	3:2:443:ILE:HG21	1.86	0.57
6:7:433:ASP:OD2	6:7:436:SER:OG	2.20	0.57
3:2:225:THR:HG22	3:2:239:LYS:HB2	1.86	0.57
7:8:444:SER:HB2	7:8:454:HIS:CE1	2.39	0.57
3:2:354:ASN:ND2	6:7:377:PRO:HB3	2.20	0.57
9:3:29:GLY:HA2	11:3:201:GTP:O5'	2.05	0.57
3:2:213:TYR:HB3	3:2:216:ARG:HB3	1.86	0.57
3:2:416:LEU:HD21	3:2:427:SER:HB2	1.85	0.57
6:7:449:ALA:C	6:7:475:ARG:HH12	2.12	0.57
1:0:12:LEU:HD21	4:4:346:VAL:HG11	1.87	0.57
8:9:263:LEU:HD13	8:9:290:PHE:HB3	1.87	0.57
3:2:283:ASP:OD2	3:2:317:TYR:OH	2.22	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:9:72:VAL:HG21	8:9:123:ILE:HD11	1.87	0.57
6:7:507:ASN:HD22	6:7:598:ASN:H	1.51	0.56
8:9:490:TYR:HA	8:9:533:LEU:HD11	1.87	0.56
8:9:607:GLU:HG2	8:9:726:ARG:HB3	1.86	0.56
1:0:7:MET:HG3	1:0:7:MET:O	2.04	0.56
1:0:19:TYR:OH	4:4:303:ASP:HB3	2.04	0.56
2:1:471:LEU:HD13	8:9:395:VAL:HG11	1.86	0.56
2:1:46:PRO:HB3	2:1:65:LEU:HD23	1.87	0.56
2:1:293:VAL:HG23	4:4:44:ILE:HG23	1.87	0.56
5:5:243:LEU:O	5:5:247:VAL:HG23	2.05	0.56
8:9:333:VAL:HG12	8:9:347:THR:HG22	1.88	0.56
9:3:32:THR:HG21	11:3:201:GTP:H8	1.69	0.56
3:2:417:ILE:HD11	3:2:443:ILE:HG21	1.88	0.56
5:5:47:ARG:NH2	8:9:380:GLU:OE2	2.38	0.56
6:7:360:ARG:HE	6:7:477:GLN:HG2	1.70	0.56
6:7:521:HIS:O	6:7:525:VAL:HG23	2.06	0.56
1:0:10:GLU:HB3	4:4:377:ASN:ND2	2.20	0.56
6:7:410:GLN:NE2	6:7:411:SER:O	2.39	0.56
8:9:304:LEU:HD12	8:9:312:LEU:HD13	1.88	0.55
8:9:535:CYS:SG	8:9:536:LEU:N	2.79	0.55
2:1:458:LEU:HD21	8:9:376:LEU:HD11	1.88	0.55
9:3:30:LYS:HB2	11:3:201:GTP:O2B	2.06	0.55
3:2:454:ASP:OD1	3:2:454:ASP:N	2.40	0.55
6:7:342:ILE:O	6:7:346:ARG:HG2	2.06	0.55
9:3:87:GLY:O	9:3:121:ARG:NH2	2.38	0.55
3:2:166:LEU:HD22	3:2:181:VAL:HG12	1.88	0.55
3:2:429:VAL:CG1	6:7:408:LEU:HD21	2.29	0.55
3:2:461:VAL:HG21	3:2:472:PHE:CD2	2.42	0.55
5:5:207:ARG:HD3	5:5:225:SER:HA	1.89	0.55
6:7:500:ILE:HD13	6:7:555:GLU:HB2	1.88	0.55
8:9:20:PHE:HE2	8:9:352:GLY:HA2	1.70	0.55
9:3:31:THR:N	11:3:201:GTP:O2B	2.38	0.55
2:1:234:GLU:HB2	2:1:236:PHE:CE2	2.42	0.55
9:3:29:GLY:HA2	11:3:201:GTP:C5'	2.37	0.55
1:0:27:VAL:H	7:8:456:ASN:HD21	1.55	0.55
4:4:274:ASN:OD1	4:4:309:ASN:ND2	2.40	0.55
2:1:247:VAL:HB	2:1:268:ARG:HD2	1.88	0.54
3:2:255:ASP:C	3:2:255:ASP:OD1	2.50	0.54
5:5:239:PRO:O	5:5:242:LYS:NZ	2.39	0.54
2:1:15:HIS:N	2:1:38:ASP:OD2	2.40	0.54
3:2:73:GLN:HG2	3:2:96:THR:HG21	1.89	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:5:238:ASP:HB3	5:5:239:PRO:HD2	1.88	0.54
6:7:64:GLN:HB2	6:7:86:ALA:HB1	1.89	0.54
6:7:426:VAL:O	6:7:445:TYR:HA	2.07	0.54
7:8:64:ILE:HD11	7:8:118:PRO:HG2	1.89	0.54
2:1:456:LEU:HD11	7:8:396:THR:HG21	1.89	0.54
6:7:381:VAL:HG12	6:7:400:VAL:HG22	1.89	0.54
8:9:112:LEU:HA	8:9:119:ASN:HB3	1.89	0.54
8:9:304:LEU:HA	8:9:313:HIS:O	2.07	0.54
8:9:481:MET:SD	8:9:483:ARG:NH2	2.80	0.54
3:2:259:GLU:HB3	3:2:272:ARG:O	2.07	0.54
3:2:340:GLU:H	3:2:340:GLU:CD	2.15	0.54
6:7:342:ILE:HD13	6:7:345:LEU:HD21	1.89	0.54
4:4:266:VAL:HG12	7:8:485:VAL:HG11	1.89	0.54
6:7:40:HIS:HD2	6:7:65:LYS:HE2	1.73	0.54
5:5:19:SER:HA	5:5:22:MET:HE2	1.90	0.54
8:9:550:ILE:HD11	8:9:613:THR:HG23	1.90	0.54
4:4:168:ASP:N	4:4:168:ASP:OD1	2.41	0.54
4:4:222:PHE:HB2	4:4:245:MET:HE1	1.89	0.54
6:7:435:GLU:HG2	6:7:436:SER:N	2.22	0.54
2:1:87:ALA:HB2	2:1:203:MET:HE3	1.90	0.53
2:1:250:PHE:HB2	2:1:266:ALA:HB3	1.90	0.53
2:1:321:LEU:HG	2:1:322:TRP:CD1	2.43	0.53
3:2:415:VAL:HB	3:2:430:VAL:CG1	2.38	0.53
4:4:29:PHE:N	4:4:30:PRO:HD2	2.22	0.53
5:5:322:LEU:HD13	8:9:345:ILE:HD11	1.90	0.53
9:3:149:LEU:HD23	9:3:157:TRP:NE1	2.23	0.53
5:5:83:THR:OG1	5:5:93:GLU:OE1	2.21	0.53
1:0:49:GLN:NE2	1:0:53:ASP:OD1	2.41	0.53
2:1:349:ALA:HB2	2:1:376:LEU:CD2	2.30	0.53
4:4:372:PRO:HB2	4:4:398:MET:HG3	1.89	0.53
6:7:336:GLN:NE2	6:7:337:GLU:OE2	2.37	0.53
3:2:287:SER:OG	3:2:288:ALA:N	2.42	0.53
4:4:152:ASP:OD1	4:4:153:LYS:N	2.40	0.53
5:5:17:VAL:N	5:5:68:ASN:OD1	2.40	0.53
8:9:455:ILE:HB	8:9:474:PHE:HB2	1.90	0.53
9:3:31:THR:H	11:3:201:GTP:PB	2.30	0.53
7:8:169:ALA:O	7:8:173:GLN:NE2	2.39	0.53
3:2:511:VAL:HG22	3:2:531:PHE:CE1	2.44	0.53
6:7:5:LEU:HD11	6:7:249:ILE:HD11	1.90	0.53
6:7:603:LYS:HG3	6:7:709:ILE:HD11	1.89	0.53
7:8:166:LEU:H	7:8:166:LEU:HD23	1.74	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:430:VAL:O	3:2:431:HIS:HB2	2.09	0.53
3:2:2:LEU:O	3:2:3:GLN:NE2	2.42	0.53
5:5:30:LEU:HD11	5:5:51:LEU:HD22	1.91	0.53
5:5:305:ASP:OD1	8:9:7:ARG:NH1	2.27	0.53
7:8:110:ARG:HG2	7:8:113:THR:HG23	1.90	0.53
1:0:20:VAL:HG12	1:0:20:VAL:O	2.08	0.52
2:1:383:ARG:HB2	9:3:101:ARG:HD3	1.91	0.52
5:5:205:GLN:HE22	5:5:227:GLN:HB2	1.74	0.52
2:1:54:HIS:CE1	9:3:99:LYS:HB3	2.44	0.52
2:1:287:GLU:OE1	4:4:165:ASN:ND2	2.42	0.52
9:3:122:ARG:NH1	9:3:154:ASP:O	2.41	0.52
9:3:141:VAL:O	9:3:145:GLN:HG2	2.09	0.52
3:2:416:LEU:HD22	3:2:418:PHE:CE2	2.44	0.52
4:4:267:ILE:HG23	4:4:268:GLU:HG3	1.90	0.52
5:5:182:ILE:HA	5:5:187:ILE:HD12	1.91	0.52
6:7:410:GLN:NE2	6:7:439:ASN:OD1	2.42	0.52
3:2:559:ASP:N	3:2:559:ASP:OD1	2.39	0.52
3:2:44:ASN:HB3	3:2:45:PRO:HD3	1.91	0.52
3:2:204:GLU:HG3	3:2:205:ILE:H	1.74	0.52
2:1:532:ARG:NH2	8:9:761:GLN:OE1	2.36	0.52
3:2:263:GLY:HA3	3:2:289:ILE:HG21	1.91	0.52
5:5:50:LEU:HD11	5:5:57:ILE:HD11	1.92	0.52
7:8:212:TRP:O	7:8:216:GLN:HG2	2.09	0.52
6:7:552:THR:HB	6:7:568:ASP:HB3	1.92	0.52
4:4:42:TYR:HB3	4:4:51:CYS:HB2	1.91	0.52
6:7:704:ASP:HB3	6:7:707:ALA:HB3	1.91	0.52
9:3:32:THR:HG21	11:3:201:GTP:H5'	1.92	0.52
3:2:622:ARG:HB3	7:8:61:ALA:HB1	1.91	0.52
6:7:186:VAL:HG21	6:7:190:PRO:HG3	1.92	0.52
7:8:201:LEU:O	7:8:204:GLU:HG3	2.10	0.52
8:9:815:PHE:HZ	8:9:825:LEU:HD11	1.74	0.52
1:0:50:ALA:O	1:0:54:THR:HG23	2.10	0.51
9:3:118:ILE:O	9:3:155:LYS:NZ	2.33	0.51
2:1:349:ALA:HA	2:1:355:VAL:HG22	1.93	0.51
3:2:166:LEU:HD23	3:2:181:VAL:HA	1.92	0.51
6:7:24:LEU:HD12	6:7:34:LYS:HB2	1.92	0.51
6:7:95:LYS:O	6:7:96:ARG:HG3	2.11	0.51
3:2:511:VAL:HG22	3:2:531:PHE:HE1	1.76	0.51
8:9:410:ASP:OD1	8:9:410:ASP:N	2.44	0.51
8:9:513:GLU:HG2	8:9:514:ARG:HD3	1.92	0.51
9:3:91:ILE:HD13	9:3:126:LEU:HB3	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:9:250:ILE:HG12	8:9:260:VAL:HG22	1.92	0.51
3:2:412:ILE:HD13	3:2:412:ILE:N	2.26	0.51
5:5:86:SER:OG	5:5:87:LYS:N	2.43	0.51
6:7:57:VAL:HG12	6:7:58:PHE:HD1	1.75	0.51
3:2:216:ARG:HA	3:2:229:TYR:O	2.11	0.51
6:7:196:HIS:CD2	6:7:218:LEU:HD11	2.45	0.51
7:8:54:ASP:OD1	7:8:54:ASP:N	2.36	0.51
2:1:513:PRO:HB2	2:1:539:LEU:HD11	1.93	0.51
4:4:83:ILE:HD13	4:4:113:LEU:HB3	1.93	0.51
7:8:400:ASN:OD1	7:8:430:ARG:NH2	2.44	0.51
8:9:18:GLU:OE2	8:9:50:ARG:NH1	2.38	0.51
3:2:639:THR:O	3:2:643:ARG:HG2	2.11	0.51
5:5:105:ARG:HD3	8:9:7:ARG:HH22	1.76	0.51
6:7:22:LYS:HB3	6:7:71:LEU:HD23	1.91	0.51
6:7:157:ARG:NH2	6:7:201:GLY:O	2.44	0.51
8:9:642:LEU:HD11	8:9:812:ILE:HG22	1.93	0.51
3:2:21:VAL:HG11	3:2:295:GLY:HA3	1.93	0.51
6:7:588:LYS:HD2	6:7:588:LYS:O	2.11	0.51
4:4:183:ASP:OD1	4:4:184:LEU:N	2.45	0.50
6:7:13:VAL:HG22	6:7:14:GLY:H	1.76	0.50
3:2:412:ILE:HG12	3:2:439:SER:O	2.11	0.50
5:5:8:TRP:HZ2	5:5:21:GLN:HB3	1.75	0.50
5:5:181:PHE:HB2	5:5:188:VAL:HG22	1.92	0.50
5:5:22:MET:SD	5:5:68:ASN:ND2	2.84	0.50
8:9:133:ARG:HH21	8:9:174:PHE:HZ	1.60	0.50
8:9:558:SER:O	8:9:561:SER:OG	2.27	0.50
2:1:50:VAL:HG21	2:1:98:LEU:HD11	1.93	0.50
2:1:106:LEU:HD11	2:1:223:THR:HG22	1.94	0.50
4:4:87:LEU:HD11	4:4:111:LEU:HD23	1.93	0.50
6:7:644:PRO:HA	6:7:647:ARG:HB2	1.94	0.50
8:9:770:GLU:HG3	8:9:802:PRO:HD3	1.93	0.50
2:1:515:LEU:HD11	8:9:751:ILE:HG12	1.92	0.50
