



Full wwPDB EM Validation Report ⓘ

May 1, 2024 – 02:37 PM JST

PDB ID : 8W56
EMDB ID : EMD-37272
Title : Cryo-EM structure of DSR2-DSAD1 state 1
Authors : Zhang, H.; Li, Z.; Li, X.Z.
Deposited on : 2023-08-25
Resolution : 3.59 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:

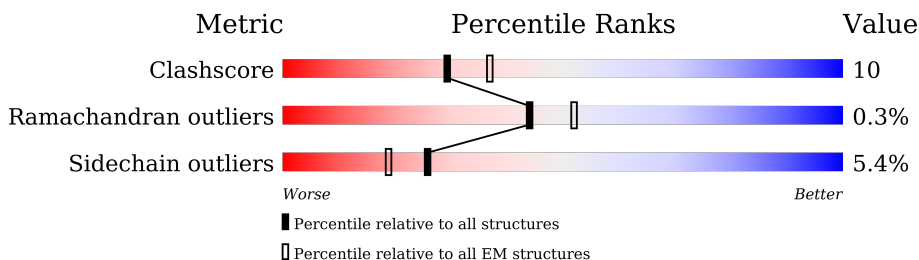
EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

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 3.59 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	1005	
1	B	1005	
1	C	1005	
1	D	1005	
2	E	120	
2	F	120	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 34051 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 SIR2-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	973	Total 8076	C 5231	N 1302	O 1514	S 29	0	0
1	B	972	Total 8059	C 5211	N 1301	O 1516	S 31	0	0
1	C	972	Total 8095	C 5237	N 1309	O 1518	S 31	0	0
1	D	973	Total 8113	C 5253	N 1315	O 1514	S 31	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	643	SER	LEU	conflict	UNP A0A162TTM4
B	643	SER	LEU	conflict	UNP A0A162TTM4
C	643	SER	LEU	conflict	UNP A0A162TTM4
D	643	SER	LEU	conflict	UNP A0A162TTM4

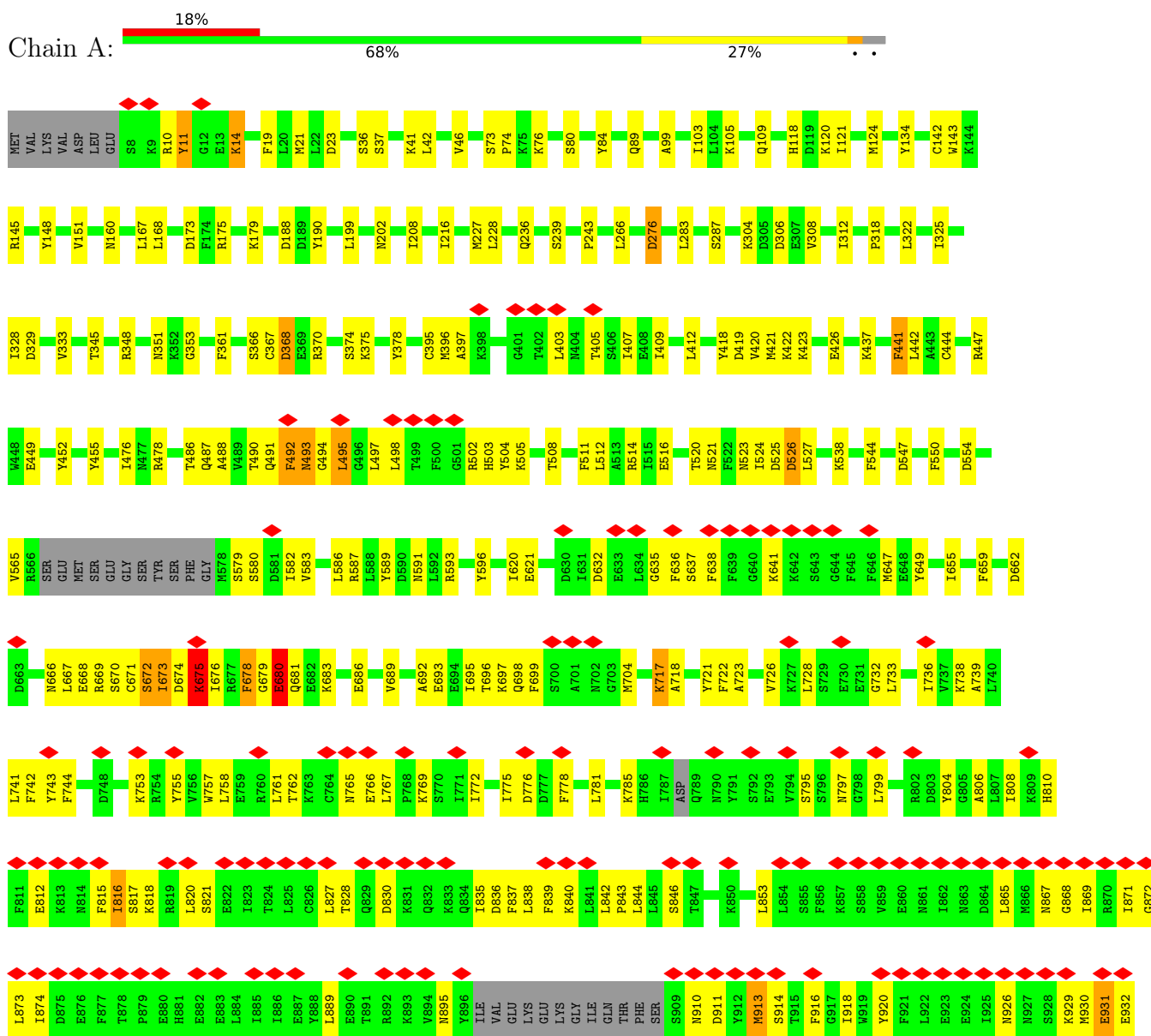
- Molecule 2 is a protein called SPbeta prophage-derived uncharacterized protein YotI.

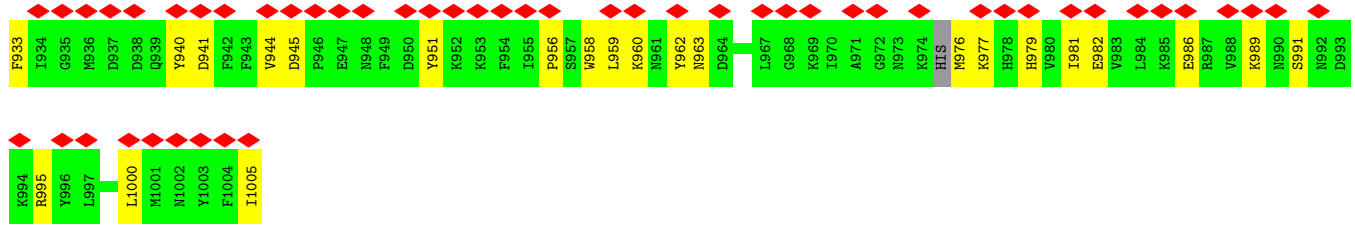
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	E	111	Total 854	C 552	N 138	O 161	S 3	0	0
2	F	111	Total 854	C 552	N 138	O 161	S 3	0	0