3:2:601:ASP:OD1	3:2:602:GLU:N	2.45	0.50
6:7:600:VAL:HA	6:7:603:LYS:HE2	1.93	0.50
9:3:23:LEU:N	9:3:91:ILE:O	2.34	0.50
1:0:14:LYS:CG	1:0:14:LYS:O	2.60	0.50
2:1:26:PHE:HA	2:1:81:THR:OG1	2.11	0.50
5:5:25:ARG:HG2	5:5:26:PRO:HD2	1.93	0.50
6:7:597:ILE:HD11	6:7:684:PHE:HD2	1.77	0.50
9:3:26:ASP:O	9:3:101:ARG:NH2	2.44	0.50
3:2:353:ARG:O	3:2:356:GLU:HG2	2.12	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:383:HIS:HE2	3:2:461:VAL:HG22	1.76	0.50
6:7:447:CYS:O	6:7:447:CYS:SG	2.70	0.50
8:9:554:LYS:NZ	8:9:632:PHE:HB2	2.27	0.50
8:9:575:VAL:HG12	8:9:576:ASN:H	1.75	0.50
5:5:155:LEU:HG	5:5:186:ARG:HH11	1.76	0.50
5:5:162:ASN:HB3	5:5:164:ILE:HD11	1.93	0.50
6:7:190:PRO:HA	6:7:211:THR:HA	1.94	0.50
7:8:176:LYS:HG3	7:8:177:LEU:HD12	1.94	0.50
7:8:241:GLN:HG2	7:8:243:MET:HE2	1.94	0.50
9:3:129:ALA:HB3	9:3:161:ALA:HA	1.92	0.50
2:1:565:LYS:HG2	2:1:581:HIS:CD2	2.46	0.50
3:2:137:ILE:HG21	3:2:179:LEU:CD2	2.42	0.50
3:2:561:ILE:HG23	3:2:681:ARG:HD2	1.94	0.50
4:4:55:ILE:HG23	4:4:69:ALA:HB1	1.94	0.50
4:4:342:MET:HG3	4:4:374:VAL:HA	1.93	0.50
6:7:66:ILE:HD12	6:7:84:ILE:HD12	1.93	0.50
8:9:20:PHE:CE1	8:9:44:SER:HB2	2.47	0.50
9:3:73:GLN:O	9:3:77:ARG:HG3	2.12	0.50
3:2:358:ASN:HD21	6:7:375:ALA:H	1.59	0.49
7:8:5:LEU:HD21	8:9:79:LEU:HD11	1.95	0.49
9:3:178:GLN:HA	9:3:181:ILE:HG22	1.94	0.49
1:0:35:PRO:HB3	7:8:106:THR:O	2.12	0.49
6:7:404:ILE:O	6:7:447:CYS:SG	2.66	0.49
8:9:108:VAL:HG22	8:9:123:ILE:HG22	1.94	0.49
8:9:679:ARG:O	8:9:683:ARG:HG2	2.12	0.49
9:3:36:LYS:HD3	9:3:43:GLN:NE2	2.27	0.49
2:1:338:GLN:NE2	2:1:386:ASN:OD1	2.30	0.49
6:7:493:LEU:O	6:7:548:THR:HG22	2.12	0.49
3:2:144:LEU:HD21	3:2:163:VAL:HG21	1.95	0.49
3:2:619:ASN:OD1	3:2:622:ARG:NH1	2.44	0.49
7:8:99:THR:HG23	7:8:105:ILE:HG22	1.95	0.49
2:1:534:PHE:HB3	8:9:460:TYR:CZ	2.48	0.49
2:1:569:LEU:HB3	2:1:576:PRO:HA	1.93	0.49
3:2:697:ALA:HB1	3:2:713:ILE:HD13	1.93	0.49
5:5:44:ASN:HD21	8:9:374:ARG:HB3	1.78	0.49
5:5:228:SER:O	5:5:228:SER:OG	2.30	0.49
7:8:58:GLU:OE2	7:8:117:ARG:NH2	2.44	0.49
2:1:536:LYS:NZ	2:1:571:GLU:OE1	2.45	0.49
8:9:44:SER:O	8:9:78:ILE:HB	2.13	0.49
1:0:17:GLN:HA	1:0:17:GLN:NE2	2.27	0.49
3:2:15:SER:HB3	3:2:18:MET:HE2	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:76:SER:OG	3:2:120:ALA:O	2.26	0.49
3:2:213:TYR:HB2	3:2:216:ARG:HE	1.77	0.49
3:2:341:LEU:HD22	6:7:345:LEU:HD13	1.95	0.49
2:1:207:LYS:HZ2	2:1:217:SER:HG	1.59	0.49
1:0:17:GLN:HE21	1:0:17:GLN:CA	2.25	0.49
6:7:623:VAL:HG21	6:7:660:TYR:CG	2.48	0.49
8:9:510:ARG:O	8:9:518:GLY:HA2	2.13	0.49
5:5:49:ARG:HE	5:5:51:LEU:HD21	1.78	0.48
2:1:200:ILE:HB	2:1:221:LEU:HD12	1.93	0.48
7:8:14:ARG:HD3	8:9:308:HIS:CE1	2.47	0.48
8:9:157:VAL:HA	8:9:181:PRO:HG3	1.93	0.48
8:9:453:GLN:HG3	8:9:509:SER:HB2	1.95	0.48
3:2:144:LEU:HD11	3:2:181:VAL:HG11	1.94	0.48
5:5:154:LEU:HD21	5:5:160:VAL:HG13	1.95	0.48
2:1:256:GLN:OE1	2:1:256:GLN:N	2.46	0.48
6:7:409:ILE:HB	6:7:443:ALA:HB3	1.94	0.48
3:2:497:SER:HB2	3:2:559:ASP:HA	1.96	0.48
5:5:76:ILE:HG22	5:5:99:THR:HG22	1.95	0.48
6:7:323:HIS:O	9:3:140:SER:OG	2.20	0.48
6:7:520:LEU:O	6:7:524:VAL:HG23	2.12	0.48
3:2:461:VAL:O	3:2:469:PHE:HB2	2.14	0.48
5:5:57:ILE:HG23	5:5:71:ILE:HB	1.96	0.48
6:7:324:LYS:HB3	9:3:161:ALA:HB3	1.96	0.48
8:9:497:PRO:HD2	8:9:534:VAL:HG21	1.96	0.48
8:9:548:LEU:HD23	8:9:609:LEU:HD23	1.95	0.48
1:0:14:LYS:O	1:0:14:LYS:HG3	2.13	0.48
3:2:178:GLU:N	3:2:178:GLU:OE1	2.46	0.48
6:7:179:ASP:OD2	6:7:179:ASP:N	2.46	0.48
8:9:826:CYS:SG	8:9:827:LEU:N	2.86	0.48
9:3:20:VAL:HG13	9:3:67:VAL:HG12	1.96	0.48
7:8:53:ILE:O	7:8:252:LYS:HD2	2.14	0.48
2:1:428:PRO:HD2	4:4:291:SER:HB3	1.96	0.48
3:2:172:ASP:C	3:2:172:ASP:OD1	2.57	0.48
6:7:360:ARG:HH21	6:7:477:GLN:HE21	1.61	0.48
8:9:588:VAL:HA	8:9:603:SER:OG	2.14	0.48
3:2:285:PHE:CD2	3:2:289:ILE:HD11	2.49	0.47
4:4:82:ASN:HD21	4:4:85:GLU:HG2	1.79	0.47
7:8:42:ARG:NH2	7:8:183:GLU:OE1	2.47	0.47
8:9:20:PHE:CE2	8:9:352:GLY:HA2	2.48	0.47
8:9:98:LEU:HD13	8:9:154:ILE:HD13	1.95	0.47
2:1:477:PRO:HG3	7:8:414:ASN:HD22	1.78	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:498:TYR:HB3	3:2:557:ASN:ND2	2.28	0.47
5:5:245:GLU:O	5:5:248:LYS:HG3	2.14	0.47
8:9:599:TYR:HE2	8:9:620:LEU:HD21	1.79	0.47
7:8:234:PHE:CE2	7:8:249:TYR:HB3	2.49	0.47
2:1:210:LEU:HB2	2:1:215:ALA:HB2	1.96	0.47
3:2:504:ALA:O	3:2:505:GLU:HG2	2.15	0.47
6:7:338:MET:HG3	6:7:341:LYS:HE2	1.96	0.47
7:8:43:ALA:O	7:8:47:MET:HG3	2.14	0.47
2:1:455:ASP:HB3	7:8:366:LEU:HD12	1.96	0.47
3:2:413:ARG:HD3	3:2:437:LEU:HD21	1.97	0.47
3:2:503:ILE:HG13	3:2:504:ALA:H	1.77	0.47
5:5:297:ASP:O	8:9:371:VAL:HG23	2.14	0.47
6:7:109:GLU:HG2	6:7:110:SER:N	2.30	0.47
6:7:643:ILE:HG12	6:7:645:GLU:H	1.79	0.47
2:1:338:GLN:HE22	2:1:385:ASP:HB3	1.80	0.47
3:2:527:GLN:HG2	3:2:528:ASN:H	1.79	0.47
3:2:607:HIS:NE2	8:9:687:LYS:HE2	2.30	0.47
4:4:128:ALA:HB2	4:4:137:ILE:HG21	1.96	0.47
6:7:507:ASN:ND2	6:7:598:ASN:H	2.11	0.47
1:0:14:LYS:O	1:0:14:LYS:HD2	2.14	0.47
2:1:538:PRO:HB3	8:9:758:PRO:HB2	1.97	0.47
4:4:361:TYR:OH	4:4:377:ASN:HB3	2.14	0.47
8:9:199:CYS:O	8:9:201:GLN:HG2	2.15	0.47
8:9:417:VAL:HG13	8:9:442:VAL:HG22	1.95	0.47
8:9:808:LEU:O	8:9:812:ILE:HG13	2.15	0.47
9:3:99:LYS:HG2	9:3:138:LEU:HD11	1.96	0.47
2:1:510:THR:OG1	2:1:511:ALA:N	2.46	0.47
6:7:357:LEU:HD22	6:7:360:ARG:HH12	1.80	0.47
9:3:20:VAL:HG23	9:3:89:ALA:HB3	1.97	0.47
3:2:120:ALA:HB2	3:2:138:ILE:HD11	1.97	0.47
3:2:460:PHE:HB3	3:2:469:PHE:CE2	2.44	0.47
6:7:477:GLN:HB3	6:7:478:PRO:HD3	1.97	0.47
6:7:655:HIS:HA	6:7:658:GLU:HG3	1.97	0.47
2:1:33:LYS:HG3	2:1:52:LYS:HB2	1.96	0.47
2:1:268:ARG:HG2	4:4:40:HIS:CD2	2.50	0.47
3:2:159:THR:HG21	3:2:163:VAL:HG23	1.97	0.47
6:7:357:LEU:HD22	6:7:360:ARG:NH1	2.30	0.47
8:9:661:LYS:O	8:9:664:GLU:HG3	2.15	0.47
2:1:473:SER:OG	8:9:515:ASN:ND2	2.48	0.46
3:2:547:LYS:HB2	3:2:555:THR:OG1	2.14	0.46
3:2:654:LEU:HD23	3:2:654:LEU:HA	1.75	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:693:GLN:O	3:2:696:THR:OG1	2.30	0.46
5:5:171:SER:HB3	8:9:115:VAL:HG11	1.97	0.46
6:7:268:VAL:HG23	6:7:280:ARG:HB2	1.96	0.46
3:2:6:PHE:CE2	3:2:316:GLY:HA3	2.50	0.46
6:7:17:SER:HG	6:7:40:HIS:CE1	2.32	0.46
5:5:136:MET:HE3	5:5:146:LEU:HD21	1.98	0.46
5:5:189:TRP:O	5:5:198:ASN:HA	2.15	0.46
6:7:15:VAL:O	6:7:40:HIS:ND1	2.49	0.46
6:7:166:ALA:HB2	6:7:193:LEU:HD21	1.96	0.46
6:7:575:ILE:O	6:7:579:VAL:HG12	2.14	0.46
2:1:314:PHE:CE1	2:1:320:ARG:HB2	2.51	0.46
3:2:247:ILE:HB	3:2:260:LEU:CD2	2.45	0.46
6:7:209:PHE:CE1	6:7:217:GLY:HA3	2.50	0.46
3:2:137:ILE:HG21	3:2:179:LEU:HD22	1.98	0.46
6:7:181:THR:HG22	6:7:182:TYR:HD1	1.81	0.46
6:7:211:THR:OG1	6:7:215:LYS:HB2	2.15	0.46
6:7:417:LEU:HD23	6:7:445:TYR:HE1	1.80	0.46
6:7:681:LYS:HE2	6:7:712:PHE:HD1	1.81	0.46
7:8:424:ALA:HB2	7:8:439:LEU:HB2	1.98	0.46
8:9:205:TYR:CE1	8:9:235:VAL:HG22	2.51	0.46
2:1:350:LEU:HD11	2:1:356:ARG:HD2	1.97	0.46
3:2:23:ARG:HA	3:2:29:PRO:HA	1.98	0.46
3:2:171:PHE:CZ	3:2:217:PHE:HE1	2.33	0.46
3:2:652:LYS:HA	3:2:652:LYS:HD3	1.66	0.46
6:7:214:GLY:O	6:7:215:LYS:HG3	2.14	0.46
6:7:247:PHE:HB3	6:7:258:LEU:HD11	1.97	0.46
3:2:416:LEU:CD2	3:2:427:SER:HB2	2.45	0.46
4:4:143:VAL:HG23	4:4:173:MET:HE2	1.98	0.46
7:8:210:ASP:OD2	7:8:213:TRP:HD1	1.98	0.46
8:9:537:PRO:HB3	8:9:566:PHE:HB3	1.98	0.46
9:3:33:ILE:HG21	9:3:93:VAL:HG11	1.98	0.46
3:2:468:GLN:HG2	6:7:376:VAL:HG11	1.98	0.46
6:7:6:ASN:ND2	6:7:320:GLU:O	2.49	0.46
6:7:199:ASN:OD1	6:7:200:GLY:N	2.49	0.46
8:9:324:THR:HG21	8:9:359:LEU:HD22	1.97	0.46
2:1:522:LEU:HB2	2:1:565:LYS:HB2	1.96	0.46
7:8:461:SER:O	7:8:465:GLY:N	2.43	0.46
2:1:380:ARG:HG3	2:1:385:ASP:OD2	2.16	0.46
3:2:419:ALA:HB2	3:2:455:LEU:HD23	1.98	0.46
6:7:85:ALA:HB2	6:7:90:ILE:HG12	1.97	0.46
6:7:205:GLU:N	6:7:205:GLU:OE1	2.48	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:7:544:TYR:CE1	6:7:555:GLU:HG3	2.50	0.46
8:9:49:LEU:HD11	8:9:95:LEU:HD21	1.98	0.46
2:1:5:ASP:OD1	2:1:400:LYS:NZ	2.49	0.45
2:1:476:SER:HA	7:8:411:VAL:HG22	1.97	0.45
3:2:248:HIS:HB3	3:2:292:VAL:HG23	1.97	0.45
4:4:414:ASP:N	4:4:415:PRO:CD	2.78	0.45
5:5:149:ASN:OD1	5:5:150:LYS:N	2.49	0.45
6:7:147:ILE:HD13	6:7:165:LEU:HD11	1.98	0.45
6:7:491:LEU:HD23	6:7:494:HIS:CE1	2.51	0.45
8:9:588:VAL:HG22	8:9:608:ASP:HB3	1.97	0.45
2:1:373:VAL:HG13	2:1:373:VAL:O	2.15	0.45
4:4:113:LEU:HD22	7:8:467:LEU:HD12	1.98	0.45
8:9:154:ILE:HD12	8:9:164:PHE:HE2	1.81	0.45
8:9:535:CYS:SG	8:9:580:PHE:HB3	2.56	0.45
2:1:441:GLU:OE2	4:4:322:SER:OG	2.27	0.45
3:2:341:LEU:HD12	3:2:341:LEU:H	1.82	0.45
6:7:17:SER:OG	6:7:40:HIS:NE2	2.50	0.45
9:3:158:HIS:HB2	9:3:176:TRP:CZ2	2.52	0.45
3:2:264:TRP:HE1	3:2:270:ASP:CG	2.21	0.45
3:2:298:ARG:NE	3:2:300:GLU:OE2	2.30	0.45
3:2:298:ARG:HD3	3:2:304:GLN:HE22	1.81	0.45
4:4:342:MET:HG3	4:4:374:VAL:HG22	1.98	0.45
5:5:299:PHE:HD1	5:5:299:PHE:H	1.64	0.45
3:2:450:ASP:OD2	3:2:484:TYR:OH	2.25	0.45
3:2:635:ARG:NH2	8:9:663:GLU:OE2	2.49	0.45
6:7:175:LEU:H	6:7:175:LEU:HD23	1.80	0.45
6:7:515:PHE:HE1	6:7:589:ILE:HG21	1.80	0.45
8:9:204:SER:O	8:9:236:ASP:HB3	2.16	0.45
8:9:307:ASN:HB3	8:9:309:ASN:H	1.81	0.45
2:1:66:PRO:HB3	2:1:86:ILE:HD11	1.99	0.45
3:2:77:CYS:HB3	3:2:123:ILE:HG12	1.97	0.45
3:2:212:MET:HG3	3:2:249:ALA:HB3	1.99	0.45
3:2:383:HIS:CE1	3:2:406:THR:HG23	2.52	0.45
3:2:565:GLY:HA2	3:2:685:LEU:HD12	1.99	0.45
1:0:29:CYS:N	7:8:422:ASN:HD21	2.15	0.45
4:4:247:GLN:NE2	4:4:275:ASN:O	2.50	0.45
6:7:300:ASP:OD1	6:7:300:ASP:N	2.49	0.45
8:9:701:GLY:O	8:9:705:GLN:HG2	2.16	0.45
9:3:44:SER:OG	9:3:45:GLN:N	2.50	0.45
2:1:326:MET:HE1	2:1:358:TYR:CZ	2.51	0.45
3:2:411:ILE:HG21	3:2:437:LEU:HB3	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:9:411:LEU:HD12	8:9:452:LEU:HD12	1.99	0.45
3:2:23:ARG:N	3:2:90:ASP:OD2	2.37	0.45
3:2:259:GLU:HG3	3:2:273:SER:HA	1.99	0.45
5:5:145:ALA:HB2	8:9:71:GLU:O	2.17	0.45
8:9:27:LEU:HD21	8:9:336:GLY:HA3	1.98	0.45
8:9:187:SER:HA	8:9:250:ILE:HG21	1.98	0.45
2:1:80:ARG:HG2	2:1:81:THR:HG22	1.98	0.44
3:2:339:ARG:O	3:2:342:SER:OG	2.32	0.44
4:4:90:PHE:CD2	4:4:106:GLN:HB3	2.52	0.44
9:3:25:LEU:HD23	9:3:77:ARG:HH22	1.82	0.44
9:3:97:SER:HA	9:3:137:ALA:HA	1.99	0.44
2:1:80:ARG:HD3	2:1:97:ASN:HD21	1.82	0.44
4:4:85:GLU:OE1	4:4:88:ARG:NH1	2.50	0.44
7:8:196:LEU:HD12	7:8:220:CYS:HB3	1.99	0.44
7:8:294:ILE:O	7:8:298:THR:HG23	2.17	0.44
8:9:453:GLN:HG2	8:9:511:PRO:HD3	1.99	0.44
9:3:25:LEU:HD12	9:3:25:LEU:H	1.82	0.44
2:1:232:ASP:CG	2:1:237:THR:H	2.25	0.44
6:7:184:ILE:HG12	6:7:226:PRO:HB3	1.99	0.44
8:9:739:GLY:HA2	8:9:744:LEU:HB2	1.99	0.44
2:1:310:SER:OG	2:1:312:HIS:NE2	2.51	0.44
3:2:529:ALA:HB3	3:2:530:PRO:HD3	1.99	0.44
6:7:41:ASP:O	6:7:63:GLY:N	2.47	0.44
6:7:370:SER:OG	6:7:371:LYS:N	2.50	0.44
5:5:161:TYR:CE1	5:5:184:ASN:HB3	2.53	0.44
5:5:299:PHE:N	5:5:299:PHE:CD1	2.85	0.44
5:5:308:LYS:HE2	8:9:2:SER:HB2	1.98	0.44
6:7:231:GLU:HG2	6:7:233:ARG:H	1.82	0.44
2:1:74:MET:HE2	2:1:96:LYS:HE2	1.99	0.44
6:7:39:ASP:OD1	6:7:40:HIS:N	2.49	0.44
6:7:208:LEU:HA	6:7:217:GLY:O	2.18	0.44
6:7:629:LEU:HB3	6:7:650:LEU:HD21	1.98	0.44
7:8:4:LEU:HB2	7:8:26:MET:HE1	1.99	0.44
2:1:23:LEU:HD22	2:1:381:TYR:HB2	1.99	0.44
2:1:53:GLY:O	2:1:381:TYR:OH	2.31	0.44
5:5:183:THR:OG1	5:5:186:ARG:O	2.27	0.44
6:7:2:ASP:OD1	6:7:2:ASP:N	2.50	0.44
8:9:456:LYS:O	8:9:506:VAL:HA	2.18	0.44
4:4:47:ASP:OD2	4:4:50:ALA:N	2.42	0.44
4:4:79:LEU:HD23	4:4:79:LEU:HA	1.82	0.44
2:1:430:LYS:HA	2:1:430:LYS:HD3	1.81	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:7:553:GLN:N	6:7:553:GLN:OE1	2.51	0.44
6:7:632:LEU:HD21	8:9:676:ILE:HG12	2.00	0.44
7:8:58:GLU:O	7:8:62:GLU:HB2	2.17	0.44
4:4:415:PRO:O	4:4:418:VAL:HG22	2.18	0.43
6:7:643:ILE:HG23	6:7:646:TYR:H	1.83	0.43
7:8:37:TRP:HZ2	7:8:161:ILE:HD12	1.83	0.43
7:8:162:ASN:HB3	7:8:165:ARG:HG2	1.99	0.43
7:8:196:LEU:HD11	7:8:221:TYR:CE1	2.53	0.43
7:8:332:LEU:HB2	7:8:355:CYS:HB3	2.00	0.43
8:9:548:LEU:HD22	8:9:737:LEU:HD11	2.00	0.43
1:0:41:LEU:HB2	7:8:111:PRO:HD3	2.00	0.43
2:1:259:VAL:HG22	2:1:260:GLU:OE1	2.18	0.43
5:5:298:ALA:O	5:5:299:PHE:C	2.61	0.43
6:7:417:LEU:HD23	6:7:445:TYR:CE1	2.52	0.43
8:9:278:GLN:HG2	8:9:279:PHE:CD2	2.52	0.43
8:9:814:LEU:HD21	8:9:818:ARG:CZ	2.48	0.43
9:3:147:LEU:HB3	9:3:149:LEU:CD1	2.48	0.43
5:5:190:HIS:HA	5:5:198:ASN:HB3	2.00	0.43
6:7:139:HIS:NE2	6:7:177:GLY:HA2	2.32	0.43
6:7:654:ASP:OD1	6:7:654:ASP:N	2.51	0.43
8:9:9:TRP:HE3	8:9:356:CYS:HB2	1.83	0.43
5:5:253:LEU:HA	5:5:256:VAL:HG12	2.00	0.43
6:7:158:LEU:HD12	6:7:160:ARG:NH2	2.34	0.43
6:7:500:ILE:HD11	6:7:502:HIS:CE1	2.53	0.43
7:8:60:ILE:HG22	7:8:139:SER:HA	2.00	0.43
8:9:374:ARG:HA	8:9:374:ARG:HD3	1.81	0.43
8:9:376:LEU:HD23	8:9:378:TYR:HE1	1.83	0.43
9:3:126:LEU:HD12	9:3:158:HIS:O	2.18	0.43
1:0:20:VAL:O	1:0:20:VAL:CG1	2.67	0.43
3:2:171:PHE:CE1	3:2:217:PHE:HE1	2.36	0.43
4:4:311:GLY:HA3	4:4:327:LEU:HG	2.00	0.43
5:5:191:ALA:C	5:5:193:MET:H	2.26	0.43
6:7:15:VAL:HG13	6:7:40:HIS:HB2	1.99	0.43
6:7:490:PRO:HB2	6:7:491:LEU:HD12	2.00	0.43
8:9:10:TRP:NE1	8:9:67:ASP:OD2	2.52	0.43
8:9:99:HIS:HB2	8:9:102:LYS:HB3	1.99	0.43
2:1:266:ALA:HB2	2:1:295:LEU:HD22	2.01	0.43
2:1:518:VAL:HG21	2:1:534:PHE:CZ	2.53	0.43
4:4:203:GLU:OE2	4:4:237:LYS:NZ	2.52	0.43
5:5:9:GLU:HB3	5:5:56:ARG:HD3	2.01	0.43
6:7:196:HIS:O	6:7:196:HIS:CG	2.72	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:9:129:HIS:NE2	8:9:168:SER:HA	2.34	0.43
8:9:272:LYS:HG3	8:9:278:GLN:HB2	2.01	0.43
9:3:17:GLU:N	9:3:64:SER:O	2.52	0.43
9:3:34:ILE:HG21	9:3:67:VAL:HG21	2.00	0.43
2:1:505:LEU:HD23	2:1:506:GLN:N	2.33	0.43
3:2:243:GLN:O	3:2:265:SER:OG	2.33	0.43
3:2:539:ARG:O	3:2:540:ASN:ND2	2.52	0.43
3:2:546:ILE:HD13	3:2:556:VAL:HG22	2.00	0.43
4:4:46:LYS:HA	4:4:48:TYR:CZ	2.54	0.43
5:5:319:GLU:O	8:9:296:VAL:HG21	2.19	0.43
6:7:428:SER:OG	6:7:444:THR:HB	2.18	0.43
7:8:24:THR:O	7:8:28:GLU:HG2	2.19	0.43
9:3:39:PRO:O	9:3:43:GLN:HB2	2.18	0.43
3:2:84:ASN:OD1	3:2:84:ASN:N	2.51	0.43
3:2:532:GLN:HG3	3:2:547:LYS:HG2	2.00	0.43
3:2:547:LYS:NZ	3:2:557:ASN:OD1	2.49	0.43
6:7:45:MET:HE3	6:7:59:LYS:HG3	2.00	0.43
7:8:278:VAL:HG13	7:8:304:VAL:HG13	1.99	0.43
8:9:154:ILE:HD12	8:9:164:PHE:CE2	2.54	0.43
8:9:669:ARG:HD3	8:9:669:ARG:HA	1.82	0.43
8:9:14:LEU:HD12	8:9:14:LEU:HA	1.72	0.43
2:1:225:ASN:O	2:1:227:GLU:N	2.52	0.43
4:4:191:TYR:O	4:4:195:VAL:HG23	2.19	0.43
6:7:235:GLU:N	6:7:235:GLU:OE1	2.52	0.43
7:8:210:ASP:OD1	7:8:210:ASP:N	2.51	0.43
8:9:48:TYR:CD1	8:9:73:HIS:HB2	2.54	0.43
3:2:533:VAL:HG23	3:2:546:ILE:HB	2.01	0.42
5:5:173:ASP:OD1	5:5:173:ASP:N	2.51	0.42
2:1:309:ASP:HB3	2:1:328:ALA:O	2.19	0.42
3:2:348:LEU:HD13	6:7:352:LEU:HB3	2.01	0.42
6:7:13:VAL:O	6:7:312:GLY:HA3	2.20	0.42
8:9:204:SER:HG	8:9:237:TRP:CD1	2.37	0.42
2:1:263:LEU:HB2	2:1:275:LEU:HB2	2.00	0.42
5:5:220:LEU:HD11	5:5:243:LEU:HG	2.02	0.42
6:7:266:VAL:O	6:7:282:ASP:HA	2.19	0.42
6:7:387:LEU:HD12	6:7:394:TYR:CZ	2.54	0.42
2:1:272:ILE:HB	2:1:286:ILE:CG1	2.49	0.42
2:1:564:ILE:HD12	2:1:584:MET:HE3	2.01	0.42
6:7:613:LEU:HG	6:7:670:LEU:HD13	2.01	0.42