3 Residue-property plots

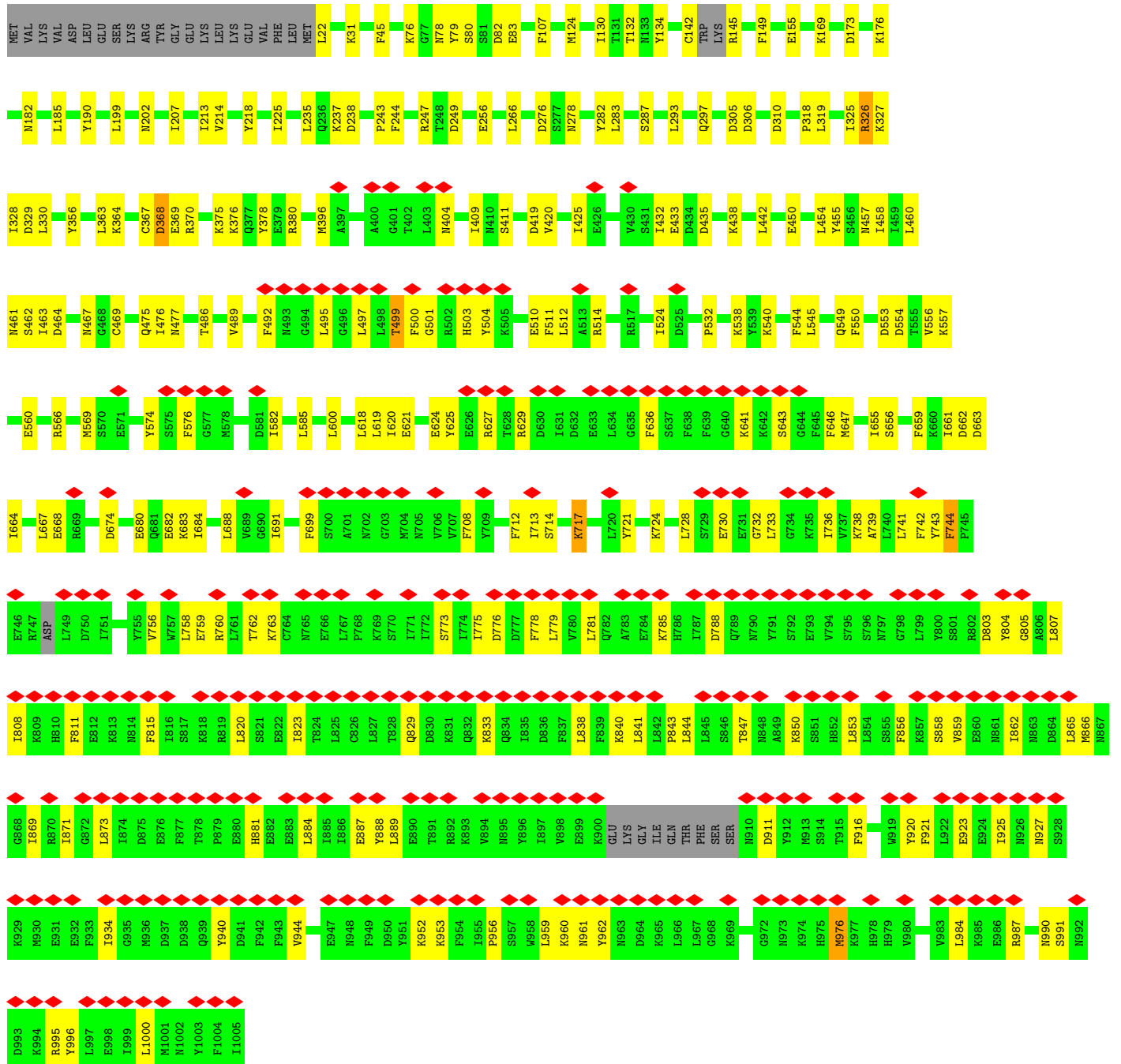
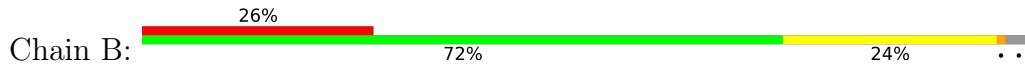
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: SIR2-like domain-containing protein

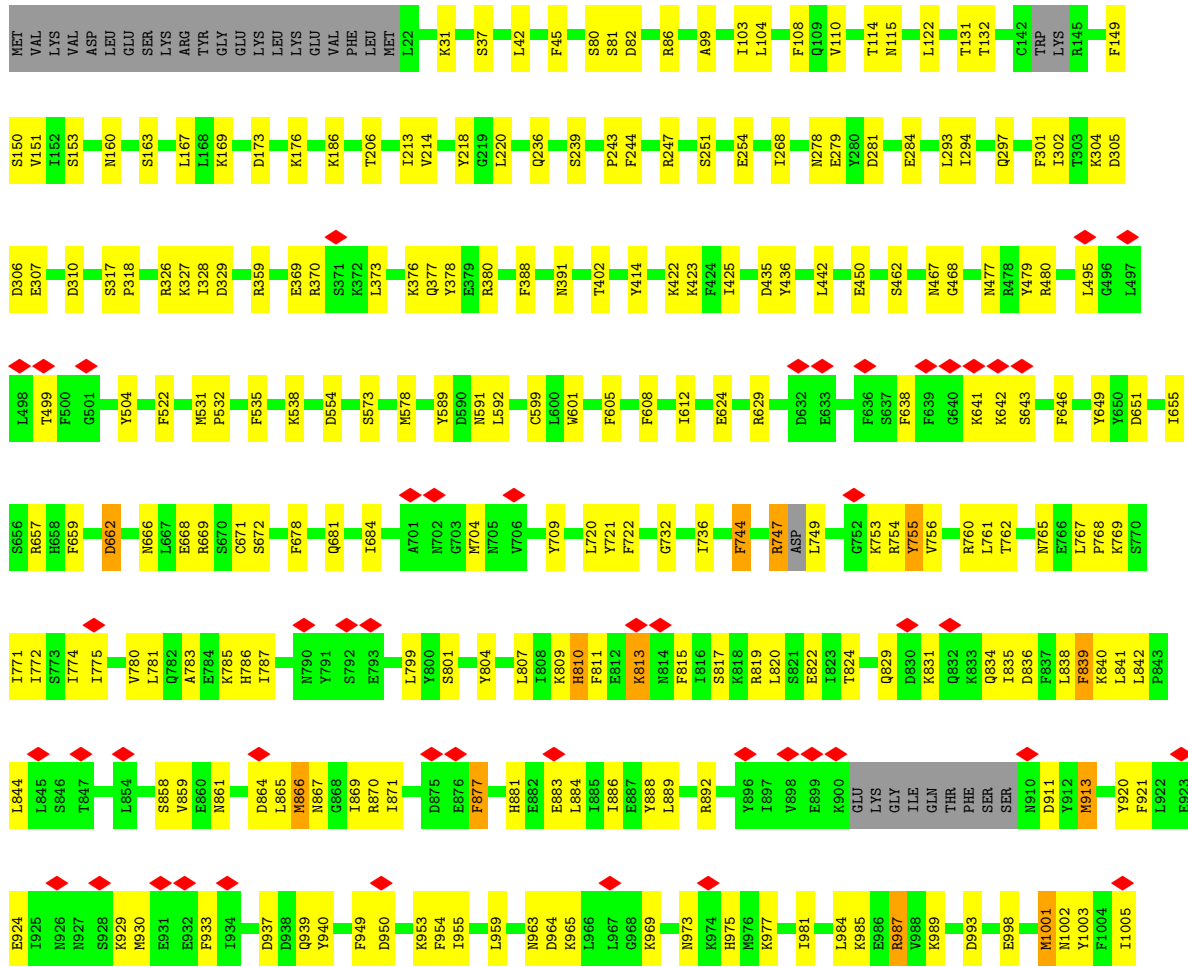
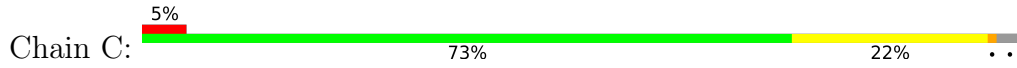




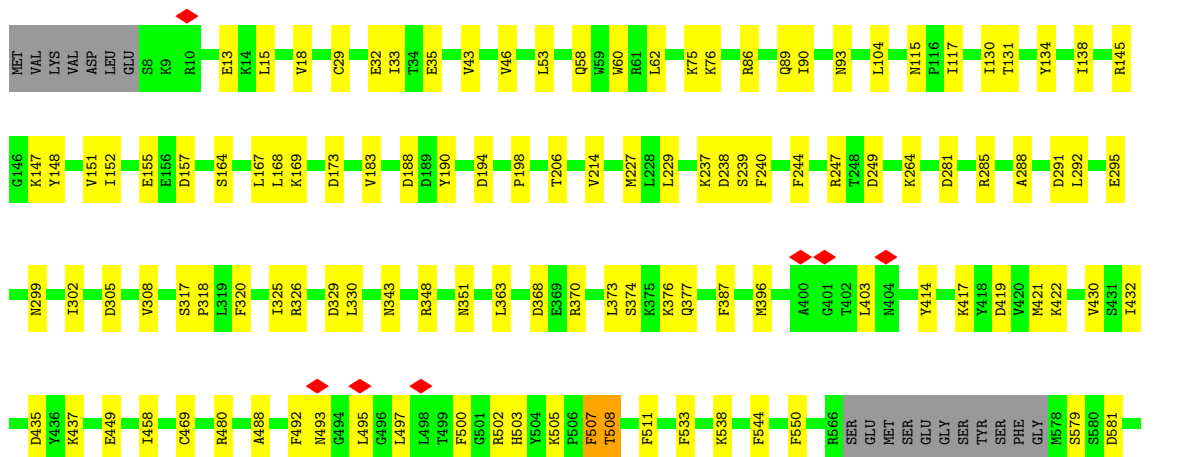
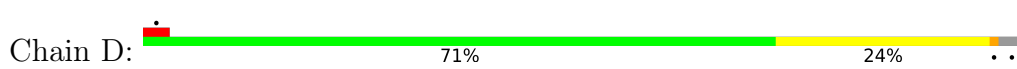
● Molecule 1: SIR2-like domain-containing protein

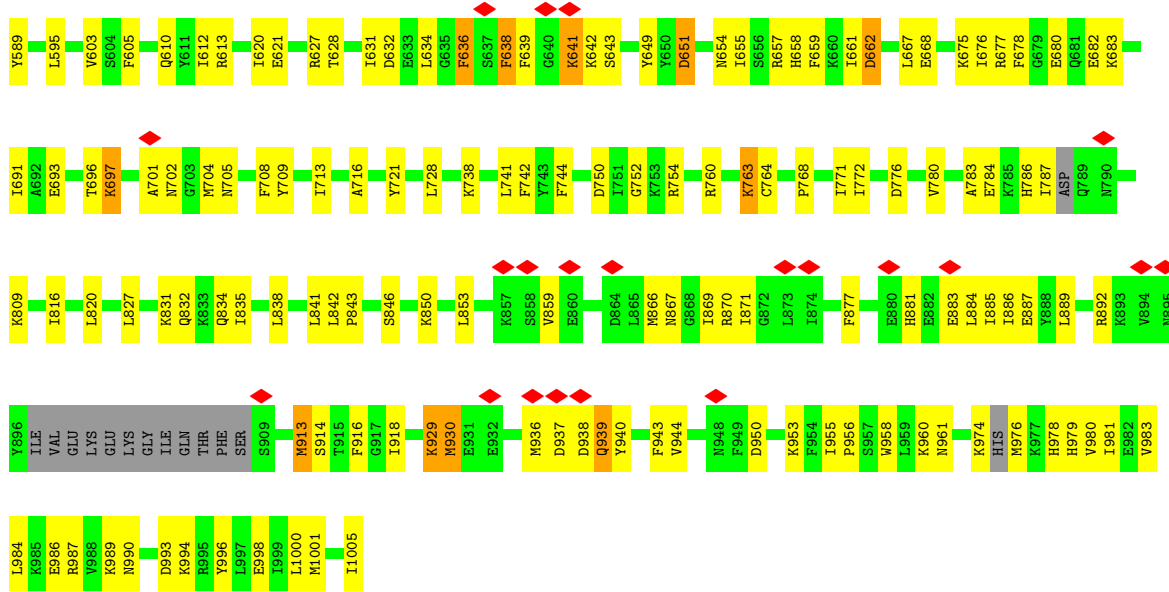


• Molecule 1: SIR2-like domain-containing protein

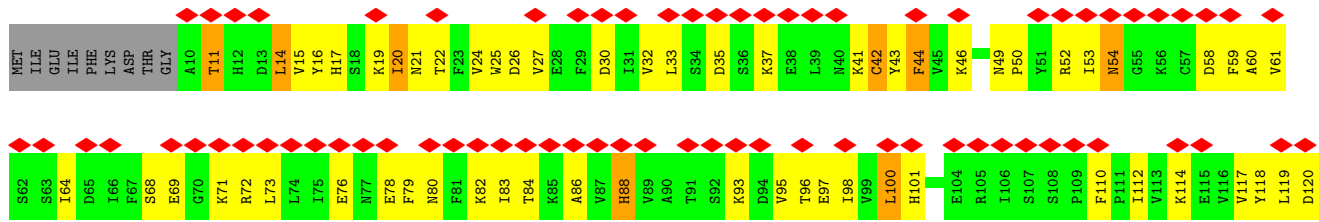
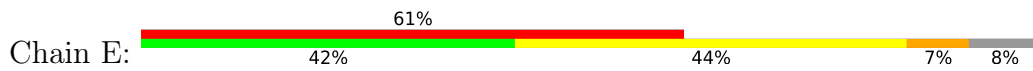