2:1:223:THR:OG1	2:1:225:ASN:O	2.24	0.42
2:1:381:TYR:HB3	2:1:387:THR:HG21	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:5:VAL:HG21	3:2:318:LEU:HD23	2.01	0.42
3:2:31:LEU:O	3:2:42:ILE:HA	2.19	0.42
4:4:317:MET:HE3	4:4:317:MET:HB3	1.87	0.42
6:7:151:ILE:HD12	6:7:194:ALA:HA	2.02	0.42
6:7:506:MET:HA	6:7:567:SER:O	2.20	0.42
8:9:124:LYS:HA	8:9:124:LYS:HD3	1.81	0.42
8:9:610:TRP:HB2	8:9:733:LEU:HB2	2.01	0.42
2:1:228:LEU:HB2	2:1:242:MET:HB2	2.01	0.42
3:2:102:ALA:HB3	3:2:111:LEU:HB2	2.01	0.42
3:2:513:TRP:HD1	3:2:574:PHE:CG	2.37	0.42
5:5:159:ASN:OD1	5:5:160:VAL:N	2.53	0.42
5:5:179:THR:HB	5:5:190:HIS:CE1	2.54	0.42
6:7:699:ILE:O	6:7:703:TYR:N	2.22	0.42
9:3:139:THR:OG1	9:3:142:LYS:HG2	2.19	0.42
2:1:487:LYS:HE3	2:1:506:GLN:HB3	2.02	0.42
3:2:383:HIS:NE2	3:2:461:VAL:HG22	2.35	0.42
6:7:22:LYS:HD3	6:7:22:LYS:HA	1.91	0.42
6:7:704:ASP:O	6:7:708:LEU:N	2.48	0.42
1:0:12:LEU:HD13	4:4:315:LEU:HB3	2.01	0.42
2:1:242:MET:SD	2:1:280:LYS:HA	2.59	0.42
3:2:15:SER:HB2	3:2:34:ALA:HB3	2.02	0.42
4:4:246:MET:HE1	4:4:258:LYS:HZ3	1.85	0.42
5:5:99:THR:OG1	5:5:106:PHE:HB2	2.19	0.42
6:7:511:LEU:HD23	6:7:591:LEU:HD22	2.01	0.42
7:8:75:ARG:O	7:8:78:THR:HG22	2.20	0.42
8:9:464:PRO:HG2	8:9:497:PRO:HA	2.00	0.42
6:7:417:LEU:HD13	6:7:441:LEU:HD21	2.02	0.42
8:9:7:ARG:HD3	8:9:7:ARG:HA	1.80	0.42
8:9:389:GLN:HG2	8:9:393:LYS:HZ3	1.84	0.42
2:1:48:LEU:HD12	2:1:86:ILE:HD13	2.02	0.42
2:1:404:ARG:HH21	9:3:77:ARG:HD3	1.85	0.42
8:9:390:LYS:HB3	8:9:390:LYS:HE2	1.81	0.42
8:9:577:VAL:HG13	8:9:591:LEU:HD23	2.02	0.42
3:2:484:TYR:HD1	3:2:537:SER:HA	1.85	0.41
3:2:501:PHE:CE2	3:2:554:ILE:HD12	2.55	0.41
5:5:15:PHE:HD1	5:5:69:LEU:HD23	1.84	0.41
6:7:170:ARG:HA	6:7:190:PRO:HD3	2.02	0.41
6:7:396:LEU:HD11	6:7:486:TYR:CE2	2.55	0.41
6:7:689:VAL:HG13	6:7:692:LYS:HD3	2.01	0.41
8:9:79:LEU:O	8:9:98:LEU:HB3	2.20	0.41
2:1:86:ILE:HG23	2:1:93:TYR:HB2	2.01	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:7:342:ILE:O	6:7:345:LEU:HG	2.20	0.41
8:9:656:ARG:NH2	8:9:770:GLU:OE2	2.48	0.41
6:7:257:LEU:HB3	6:7:269:TYR:HB2	2.02	0.41
6:7:491:LEU:HB3	6:7:494:HIS:ND1	2.34	0.41
8:9:593:SER:HB3	8:9:598:ARG:O	2.20	0.41
1:0:8:PHE:HE2	4:4:420:VAL:HA	1.84	0.41
2:1:272:ILE:HB	2:1:286:ILE:HG13	2.03	0.41
2:1:373:VAL:HG21	2:1:390:MET:HB2	2.03	0.41
3:2:709:MET:O	3:2:713:ILE:HG13	2.20	0.41
4:4:218:TYR:CE1	4:4:245:MET:HG2	2.55	0.41
4:4:412:GLU:O	4:4:415:PRO:HD2	2.20	0.41
6:7:381:VAL:HA	6:7:399:GLU:O	2.19	0.41
7:8:2:GLU:OE1	8:9:134:THR:OG1	2.28	0.41
8:9:375:GLU:HG2	8:9:376:LEU:N	2.36	0.41
8:9:676:ILE:HG23	8:9:695:LEU:HD22	2.02	0.41
9:3:22:CYS:HA	9:3:91:ILE:HB	2.01	0.41
2:1:334:ASN:ND2	2:1:376:LEU:O	2.48	0.41
2:1:477:PRO:HG3	7:8:414:ASN:ND2	2.34	0.41
2:1:530:LEU:HD23	2:1:530:LEU:HA	1.83	0.41
2:1:534:PHE:HB3	8:9:460:TYR:CE2	2.55	0.41
3:2:417:ILE:HG23	3:2:457:LEU:HD23	2.02	0.41
3:2:623:SER:O	3:2:627:GLN:HG3	2.20	0.41
4:4:210:LEU:O	4:4:214:GLN:HG2	2.20	0.41
5:5:246:SER:O	5:5:249:GLU:HG3	2.21	0.41
6:7:540:CYS:HB2	6:7:559:ARG:HG3	2.03	0.41
9:3:54:SER:OG	9:3:55:ILE:N	2.54	0.41
2:1:207:LYS:HE3	2:1:207:LYS:HA	2.03	0.41
3:2:8:LEU:HD12	3:2:8:LEU:HA	1.88	0.41
5:5:41:LYS:HG2	5:5:107:GLU:O	2.21	0.41
8:9:27:LEU:HD11	8:9:338:LEU:HD21	2.02	0.41
8:9:526:LYS:HE2	8:9:526:LYS:HB3	1.95	0.41
9:3:32:THR:HG22	11:3:201:GTP:O5'	2.21	0.41
9:3:142:LYS:O	9:3:146:LEU:HG	2.20	0.41
2:1:206:LEU:HD12	2:1:207:LYS:H	1.85	0.41
2:1:516:GLY:O	2:1:570:ARG:HD3	2.19	0.41
3:2:6:PHE:CZ	3:2:316:GLY:HA3	2.56	0.41
5:5:48:GLY:HA2	5:5:61:SER:C	2.46	0.41
5:5:105:ARG:HD3	8:9:7:ARG:NH2	2.35	0.41
7:8:182:PHE:CE2	7:8:216:GLN:HB3	2.56	0.41
1:0:26:MET:HE3	7:8:456:ASN:HB3	2.03	0.41
2:1:206:LEU:HD13	2:1:253:ALA:HB1	2.01	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:258:ASP:OD2	2:1:259:VAL:N	2.54	0.41
2:1:355:VAL:CG2	2:1:373:VAL:HG11	2.51	0.41
2:1:380:ARG:HA	2:1:384:GLU:O	2.21	0.41
2:1:487:LYS:HE3	2:1:487:LYS:HB3	1.93	0.41
3:2:103:TYR:OH	3:2:108:ASN:HB2	2.21	0.41
4:4:342:MET:O	4:4:346:VAL:HG23	2.21	0.41
6:7:607:LYS:HE3	6:7:607:LYS:HB2	1.87	0.41
7:8:381:GLU:O	7:8:385:VAL:HG23	2.21	0.41
1:0:7:MET:O	1:0:7:MET:CG	2.68	0.41
2:1:63:PRO:HG3	2:1:93:TYR:CZ	2.55	0.41
2:1:234:GLU:HB2	2:1:236:PHE:CD2	2.56	0.41
2:1:356:ARG:HD3	2:1:358:TYR:HE2	1.85	0.41
2:1:513:PRO:HG3	8:9:778:HIS:CD2	2.56	0.41
2:1:588:GLU:OE1	7:8:139:SER:OG	2.25	0.41
3:2:186:PHE:HE1	3:2:205:ILE:HG23	1.86	0.41
3:2:386:ALA:HB3	3:2:403:CYS:SG	2.61	0.41
3:2:431:HIS:O	3:2:431:HIS:ND1	2.53	0.41
3:2:499:VAL:HA	3:2:584:ALA:HA	2.03	0.41
3:2:684:HIS:HA	3:2:691:LYS:HE2	2.03	0.41
4:4:247:GLN:NE2	4:4:259:TYR:HE2	2.19	0.41
5:5:22:MET:HA	5:5:56:ARG:NH1	2.36	0.41
6:7:22:LYS:O	6:7:23:LEU:HD23	2.21	0.41
6:7:396:LEU:HD22	6:7:456:LEU:HD21	2.03	0.41
7:8:280:LEU:O	7:8:284:ILE:HG13	2.21	0.41
7:8:458:ALA:HB2	7:8:473:ALA:HB3	2.02	0.41
8:9:776:LEU:HD23	8:9:776:LEU:HA	1.93	0.41
3:2:74:THR:O	3:2:96:THR:HG23	2.21	0.41
3:2:230:ASP:OD1	3:2:233:ALA:N	2.54	0.41
4:4:108:ALA:HB2	4:4:123:VAL:HB	2.02	0.41
2:1:434:TYR:O	2:1:438:THR:HG23	2.21	0.40
3:2:283:ASP:OD1	3:2:284:ASN:N	2.54	0.40
5:5:308:LYS:HE3	5:5:310:GLN:O	2.21	0.40
6:7:121:LEU:HD21	6:7:123:LEU:HD23	2.03	0.40
2:1:433:LEU:HD11	7:8:333:ARG:HD2	2.03	0.40
2:1:529:ALA:HB2	2:1:555:LEU:HD11	2.03	0.40
3:2:429:VAL:HG23	6:7:430:SER:OG	2.21	0.40
3:2:486:LEU:HA	3:2:535:PHE:HD1	1.85	0.40
5:5:137:TYR:CD1	5:5:264:GLY:HA3	2.55	0.40
8:9:686:ASP:OD1	8:9:687:LYS:N	2.54	0.40
8:9:788:SER:HA	8:9:791:GLN:HB2	2.03	0.40
2:1:319:LYS:HD2	2:1:319:LYS:HA	1.81	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:384:GLU:OE1	2:1:384:GLU:N	2.54	0.40
3:2:5:VAL:N	3:2:316:GLY:O	2.55	0.40
3:2:13:LYS:H	3:2:13:LYS:HG2	1.72	0.40
3:2:416:LEU:CD2	3:2:416:LEU:C	2.94	0.40
3:2:569:GLN:HE22	3:2:691:LYS:NZ	2.19	0.40
4:4:266:VAL:O	4:4:266:VAL:HG23	2.21	0.40
5:5:182:ILE:HD13	5:5:249:GLU:OE2	2.21	0.40
5:5:184:ASN:OD1	5:5:185:VAL:HG13	2.21	0.40
6:7:160:ARG:H	6:7:160:ARG:HD3	1.85	0.40
6:7:504:ARG:HD3	6:7:568:ASP:OD2	2.21	0.40
7:8:238:LEU:HD22	7:8:242:GLU:HG3	2.03	0.40
2:1:349:ALA:HB2	2:1:376:LEU:HD11	2.02	0.40
3:2:35:THR:HG22	3:2:36:GLN:N	2.36	0.40
3:2:429:VAL:HG12	3:2:430:VAL:O	2.21	0.40
3:2:624:LEU:HA	3:2:624:LEU:HD23	1.89	0.40
6:7:164:VAL:HG21	6:7:207:LEU:HD22	2.04	0.40
7:8:22:LEU:O	7:8:25:GLN:HB2	2.20	0.40
7:8:234:PHE:HB3	7:8:250:LEU:HG	2.02	0.40
8:9:333:VAL:O	8:9:334:ARG:NH1	2.51	0.40
8:9:342:LYS:HB3	8:9:342:LYS:HE2	1.73	0.40
8:9:599:TYR:CD2	8:9:616:LEU:HD11	2.57	0.40
9:3:27:ASN:N	11:3:201:GTP:O2G	2.48	0.40
9:3:149:LEU:HD23	9:3:157:TRP:CD1	2.56	0.40
2:1:244:LEU:HD12	2:1:245:PRO:HD2	2.04	0.40
3:2:402:LEU:HD21	3:2:457:LEU:HD11	2.03	0.40
3:2:483:MET:HB3	3:2:538:LEU:HD12	2.04	0.40
3:2:527:GLN:HG2	3:2:528:ASN:N	2.37	0.40
3:2:655:LEU:O	3:2:659:LYS:HG2	2.21	0.40
6:7:55:VAL:HG23	6:7:55:VAL:O	2.20	0.40
8:9:103:LEU:HD13	8:9:154:ILE:HD11	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	0	50/69 (72%)	49 (98%)	1 (2%)	0	100	100
2	1	478/592 (81%)	439 (92%)	39 (8%)	0	100	100
3	2	649/721 (90%)	598 (92%)	50 (8%)	1 (0%)	43	74
4	4	387/519 (75%)	373 (96%)	14 (4%)	0	100	100
5	5	294/341 (86%)	259 (88%)	34 (12%)	1 (0%)	36	67
6	7	700/715 (98%)	629 (90%)	70 (10%)	1 (0%)	48	79
7	8	469/501 (94%)	449 (96%)	20 (4%)	0	100	100
8	9	752/887 (85%)	705 (94%)	47 (6%)	0	100	100
9	3	165/186 (89%)	156 (94%)	9 (6%)	0	100	100
All	All	3944/4531 (87%)	3657 (93%)	284 (7%)	3 (0%)	49	79