• Molecule 1: SIR2-like domain-containing protein

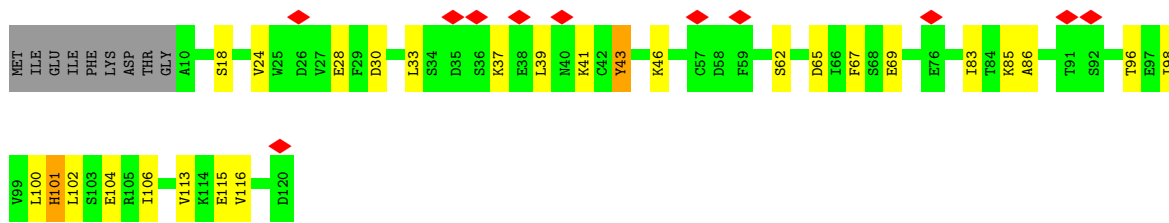




• Molecule 2: SPbeta prophage-derived uncharacterized protein YotI



• Molecule 2: SPbeta prophage-derived uncharacterized protein YotI



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	200000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.583	Depositor
Minimum map value	-0.905	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.040	Depositor
Recommended contour level	0.266	Depositor
Map size (\AA)	425.0, 425.0, 425.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.85, 0.85, 0.85	Depositor

5 Model quality

5.1 Standard geometry

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	0.32	0/8261	0.50	0/11129
1	B	0.30	0/8243	0.48	0/11107
1	C	0.25	0/8281	0.46	0/11152
1	D	0.25	0/8298	0.46	0/11171
2	E	0.71	0/873	0.65	0/1188
2	F	0.28	0/873	0.54	0/1188
All	All	0.30	0/34829	0.48	0/46935

There are no bond length outliers.

There are no bond angle outliers.

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	8076	0	7887	177	0
1	B	8059	0	7863	157	0
1	C	8095	0	7926	153	0
1	D	8113	0	7965	150	0
2	E	854	0	806	58	0
2	F	854	0	806	20	0
All	All	34051	0	33253	684	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 10.

All (684) 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:A:498:LEU:HA	1:A:503:HIS:CE1	2.09	0.86
2:E:30:ASP:HB2	2:E:41:LYS:HE3	1.60	0.83
1:B:499:THR:HB	1:B:503:HIS:HB2	1.61	0.82
1:A:739:ALA:HA	1:A:743:TYR:H	1.42	0.82
1:D:493:ASN:HA	1:D:503:HIS:CD2	2.15	0.81
1:A:488:ALA:HA	1:A:491:GLN:HE21	1.45	0.80
1:D:493:ASN:HA	1:D:503:HIS:HD2	1.47	0.80
1:A:963:ASN:HA	2:E:61:VAL:HG13	1.65	0.79
1:C:913:MET:N	1:C:913:MET:SD	2.56	0.78
1:A:868:GLY:O	1:A:872:GLY:N	2.18	0.76
1:C:284:GLU:OE1	1:C:284:GLU:N	2.19	0.76
2:E:68:SER:HB3	2:E:73:LEU:HB2	1.69	0.75
1:A:868:GLY:HA2	1:A:871:ILE:HG22	1.69	0.74
1:A:816:ILE:HD11	1:A:821:SER:HB2	1.70	0.73
1:D:488:ALA:O	1:D:492:PHE:HB3	1.89	0.73
2:E:26:ASP:HB3	2:E:88:HIS:CE1	2.24	0.73
1:C:662:ASP:OD1	1:C:662:ASP:N	2.24	0.71
1:C:753:LYS:HA	1:C:756:VAL:HG12	1.71	0.71
1:A:797:ASN:HB3	2:E:117:VAL:HG11	1.74	0.70
1:A:986:GLU:HA	1:A:989:LYS:HD2	1.74	0.69
1:B:76:LYS:O	1:B:76:LYS:NZ	2.20	0.69
1:C:787:ILE:HG12	1:C:834:GLN:HE21	1.58	0.68
2:E:11:THR:HA	2:E:25:TRP:CH2	2.29	0.68
2:E:27:VAL:HG11	2:E:86:ALA:HB1	1.76	0.68
1:C:153:SER:OG	1:C:176:LYS:NZ	2.28	0.67
1:A:120:LYS:NZ	1:A:287:SER:OG	2.29	0.66
1:C:981:ILE:O	1:C:985:LYS:HG2	1.96	0.66
1:D:955:ILE:HD12	1:D:956:PRO:HD2	1.78	0.66
1:B:841:LEU:HD11	1:B:844:LEU:HD12	1.78	0.66
2:E:52:ARG:HE	2:E:53:ILE:H	1.43	0.66
1:A:437:LYS:O	1:A:441:PHE:HB2	1.96	0.66
1:A:871:ILE:HG23	1:A:873:LEU:HD23	1.77	0.66
1:A:739:ALA:HB2	1:A:743:TYR:HD2	1.60	0.66
1:D:492:PHE:O	1:D:503:HIS:NE2	2.27	0.66
1:A:778:PHE:HA	1:A:781:LEU:HD12	1.77	0.66
1:D:343:ASN:HB2	1:D:403:LEU:HG	1.77	0.65
1:A:739:ALA:H	1:A:742:PHE:HB2	1.62	0.65
1:B:680:GLU:HB3	1:B:683:LYS:HD2	1.79	0.65
1:B:741:LEU:HD21	1:B:758:LEU:HD21	1.79	0.65
1:D:976:MET:SD	1:D:976:MET:N	2.69	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:788:ASP:O	1:B:833:LYS:NZ	2.27	0.65
1:D:373:LEU:HB3	1:D:377:GLN:HB2	1.78	0.65
2:E:30:ASP:O	2:E:84:THR:HA	1.98	0.64
2:E:88:HIS:HB2	2:E:93:LYS:H	1.63	0.64
1:C:649:TYR:HA	1:C:684:ILE:HD11	1.80	0.64
1:C:787:ILE:O	1:C:831:LYS:NZ	2.31	0.64
1:D:783:ALA:O	1:D:786:HIS:HB2	1.98	0.64
1:A:838:LEU:HD23	1:A:853:LEU:HD12	1.80	0.63
1:D:831:LYS:HE2	1:D:834:GLN:H	1.63	0.63
1:D:867:ASN:HA	1:D:870:ARG:HD3	1.80	0.63
2:F:96:THR:HG22	2:F:100:LEU:HD23	1.81	0.63
1:B:838:LEU:HD23	1:B:841:LEU:HD23	1.81	0.62
1:B:862:ILE:HG23	1:B:866:MET:HE3	1.81	0.62
1:A:498:LEU:HA	1:A:503:HIS:HE1	1.62	0.62
1:D:950:ASP:HB3	1:D:953:LYS:HE3	1.81	0.62
1:A:674:ASP:C	1:A:676:ILE:H	2.02	0.62
1:B:364:LYS:O	1:B:370:ARG:NH2	2.32	0.62
2:E:50:PRO:HD2	2:E:120:ASP:HA	1.82	0.62
1:D:58:GLN:HB2	1:D:60:TRP:HD1	1.63	0.62
1:A:494:GLY:HA2	1:A:505:LYS:HD2	1.82	0.62
1:A:755:TYR:HB2	1:A:804:TYR:HE1	1.65	0.62
1:A:492:PHE:O	1:A:497:LEU:HB2	1.99	0.62
2:E:52:ARG:HG3	2:E:54:ASN:H	1.65	0.61
1:C:82:ASP:OD2	1:C:86:ARG:NH2	2.33	0.61
1:A:554:ASP:OD1	1:A:587:ARG:NH1	2.33	0.61
1:B:684:ILE:HD12	1:B:684:ILE:H	1.64	0.61
1:B:730:GLU:HA	1:B:733:LEU:HD12	1.83	0.61
1:D:435:ASP:HB2	1:D:458:ILE:HD11	1.81	0.61
1:D:721:TYR:O	1:D:760:ARG:NH1	2.31	0.61
1:B:728:LEU:HD11	1:B:732:GLY:HA3	1.83	0.61
2:E:11:THR:HA	2:E:25:TRP:HH2	1.65	0.61
1:A:635:GLY:HA3	1:A:638:PHE:HB3	1.81	0.61
1:A:828:THR:OG1	1:A:830:ASP:OD1	2.19	0.61
2:F:98:ILE:HA	2:F:101:HIS:CE1	2.35	0.61
1:C:327:LYS:NZ	1:C:391:ASN:O	2.32	0.60
1:A:668:GLU:HG2	1:A:673:ILE:HD11	1.82	0.60
1:B:641:LYS:NZ	1:B:643:SER:O	2.34	0.60
1:B:925:ILE:HD12	1:B:927:ASN:H	1.66	0.60
1:B:976:MET:SD	1:B:976:MET:N	2.75	0.60
1:A:565:VAL:HA	1:B:662:ASP:OD2	2.01	0.60
1:B:442:LEU:HD13	1:B:450:GLU:HG3	1.83	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:669:ARG:HH22	1:B:566:ARG:HB3	1.66	0.60
1:D:691:ILE:HD11	1:D:716:ALA:HA	1.83	0.60
2:E:50:PRO:HA	2:E:61:VAL:HB	1.83	0.60
1:A:143:TRP:CZ2	1:B:463:ILE:HA	2.36	0.59
1:A:579:SER:O	1:A:582:ILE:HG22	2.00	0.59
1:B:682:GLU:OE2	1:B:683:LYS:NZ	2.33	0.59
2:F:30:ASP:HB3	2:F:85:LYS:HB2	1.83	0.59
1:C:755:TYR:HE2	1:C:799:LEU:HD13	1.67	0.59
1:A:739:ALA:HA	1:A:743:TYR:N	2.15	0.59
1:B:838:LEU:HB3	1:B:853:LEU:HD21	1.84	0.59
1:C:865:LEU:HD12	1:C:881:HIS:HB3	1.83	0.59
1:C:824:THR:HG22	1:C:838:LEU:HD22	1.84	0.59
1:D:589:TYR:OH	1:D:651:ASP:OD1	2.19	0.59
1:A:409:ILE:HG12	1:A:593:ARG:HG3	1.84	0.59
1:B:805:GLY:C	1:B:807:LEU:N	2.53	0.59
1:D:579:SER:OG	1:D:581:ASP:OD1	2.18	0.59
1:D:886:ILE:HG12	1:D:929:LYS:HD3	1.85	0.59
1:A:632:ASP:OD2	1:B:991:SER:OG	2.14	0.59
1:A:368:ASP:N	1:A:368:ASP:OD1	2.35	0.58
1:D:930:MET:HE3	1:D:930:MET:H	1.67	0.58