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	2	431	HIS
5	5	87	LYS
6	7	444	THR

5.3.2 Protein sidechains [i](#)

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	0	49/65 (75%)	48 (98%)	1 (2%)	48	67
2	1	413/499 (83%)	409 (99%)	4 (1%)	68	75
3	2	567/618 (92%)	559 (99%)	8 (1%)	59	71
4	4	336/438 (77%)	333 (99%)	3 (1%)	70	76
5	5	268/307 (87%)	267 (100%)	1 (0%)	84	81
6	7	629/638 (99%)	627 (100%)	2 (0%)	86	83
7	8	402/423 (95%)	399 (99%)	3 (1%)	76	78

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	9	680/787 (86%)	677 (100%)	3 (0%)	84	81
9	3	151/167 (90%)	151 (100%)	0	100	100
All	All	3495/3942 (89%)	3470 (99%)	25 (1%)	73	78

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	17	GLN
2	1	376	LEU
2	1	391	THR
2	1	392	THR
2	1	488	LEU
3	2	171	PHE
3	2	172	ASP
3	2	252	LEU
3	2	257	VAL
3	2	260	LEU
3	2	412	ILE
3	2	416	LEU
3	2	461	VAL
4	4	409	SER
4	4	411	LEU
4	4	413	PHE
5	5	299	PHE
6	7	444	THR
6	7	447	CYS
7	8	18	LEU
7	8	19	CYS
7	8	22	LEU
8	9	361	THR
8	9	364	SER
8	9	365	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (83) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	17	GLN
2	1	15	HIS
2	1	45	GLN
2	1	54	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	1	97	ASN
2	1	225	ASN
2	1	291	GLN
2	1	359	HIS
3	2	3	GLN
3	2	28	HIS
3	2	107	ASN
3	2	343	GLN
3	2	347	ASN
3	2	358	ASN
3	2	468	GLN
3	2	470	HIS
3	2	532	GLN
3	2	540	ASN
3	2	569	GLN
3	2	627	GLN
3	2	642	ASN
3	2	651	ASN
3	2	656	ASN
3	2	665	HIS
3	2	684	HIS
4	4	35	GLN
4	4	40	HIS
4	4	58	GLN
4	4	91	GLN
4	4	167	HIS
4	4	224	HIS
4	4	375	ASN
4	4	377	ASN
5	5	44	ASN
5	5	78	ASN
5	5	165	ASN
5	5	176	ASN
5	5	190	HIS
5	5	192	ASN
5	5	205	GLN
5	5	251	ASN
6	7	6	ASN
6	7	99	GLN
6	7	196	HIS
6	7	293	GLN
6	7	477	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	7	498	HIS
6	7	502	HIS
6	7	507	ASN
6	7	569	ASN
6	7	604	HIS
6	7	635	HIS
6	7	663	GLN
7	8	216	GLN
7	8	233	GLN
7	8	241	GLN
7	8	350	ASN
7	8	351	ASN
7	8	360	GLN
7	8	388	ASN
7	8	422	ASN
7	8	435	GLN
7	8	449	HIS
7	8	454	HIS
7	8	456	ASN
7	8	496	GLN
8	9	22	GLN
8	9	37	GLN
8	9	201	GLN
8	9	276	GLN
8	9	313	HIS
8	9	448	ASN
8	9	515	ASN
8	9	652	HIS
8	9	693	GLN
8	9	705	GLN
8	9	742	GLN
8	9	748	GLN
8	9	778	HIS
9	3	19	HIS
9	3	27	ASN
9	3	35	ASN
9	3	43	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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
11	GTP	3	201	-	33,34,34	0.57	0	50,54,54	0.69	0

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
11	GTP	3	201	-	-	3/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

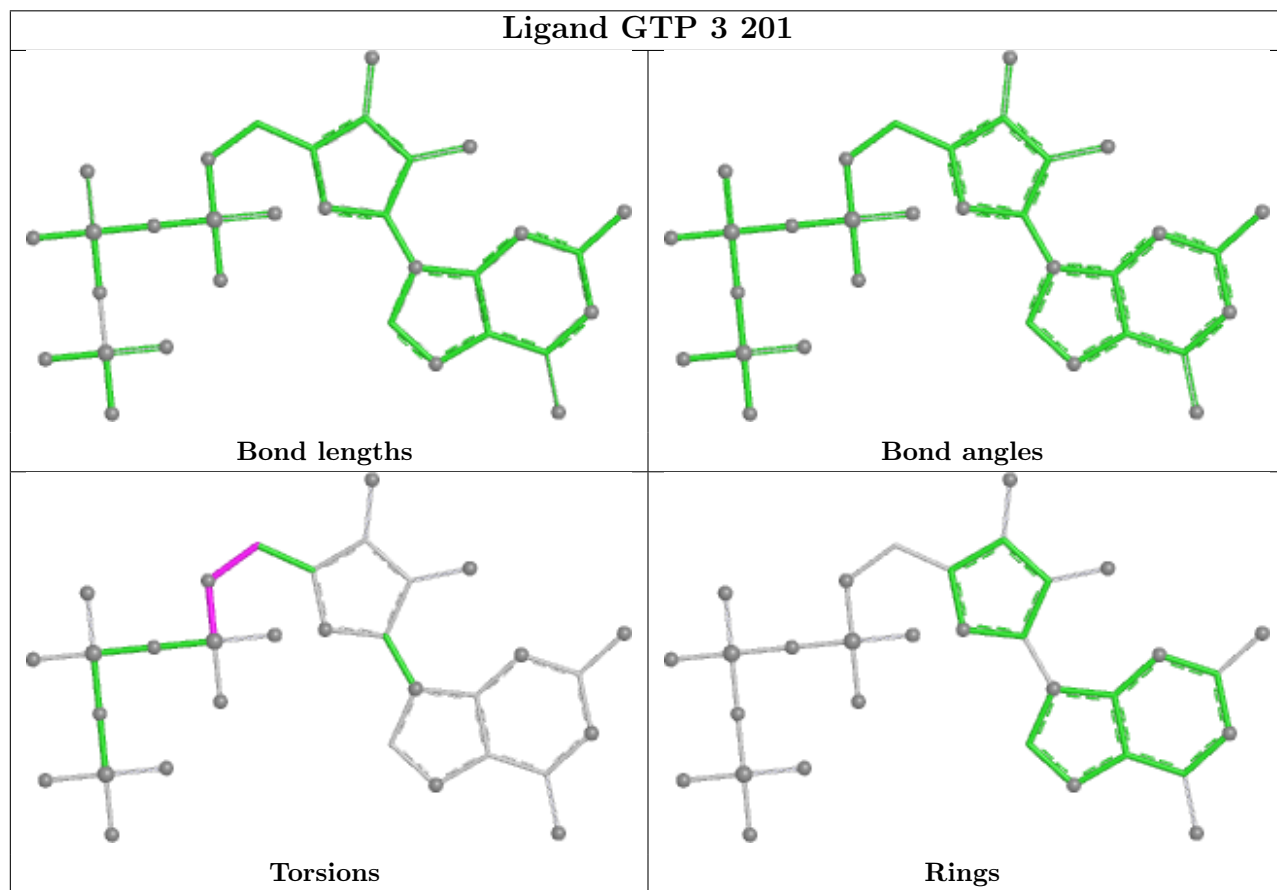
Mol	Chain	Res	Type	Atoms
11	3	201	GTP	C5'-O5'-PA-O3A
11	3	201	GTP	C4'-C5'-O5'-PA
11	3	201	GTP	C5'-O5'-PA-O1A

There are no ring outliers.

1 monomer is involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	3	201	GTP	14	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 [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

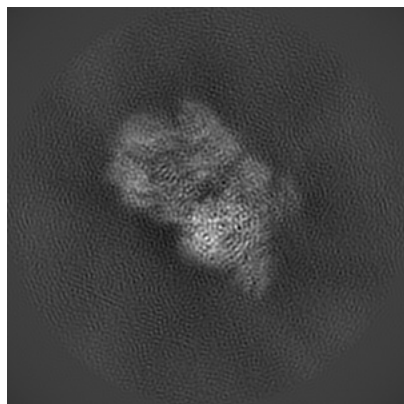
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21145. These allow visual inspection of the internal detail of the map and identification of artifacts.

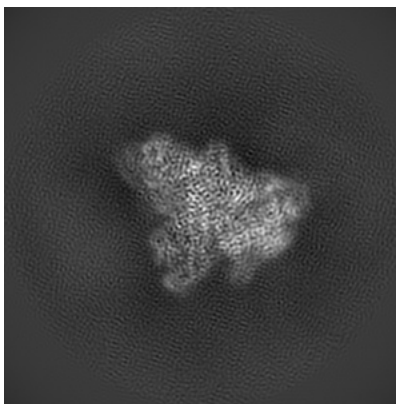
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

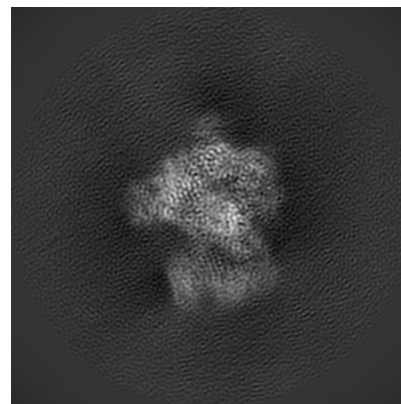
6.1.1 Primary map



X

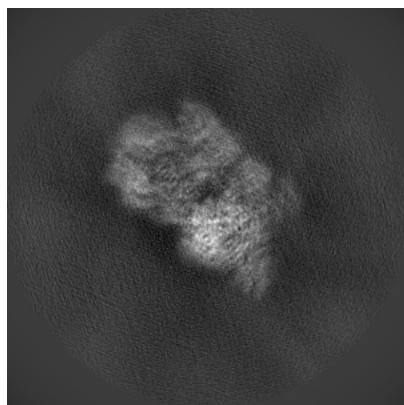


Y

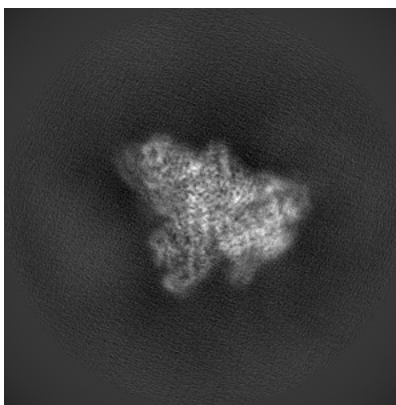


Z

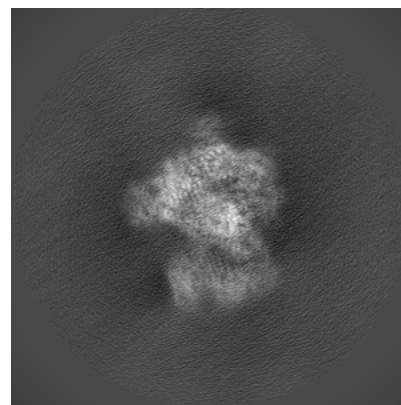
6.1.2 Raw map



X



Y

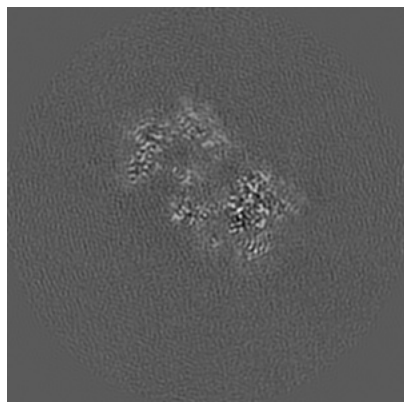


Z

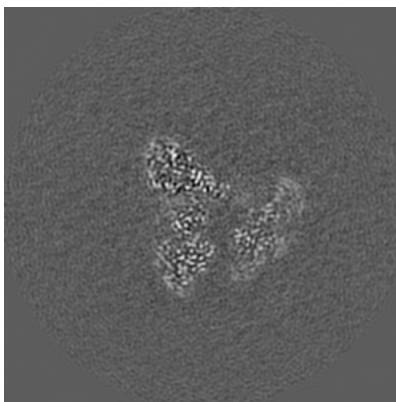
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