2:E:53:ILE:O	2:E:54:ASN:C	2.41	0.58
1:D:914:SER:O	1:D:918:ILE:HG12	2.02	0.58
1:D:889:LEU:HB3	1:D:892:ARG:HH21	1.69	0.58
1:B:923:GLU:N	1:B:923:GLU:OE1	2.37	0.58
1:C:359:ARG:NH2	1:C:369:GLU:OE1	2.37	0.58
1:C:80:SER:OG	1:C:82:ASP:OD1	2.20	0.58
1:C:963:ASN:OD1	1:C:965:LYS:NZ	2.35	0.58
1:C:749:LEU:HD12	1:C:753:LYS:HG3	1.84	0.58
1:B:176:LYS:HE2	1:B:182:ASN:HD21	1.69	0.58
1:C:104:LEU:O	1:C:108:PHE:HB2	2.04	0.58
1:A:913:MET:HA	1:A:916:PHE:HD2	1.69	0.57
1:A:318:PRO:HB3	1:A:538:LYS:HD3	1.86	0.57
1:B:492:PHE:CE2	1:B:503:HIS:HB3	2.38	0.57
1:A:956:PRO:HA	1:A:959:LEU:HD23	1.85	0.57
1:B:310:ASP:OD1	1:B:380:ARG:NH1	2.38	0.57
1:A:508:THR:HG23	1:A:511:PHE:HB2	1.85	0.57
1:A:620:ILE:HD12	1:A:667:LEU:HD11	1.85	0.57
1:A:960:LYS:HB3	1:A:995:ARG:HH22	1.68	0.57
2:F:33:LEU:HB3	2:F:37:LYS:HB2	1.85	0.57
1:B:214:VAL:HG22	1:B:244:PHE:HB2	1.86	0.57
1:A:641:LYS:O	1:A:675:LYS:NZ	2.36	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:678:PHE:CE1	1:A:726:VAL:HG12	2.40	0.57
1:C:761:LEU:O	1:C:765:ASN:ND2	2.38	0.57
1:B:425:ILE:HG22	1:B:438:LYS:HG2	1.86	0.57
1:A:145:ARG:NH1	1:A:145:ARG:O	2.38	0.57
1:A:488:ALA:HA	1:A:491:GLN:NE2	2.19	0.57
1:C:858:SER:OG	1:C:859:VAL:N	2.37	0.57
1:B:247:ARG:NH1	1:B:249:ASP:OD2	2.38	0.56
1:B:858:SER:OG	1:B:859:VAL:N	2.38	0.56
1:D:281:ASP:O	1:D:285:ARG:NH2	2.37	0.56
1:D:914:SER:HA	1:D:939:GLN:HE22	1.68	0.56
1:C:45:PHE:HD2	1:C:213:ILE:HD11	1.70	0.56
1:C:151:VAL:HG12	1:C:167:LEU:HD23	1.86	0.56
1:D:610:GLN:HG3	1:D:613:ARG:HH21	1.70	0.56
1:C:813:LYS:H	1:C:813:LYS:HD2	1.70	0.56
1:A:799:LEU:HD11	2:E:119:LEU:HD22	1.87	0.56
1:B:419:ASP:OD1	1:B:420:VAL:N	2.39	0.56
2:E:42:CYS:SG	2:E:43:TYR:N	2.79	0.56
1:D:13:GLU:OE1	1:D:13:GLU:N	2.31	0.56
1:D:89:GLN:NE2	1:D:93:ASN:OD1	2.38	0.56
1:A:348:ARG:HE	1:A:351:ASN:HB3	1.71	0.56
1:D:502:ARG:HD2	1:D:503:HIS:H	1.71	0.56
1:A:817:SER:HB2	1:A:820:LEU:HB3	1.87	0.56
1:A:678:PHE:HB3	1:A:681:GLN:HE22	1.70	0.55
1:A:755:TYR:HB2	1:A:804:TYR:CE1	2.41	0.55
1:B:45:PHE:HD2	1:B:213:ILE:HD11	1.71	0.55
1:C:911:ASP:OD1	1:C:911:ASP:N	2.39	0.55
1:D:368:ASP:N	1:D:368:ASP:OD1	2.39	0.55
1:C:987:ARG:NH1	1:D:632:ASP:OD1	2.37	0.55
1:A:755:TYR:HA	1:A:758:LEU:HG	1.88	0.55
1:A:521:ASN:HD21	1:B:297:GLN:HG2	1.72	0.55
1:C:310:ASP:OD1	1:C:380:ARG:NH1	2.39	0.55
1:A:202:ASN:ND2	1:B:202:ASN:OD1	2.34	0.55
1:A:487:GLN:O	1:A:491:GLN:HG3	2.07	0.55
1:C:554:ASP:OD2	1:C:591:ASN:ND2	2.26	0.55
1:D:827:LEU:HD11	1:D:835:ILE:HG22	1.89	0.55
1:A:151:VAL:HG12	1:A:167:LEU:HD23	1.89	0.55
1:A:806:ALA:HB1	2:E:53:ILE:HG21	1.88	0.55
1:D:595:LEU:HB3	1:D:603:VAL:HG12	1.89	0.55
1:B:576:PHE:HB2	2:E:14:LEU:HD21	1.88	0.55
1:C:744:PHE:O	1:C:754:ARG:NH2	2.39	0.54
1:A:775:ILE:HD12	1:A:776:ASP:N	2.23	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:771:ILE:O	1:C:775:ILE:HG13	2.07	0.54
1:C:913:MET:HB3	1:C:940:TYR:CE2	2.42	0.54
1:C:214:VAL:HG22	1:C:244:PHE:HB2	1.89	0.54
1:D:885:ILE:O	1:D:889:LEU:HG	2.08	0.54
2:F:98:ILE:O	2:F:102:LEU:HB2	2.07	0.54
1:D:325:ILE:HD11	1:D:329:ASP:HB2	1.90	0.54
1:A:580:SER:HA	1:A:583:VAL:HG12	1.90	0.54
1:B:775:ILE:HB	1:B:804:TYR:HE1	1.72	0.54
1:B:820:LEU:HD13	1:B:823:ILE:HD12	1.89	0.53
1:D:631:ILE:HG13	1:D:636:PHE:HA	1.90	0.53
1:B:624:GLU:OE2	1:B:627:ARG:NH2	2.37	0.53
1:C:780:VAL:HG11	1:C:819:ARG:HD2	1.89	0.53
1:D:507:PHE:HB3	1:D:511:PHE:HD2	1.73	0.53
1:A:995:ARG:NH2	2:E:19:LYS:O	2.41	0.53
1:C:247:ARG:NH1	1:C:251:SER:O	2.39	0.53
1:A:173:ASP:OD2	1:A:175:ARG:NH1	2.41	0.53
1:B:463:ILE:HG23	1:B:464:ASP:H	1.72	0.53
1:B:668:GLU:OE2	1:B:760:ARG:NH2	2.42	0.53
1:B:805:GLY:HA2	1:B:808:ILE:HG12	1.91	0.53
1:B:960:LYS:HD3	1:B:995:ARG:NH2	2.22	0.53
1:B:80:SER:H	1:B:83:GLU:HG3	1.74	0.53
1:D:53:LEU:HB2	1:D:115:ASN:ND2	2.24	0.53
1:A:674:ASP:C	1:A:676:ILE:N	2.62	0.52
1:B:132:THR:OG1	1:B:218:TYR:OH	2.26	0.52
2:F:69:GLU:N	2:F:69:GLU:OE1	2.41	0.52
1:A:671:CYS:O	1:A:672:SER:C	2.47	0.52
1:C:531:MET:HG3	1:C:532:PRO:HD2	1.91	0.52
2:E:52:ARG:HH21	2:E:53:ILE:HD13	1.73	0.52
1:A:766:GLU:CD	1:A:767:LEU:H	2.13	0.52
1:B:805:GLY:C	1:B:807:LEU:H	2.12	0.52
1:C:414:TYR:O	1:C:657:ARG:NH2	2.42	0.52
1:D:913:MET:HE2	1:D:937:ASP:HB3	1.90	0.52
1:B:911:ASP:OD1	1:B:911:ASP:N	2.38	0.52
2:E:22:THR:HG21	2:E:46:LYS:HD3	1.91	0.52
1:A:842:LEU:HG	1:A:843:PRO:HD3	1.90	0.52
1:B:629:ARG:HH22	1:B:643:SER:HB2	1.73	0.52
1:C:783:ALA:O	1:C:786:HIS:ND1	2.43	0.52
1:C:839:PHE:HZ	1:C:864:ASP:HA	1.75	0.52
1:C:964:ASP:OD1	1:C:965:LYS:N	2.43	0.52
1:D:884:LEU:O	1:D:887:GLU:HG3	2.09	0.52