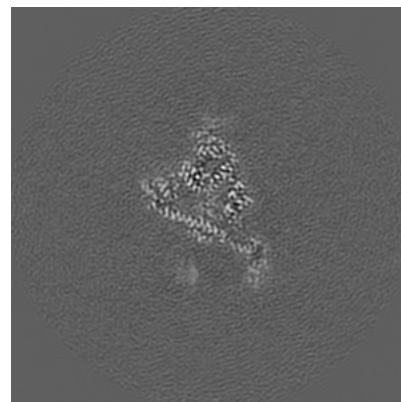
6.2.1 Primary map



X Index: 160

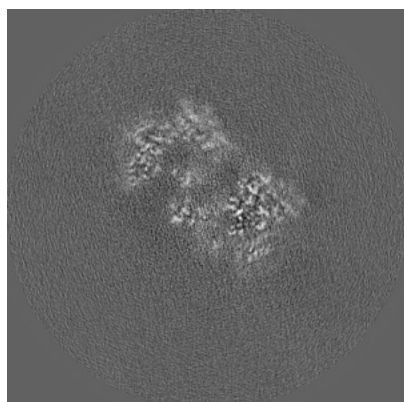


Y Index: 160

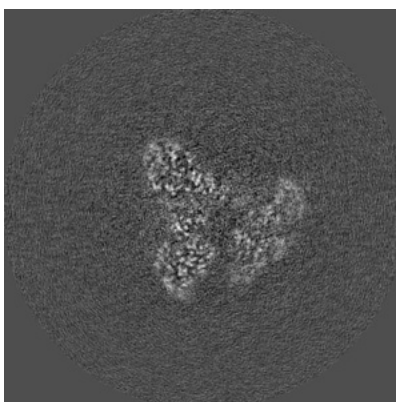


Z Index: 160

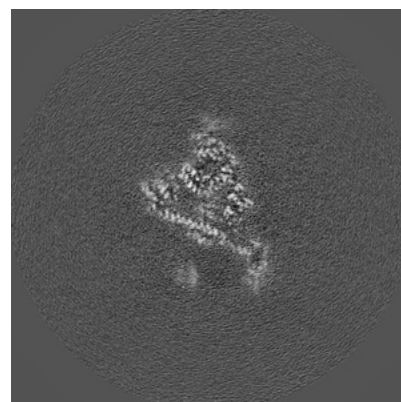
6.2.2 Raw map



X Index: 160



Y Index: 160

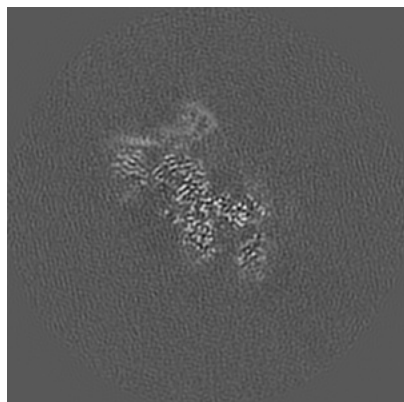


Z Index: 160

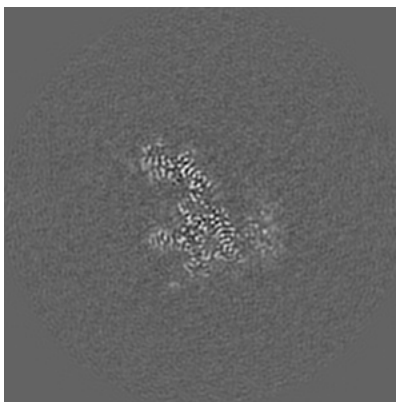
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

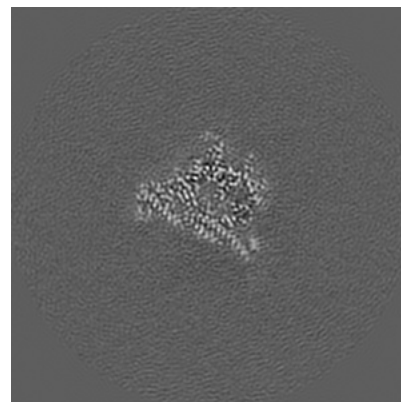
6.3.1 Primary map



X Index: 175

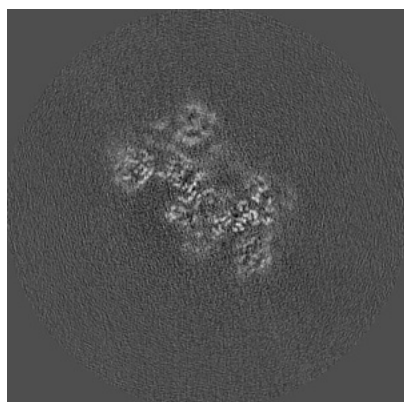


Y Index: 178

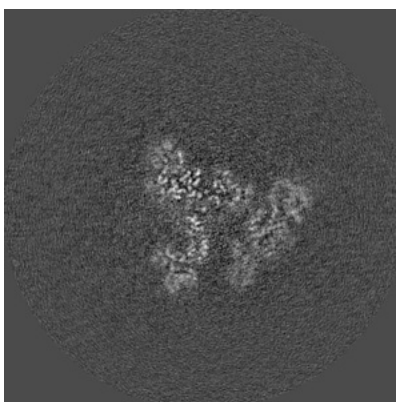


Z Index: 150

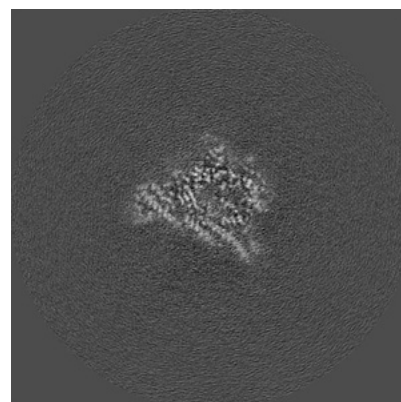
6.3.2 Raw map



X Index: 168



Y Index: 153

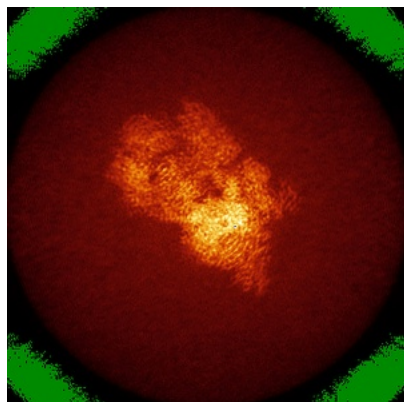


Z Index: 149

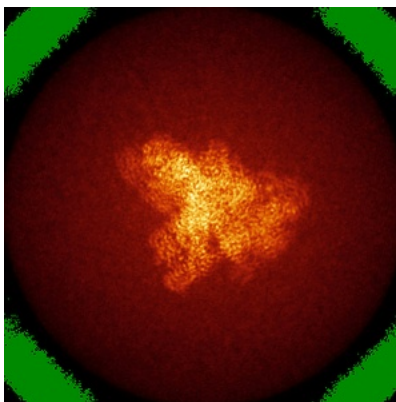
The images above show the largest variance slices of the map in three orthogonal directions.

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

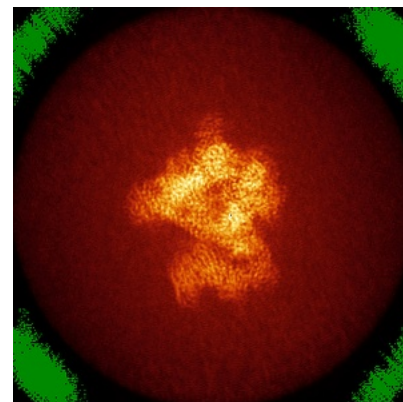
6.4.1 Primary map



X

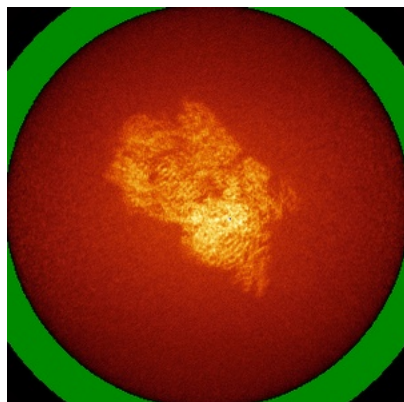


Y

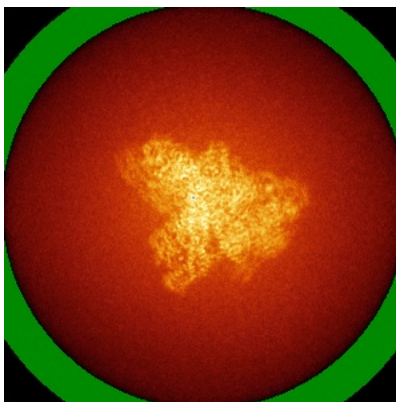


Z

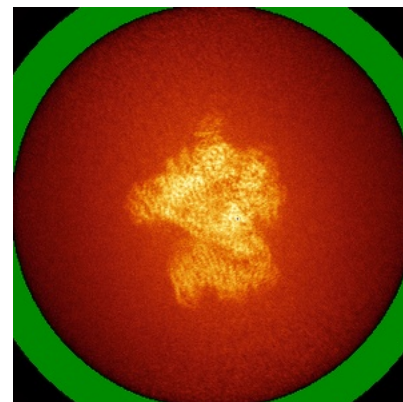
6.4.2 Raw map



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](#)

This section was not generated.

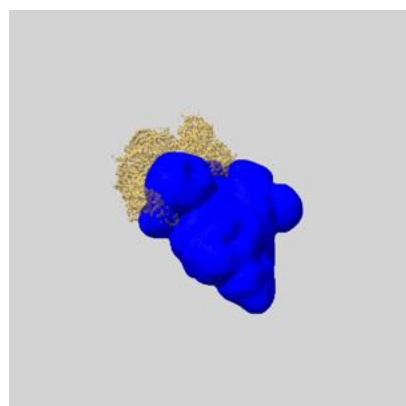
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

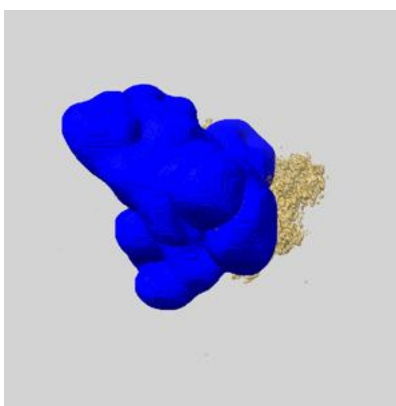
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

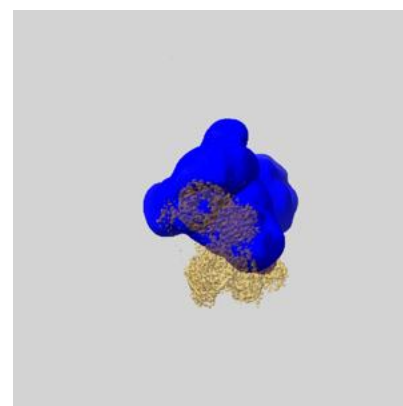
6.6.1 emd_21145_msk_1.map [i](#)



X

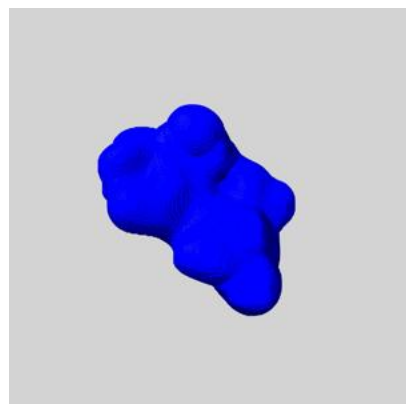


Y

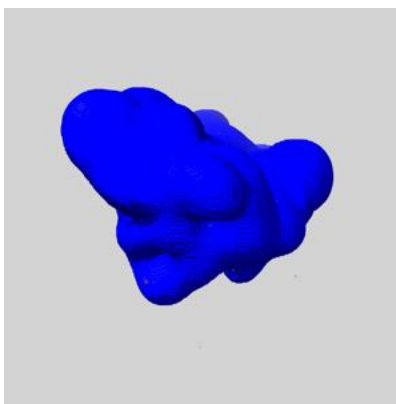


Z

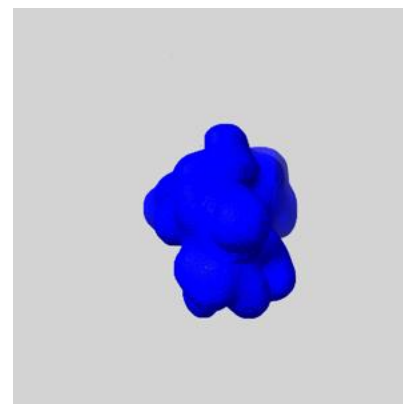
6.6.2 emd_21145_msk_4.map [i](#)



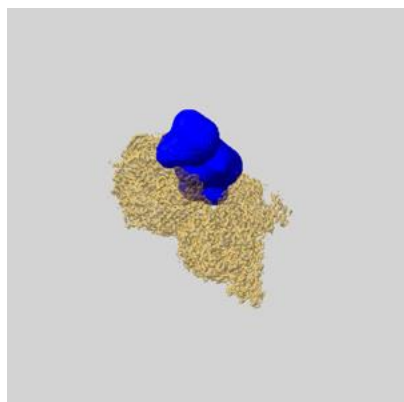
X



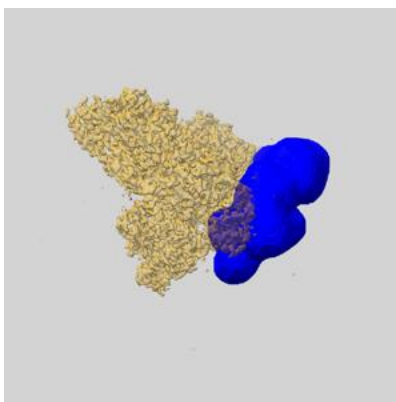
Y



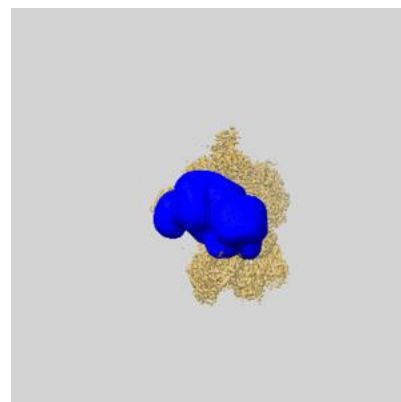
Z

6.6.3 emd_21145_msk_3.map [i](#)