1:D:655:ILE:O	1:D:659:PHE:HB2	2.10	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:771:ILE:HD12	1:C:771:ILE:H	1.74	0.52
1:C:783:ALA:HA	1:C:786:HIS:HD1	1.75	0.52
1:C:866:MET:HA	1:C:869:ILE:HG12	1.90	0.52
1:B:283:LEU:O	1:B:287:SER:OG	2.25	0.52
2:F:98:ILE:HA	2:F:101:HIS:HE1	1.73	0.51
1:B:278:ASN:OD1	1:B:278:ASN:N	2.43	0.51
1:B:820:LEU:HG	1:B:841:LEU:HD21	1.93	0.51
1:C:666:ASN:HD22	1:C:669:ARG:HH21	1.58	0.51
1:B:454:LEU:O	1:B:458:ILE:HG13	2.09	0.51
1:B:724:LYS:HE2	1:B:763:LYS:HD3	1.93	0.51
1:C:608:PHE:O	1:C:612:ILE:HG12	2.10	0.51
1:A:959:LEU:HD13	1:A:962:TYR:HE2	1.76	0.51
1:B:455:TYR:OH	1:B:477:ASN:ND2	2.44	0.51
1:B:866:MET:HA	1:B:869:ILE:HG22	1.92	0.51
1:A:243:PRO:HG2	1:A:266:LEU:HD23	1.93	0.51
1:A:455:TYR:HB3	1:A:478:ARG:HG3	1.92	0.51
1:B:560:GLU:OE2	1:B:560:GLU:N	2.43	0.51
1:B:990:ASN:OD1	1:B:991:SER:N	2.42	0.51
1:D:620:ILE:HD12	1:D:667:LEU:HD11	1.92	0.51
2:E:17:HIS:O	2:E:21:ASN:N	2.44	0.51
1:B:739:ALA:HA	1:B:743:TYR:HD1	1.74	0.51
1:D:842:LEU:HG	1:D:843:PRO:HD3	1.92	0.51
1:C:989:LYS:NZ	1:D:998:GLU:OE1	2.44	0.51
1:D:750:ASP:OD1	1:D:752:GLY:N	2.41	0.51
1:D:780:VAL:HG12	1:D:820:LEU:CD2	2.40	0.51
1:A:839:PHE:HD1	1:A:853:LEU:HD11	1.75	0.50
1:C:771:ILE:HA	1:C:774:ILE:HG12	1.92	0.50
1:D:46:VAL:HG11	1:D:138:ILE:HD11	1.93	0.50
1:D:930:MET:H	1:D:930:MET:CE	2.23	0.50
2:E:41:LYS:HB2	2:E:69:GLU:OE1	2.10	0.50
1:A:523:ASN:HB3	1:A:526:ASP:OD1	2.10	0.50
1:A:704:MET:SD	1:A:704:MET:N	2.83	0.50
1:B:319:LEU:HB3	1:B:325:ILE:CD1	2.41	0.50
1:A:512:LEU:O	1:A:516:GLU:HG2	2.11	0.50
1:A:236:GLN:O	1:A:239:SER:OG	2.28	0.50
1:C:977:LYS:O	1:C:981:ILE:HB	2.11	0.50
1:A:36:SER:OG	1:A:41:LYS:O	2.30	0.50
1:B:476:ILE:HD13	1:B:524:ILE:HD11	1.92	0.50
1:C:302:ILE:HG22	1:C:307:GLU:HB3	1.92	0.50
2:E:97:GLU:O	2:E:100:LEU:HG	2.12	0.50
1:A:621:GLU:HG2	1:A:671:CYS:SG	2.52	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:881:HIS:HA	1:C:884:LEU:HD12	1.93	0.50
1:B:741:LEU:HD11	1:B:758:LEU:HD11	1.93	0.50
1:C:37:SER:HB2	1:C:42:LEU:HD13	1.93	0.50
1:D:643:SER:HB2	1:D:676:ILE:HD13	1.93	0.50
1:B:987:ARG:HD3	1:B:996:TYR:HE2	1.76	0.50
1:B:582:ILE:HD13	1:B:585:LEU:HD23	1.93	0.49
1:B:432:ILE:HD12	1:B:433:GLU:N	2.26	0.49
1:D:414:TYR:OH	1:D:654:ASN:OD1	2.27	0.49
1:A:367:CYS:HA	1:A:370:ARG:HE	1.76	0.49
1:B:847:THR:HA	1:B:850:LYS:HG2	1.94	0.49
1:C:373:LEU:HB3	1:C:377:GLN:HB2	1.94	0.49
1:D:130:ILE:HG23	1:D:168:LEU:HB3	1.94	0.49
1:D:662:ASP:OD1	1:D:662:ASP:N	2.46	0.49
2:E:27:VAL:HG21	2:E:95:VAL:HG21	1.94	0.49
1:A:695:ILE:HG13	1:A:698:GLN:HE21	1.78	0.49
1:A:808:ILE:O	1:A:812:GLU:N	2.45	0.49
1:A:827:LEU:HD22	1:A:838:LEU:HD22	1.93	0.49
2:E:15:VAL:HB	2:E:24:VAL:HB	1.94	0.49
1:A:304:LYS:HG2	1:A:306:ASP:HB3	1.94	0.49
1:B:327:LYS:O	1:B:330:LEU:HB2	2.12	0.49
1:C:318:PRO:HG3	1:C:538:LYS:HG2	1.93	0.49
1:B:318:PRO:HB3	1:B:538:LYS:HD3	1.95	0.49
1:C:817:SER:HB3	1:C:844:LEU:HD11	1.93	0.49
1:B:80:SER:OG	1:B:82:ASP:OD1	2.29	0.49
1:B:432:ILE:HA	1:B:435:ASP:OD2	2.13	0.49
2:F:28:GLU:OE2	2:F:28:GLU:HA	2.13	0.49
2:F:104:GLU:OE1	2:F:104:GLU:N	2.39	0.49
1:A:199:LEU:HG	1:B:235:LEU:HD11	1.95	0.49
1:A:276:ASP:OD1	1:A:276:ASP:N	2.44	0.49
1:D:164:SER:O	1:D:164:SER:OG	2.31	0.49
1:B:501:GLY:HA2	1:B:504:TYR:CE1	2.48	0.49
1:C:888:TYR:O	1:C:892:ARG:HG2	2.13	0.49
1:D:741:LEU:O	1:D:754:ARG:NH1	2.46	0.49
1:A:419:ASP:N	1:A:419:ASP:OD1	2.46	0.49
1:B:367:CYS:O	1:B:370:ARG:HB2	2.12	0.49
1:B:714:SER:HA	1:B:717:LYS:HE3	1.94	0.49
1:B:829:GLN:NE2	1:B:856:PHE:O	2.37	0.49
2:E:27:VAL:HG22	2:E:88:HIS:HA	1.95	0.49
1:D:32:GLU:O	1:D:35:GLU:HG3	2.13	0.48
2:F:28:GLU:HG3	2:F:41:LYS:HB3	1.95	0.48
1:A:544:PHE:HD2	1:A:550:PHE:HB2	1.77	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:574:TYR:HB2	2:E:16:TYR:HB3	1.96	0.48
1:D:497:LEU:HB3	1:D:503:HIS:HE1	1.78	0.48
1:A:867:ASN:ND2	2:E:76:GLU:O	2.42	0.48
1:B:940:TYR:O	1:B:944:VAL:HG22	2.14	0.48
1:C:886:ILE:HG12	1:C:929:LYS:HZ2	1.78	0.48
1:D:247:ARG:NH1	1:D:249:ASP:OD2	2.46	0.48
1:A:931:GLU:C	1:A:933:PHE:H	2.15	0.48
1:C:883:GLU:HA	1:C:886:ILE:HD12	1.94	0.48
1:A:422:LYS:O	1:A:426:GLU:HG2	2.14	0.48
1:B:953:LYS:HA	1:B:953:LYS:HD3	1.71	0.48
2:E:52:ARG:HE	2:E:53:ILE:N	2.09	0.48
1:A:758:LEU:HD21	1:A:804:TYR:CE1	2.49	0.48
1:C:132:THR:HG1	1:C:218:TYR:HH	1.57	0.48
1:C:370:ARG:HB3	1:C:378:TYR:HE1	1.78	0.48
1:C:425:ILE:HG12	1:C:442:LEU:HD12	1.96	0.48
1:C:807:LEU:O	1:C:810:HIS:ND1	2.33	0.48
1:C:310:ASP:OD2	1:C:377:GLN:NE2	2.47	0.48
1:C:442:LEU:HD21	1:C:450:GLU:HB3	1.95	0.48
1:D:318:PRO:HB3	1:D:538:LYS:HD3	1.94	0.48