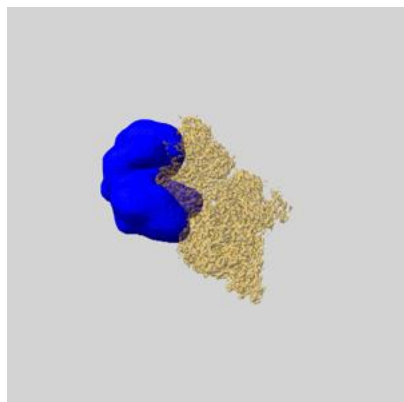
X



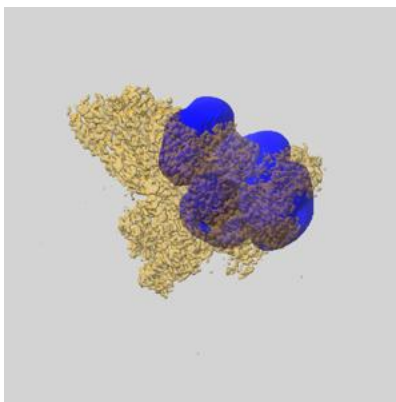
Y



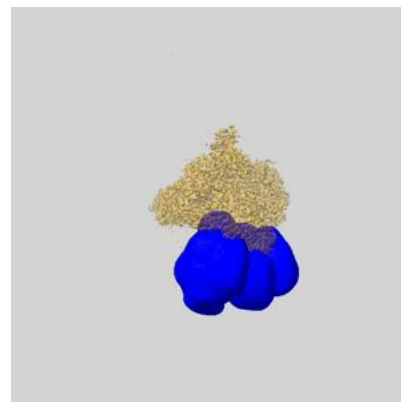
Z

6.6.4 emd_21145_msk_2.map [i](#)

X



Y

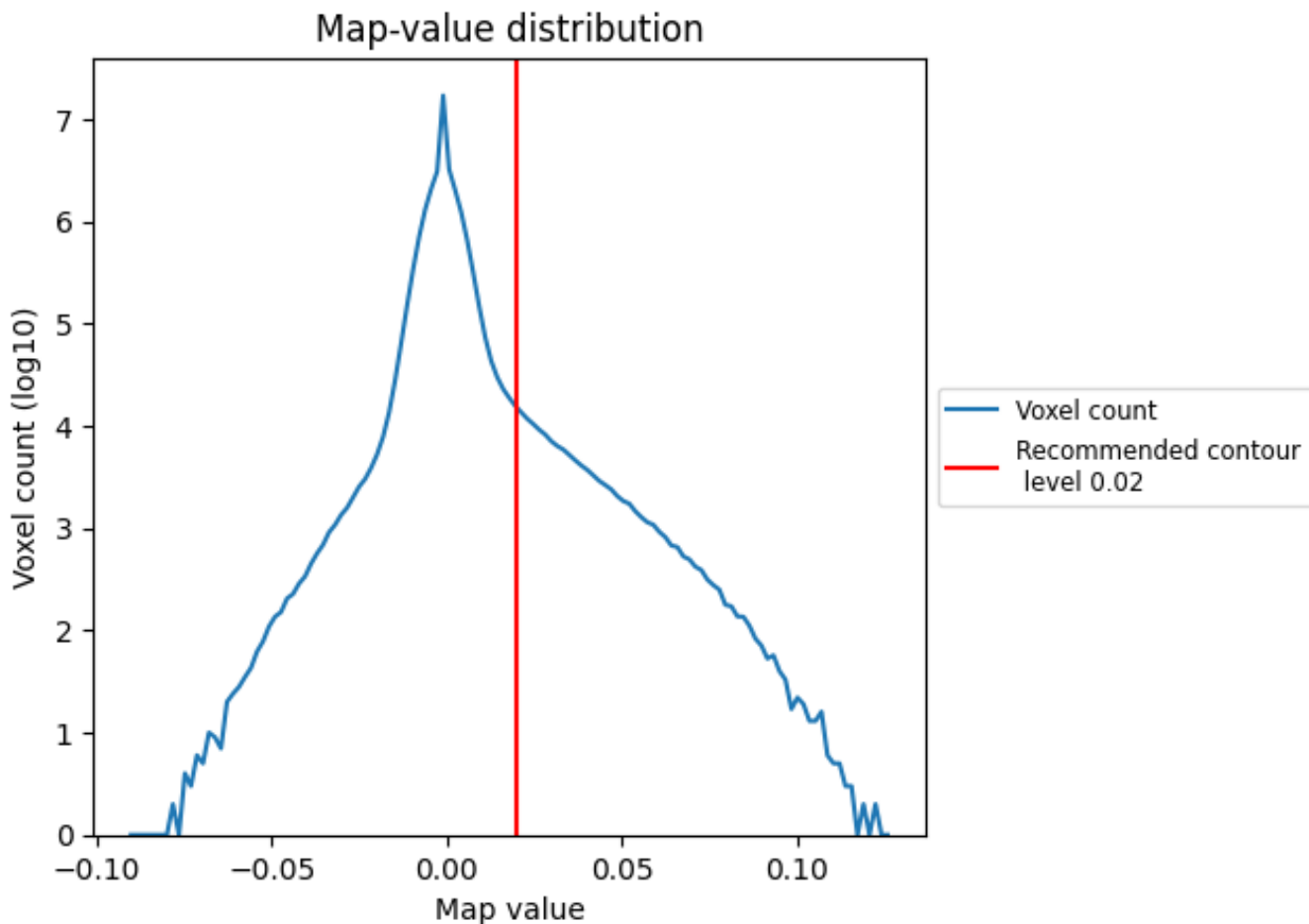


Z

7 Map analysis [i](#)

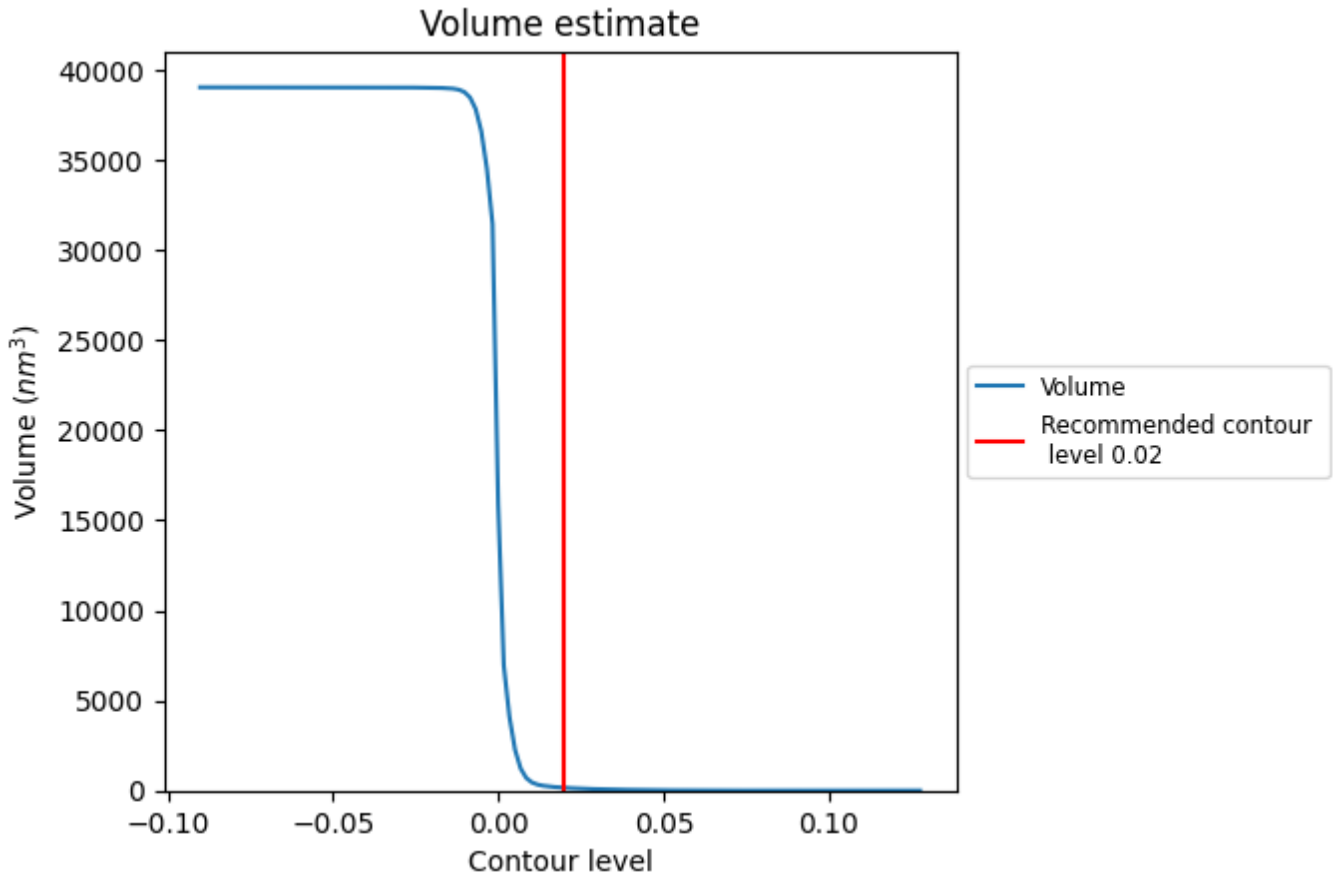
This section contains the results of statistical analysis of the map.

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.

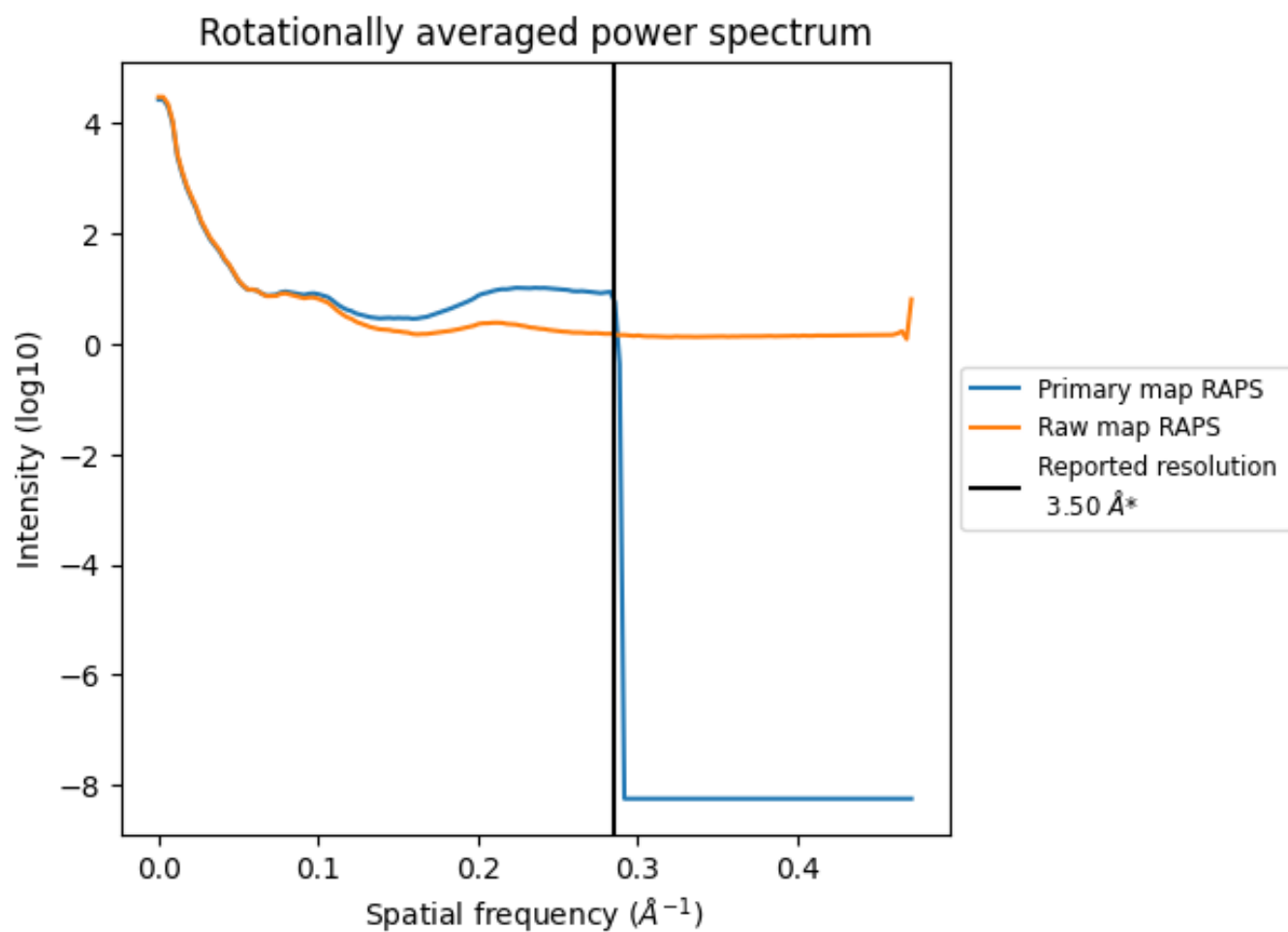
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 155 nm^3 ; this corresponds to an approximate mass of 140 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 i

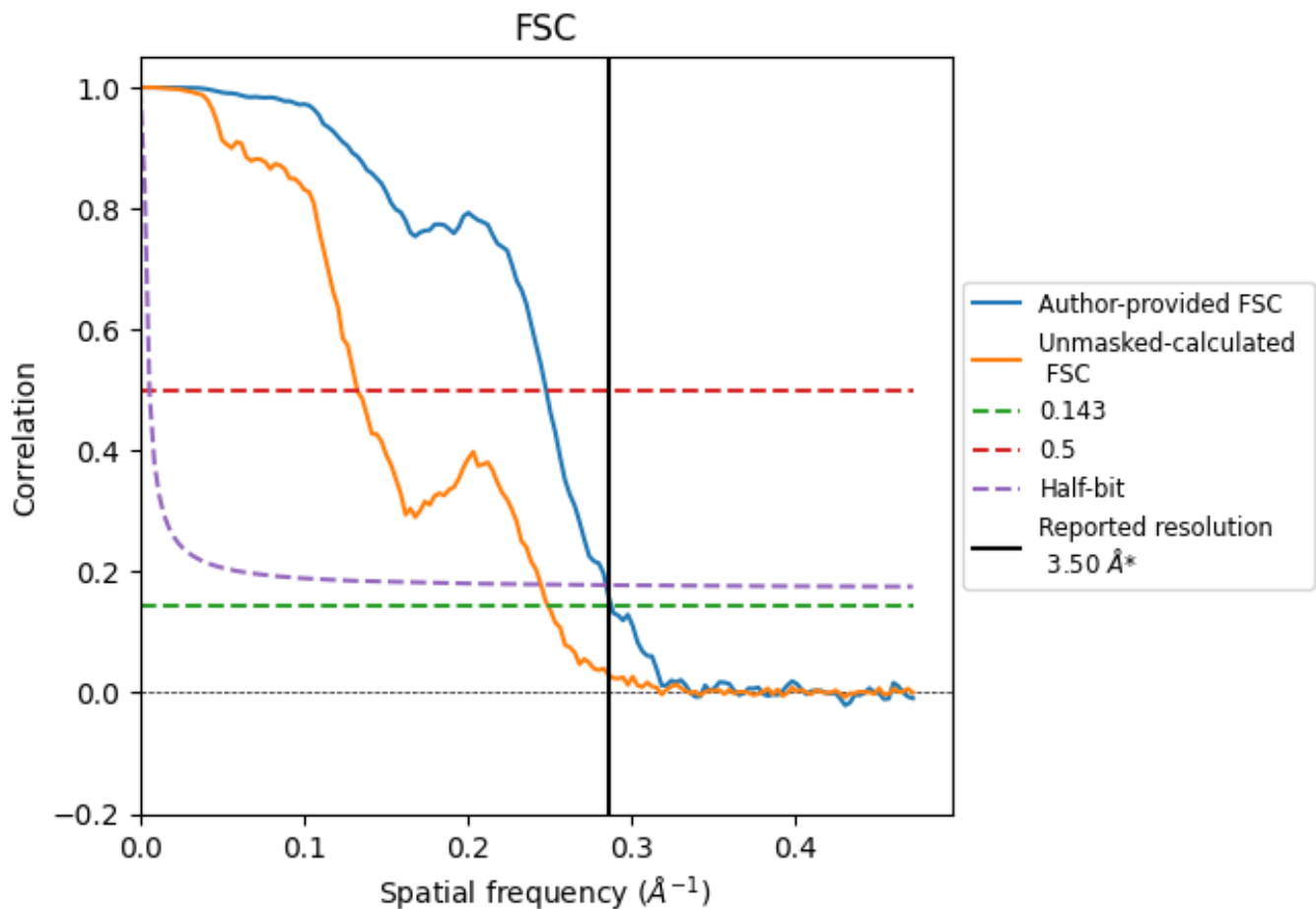


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

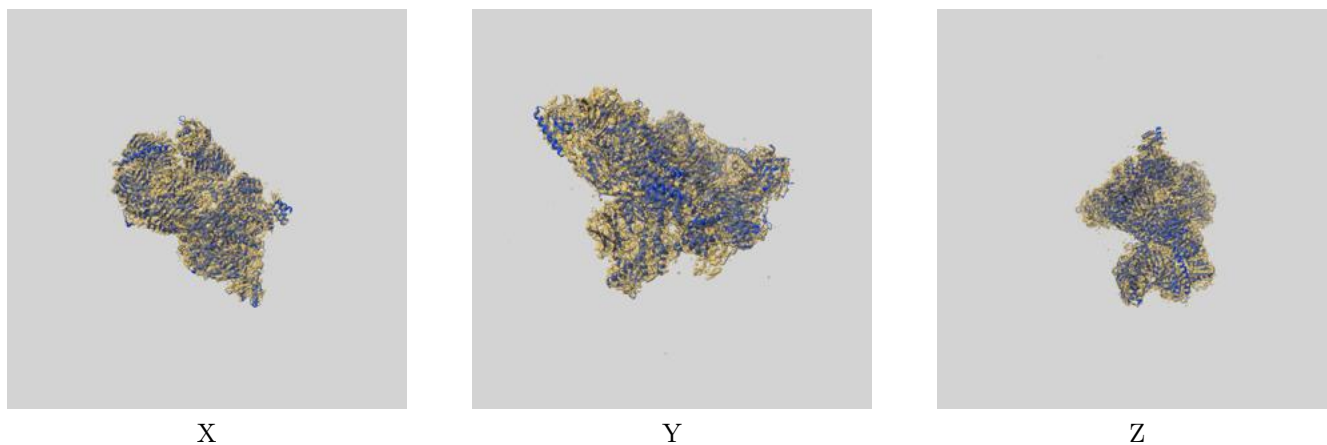
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.48	4.03	3.51
Unmasked-calculated*	4.01	7.55	4.09

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.01 differs from the reported value 3.5 by more than 10 %

9 Map-model fit [i](#)

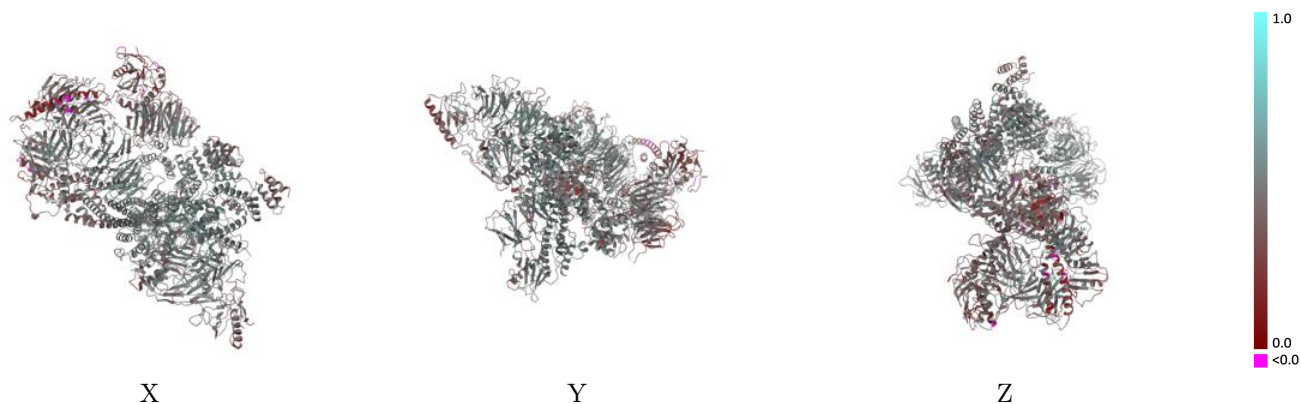
This section contains information regarding the fit between EMDB map EMD-21145 and PDB model 6VBV. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



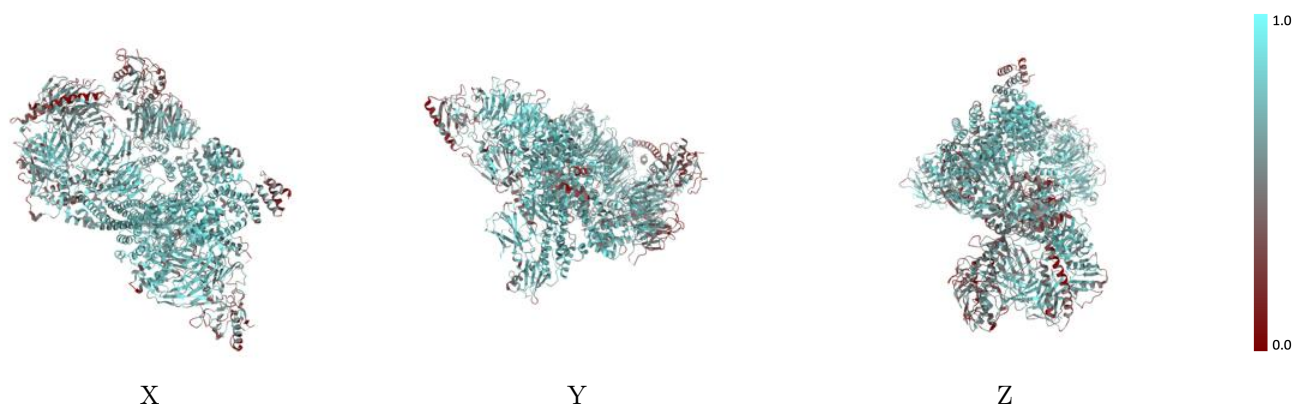
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



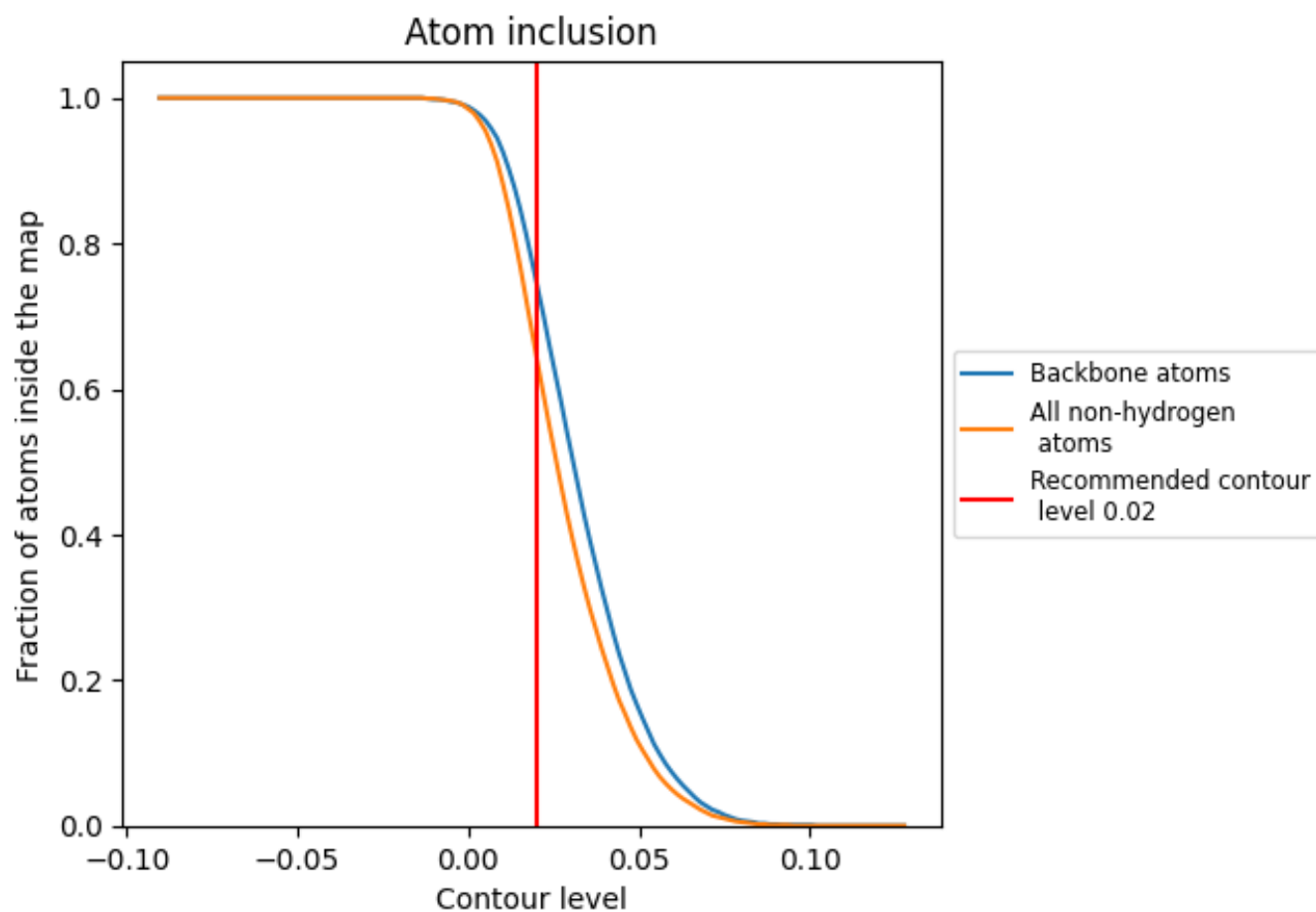
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).





















9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 64% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6440	 0.4530
0	 0.6320	 0.4900
1	 0.6390	 0.4470
2	 0.6870	 0.4620
3	 0.4070	 0.3310
4	 0.6730	 0.4670
5	 0.5450	 0.4410
7	 0.5110	 0.3990
8	 0.7880	 0.5140
9	 0.7200	 0.4840