1:D:768:PRO:HD2	1:D:771:ILE:HD11	1.96	0.48
1:B:775:ILE:HB	1:B:804:TYR:CE1	2.49	0.48
1:C:304:LYS:HE2	1:C:306:ASP:HB2	1.95	0.48
1:B:738:LYS:O	1:B:742:PHE:HB2	2.13	0.48
1:C:671:CYS:SG	1:C:672:SER:N	2.87	0.48
1:C:780:VAL:HG22	1:C:820:LEU:HD21	1.96	0.48
1:D:155:GLU:OE2	1:D:198:PRO:HD2	2.14	0.48
1:D:502:ARG:HH11	1:D:503:HIS:H	1.59	0.48
2:E:119:LEU:O	2:E:120:ASP:C	2.51	0.48
1:A:910:ASN:ND2	2:E:79:PHE:H	2.11	0.48
1:C:169:LYS:HD3	1:C:173:ASP:HB3	1.95	0.48
1:C:771:ILE:HG23	1:C:774:ILE:HD11	1.96	0.47
1:B:457:ASN:O	1:B:460:LEU:HG	2.14	0.47
1:B:641:LYS:HA	1:B:641:LYS:HD2	1.63	0.47
1:D:771:ILE:HD12	1:D:772:ILE:N	2.29	0.47
1:D:776:ASP:O	1:D:780:VAL:HG13	2.14	0.47
1:A:761:LEU:HD12	1:A:762:THR:HG23	1.97	0.47
1:B:544:PHE:HB3	1:B:550:PHE:HB3	1.96	0.47
1:C:761:LEU:HD23	1:C:765:ASN:HD22	1.78	0.47
1:A:679:GLY:O	1:A:680:GLU:C	2.53	0.47
1:A:920:TYR:CD2	1:A:944:VAL:HG22	2.50	0.47
1:B:176:LYS:HB2	1:B:182:ASN:HD21	1.79	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243:PRO:HG2	1:B:266:LEU:HD23	1.97	0.47
1:B:409:ILE:HG22	1:B:411:SER:H	1.80	0.47
1:B:620:ILE:HG21	1:B:667:LEU:HD21	1.95	0.47
1:C:1005:ILE:HG12	1:D:1005:ILE:HD11	1.95	0.47
1:A:632:ASP:OD2	1:B:987:ARG:NE	2.48	0.47
1:B:688:LEU:HD23	1:B:691:ILE:HD11	1.95	0.47
2:E:25:TRP:HA	2:E:25:TRP:CE3	2.49	0.47
1:B:674:ASP:OD1	1:B:674:ASP:N	2.47	0.47
1:B:959:LEU:HD13	1:B:984:LEU:HD21	1.96	0.47
1:C:877:PHE:CE2	1:C:924:GLU:HB3	2.50	0.47
1:D:705:ASN:HB2	1:D:708:PHE:HB3	1.97	0.47
1:A:686:GLU:HA	1:A:689:VAL:HG12	1.97	0.47
1:B:489:VAL:HG21	1:B:512:LEU:HD21	1.97	0.47
1:C:499:THR:O	1:C:747:ARG:NE	2.48	0.47
1:C:820:LEU:O	1:C:824:THR:HG23	2.14	0.47
1:A:810:HIS:HD2	2:E:53:ILE:HG13	1.80	0.47
1:A:963:ASN:HB3	2:E:60:ALA:C	2.35	0.47
1:B:305:ASP:HB2	1:B:363:LEU:HD11	1.96	0.47
1:D:437:LYS:HE2	1:D:437:LYS:HB3	1.72	0.47
1:B:569:MET:HG3	1:B:625:TYR:CD2	2.50	0.46
1:B:773:SER:HA	1:B:776:ASP:OD2	2.15	0.46
1:C:31:LYS:HE2	1:C:301:PHE:HD2	1.80	0.46
1:C:985:LYS:HD2	1:D:1001:MET:CE	2.45	0.46
1:D:188:ASP:OD1	1:D:188:ASP:N	2.48	0.46
1:D:883:GLU:HA	1:D:886:ILE:HD12	1.97	0.46
2:E:71:LYS:HE3	2:E:72:ARG:H	1.79	0.46
2:F:115:GLU:N	2:F:115:GLU:OE1	2.48	0.46
1:A:452:TYR:HE1	1:A:478:ARG:HG2	1.80	0.46
1:A:486:THR:O	1:A:490:THR:HG22	2.16	0.46
1:B:510:GLU:OE2	1:B:514:ARG:NH2	2.43	0.46
1:B:618:LEU:O	1:B:621:GLU:HG2	2.15	0.46
1:D:239:SER:O	1:D:239:SER:OG	2.32	0.46
1:B:733:LEU:HA	1:B:736:ILE:HG12	1.97	0.46
1:B:884:LEU:O	1:B:887:GLU:HG3	2.15	0.46
1:C:799:LEU:HD23	1:C:799:LEU:HA	1.78	0.46
1:D:363:LEU:O	1:D:370:ARG:NH1	2.31	0.46
1:A:283:LEU:O	1:A:287:SER:HB2	2.15	0.46
1:C:769:LYS:HA	1:C:772:ILE:HD12	1.98	0.46
1:C:132:THR:OG1	1:C:218:TYR:OH	2.30	0.46
1:C:959:LEU:HD12	1:C:984:LEU:HD21	1.97	0.46
1:A:511:PHE:HE1	1:A:514:ARG:HH21	1.64	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:756:VAL:O	1:B:759:GLU:HG3	2.14	0.46
1:C:655:ILE:O	1:C:659:PHE:HB2	2.16	0.46
1:C:781:LEU:O	1:C:785:LYS:HG2	2.16	0.46
1:D:229:LEU:HD12	1:D:264:LYS:HD3	1.98	0.46
1:A:959:LEU:HA	1:A:962:TYR:CE2	2.51	0.46
1:B:319:LEU:HB3	1:B:325:ILE:HD11	1.98	0.46
1:C:376:LYS:HZ2	1:C:377:GLN:HG2	1.81	0.46
1:C:668:GLU:OE2	1:C:760:ARG:NH2	2.49	0.46
1:C:801:SER:O	1:C:804:TYR:HB2	2.16	0.46
1:C:842:LEU:HB2	1:C:871:ILE:HD13	1.97	0.46
2:F:28:GLU:HG3	2:F:41:LYS:HE2	1.98	0.46
1:A:452:TYR:CE1	1:A:478:ARG:HG2	2.51	0.46
1:A:930:MET:O	1:A:933:PHE:HD2	1.98	0.46
1:C:749:LEU:HA	1:C:753:LYS:HD2	1.97	0.46
1:C:786:HIS:NE2	1:C:834:GLN:HA	2.31	0.46
1:D:299:ASN:HB3	1:D:302:ILE:HD11	1.98	0.46
1:A:732:GLY:O	1:A:736:ILE:HG12	2.16	0.46
1:C:307:GLU:OE1	1:C:307:GLU:N	2.46	0.46
1:C:920:TYR:HE1	1:C:930:MET:HB2	1.81	0.46
1:D:784:GLU:C	1:D:786:HIS:N	2.67	0.46
1:D:986:GLU:O	1:D:989:LYS:HG2	2.16	0.46
2:E:97:GLU:HG2	2:E:98:ILE:N	2.31	0.46
1:A:493:ASN:OD1	1:A:503:HIS:HA	2.15	0.45
1:B:840:LYS:HB2	1:B:840:LYS:HE3	1.67	0.45
1:D:417:LYS:O	1:D:421:MET:HG2	2.15	0.45
2:E:27:VAL:HA	2:E:88:HIS:HA	1.97	0.45
1:A:1000:LEU:O	1:A:1005:ILE:HG13	2.16	0.45
1:B:45:PHE:HD1	1:B:218:TYR:HE2	1.63	0.45
1:C:809:LYS:HD3	1:C:815:PHE:HE1	1.81	0.45
1:D:305:ASP:HA	1:D:308:VAL:HG12	1.98	0.45
1:D:505:LYS:HD2	1:D:508:THR:HA	1.99	0.45
1:C:328:ILE:HG13	1:C:329:ASP:N	2.32	0.45
1:D:680:GLU:OE1	1:D:683:LYS:N	2.40	0.45
1:D:831:LYS:HG2	1:D:834:GLN:HB3	1.99	0.45
1:A:865:LEU:O	1:A:869:ILE:HD12	2.16	0.45
1:B:169:LYS:HD3	1:B:173:ASP:HB3	1.98	0.45
1:B:305:ASP:OD1	1:B:305:ASP:N	2.50	0.45
1:B:713:ILE:HD11	1:B:744:PHE:CE1	2.52	0.45
1:C:436:TYR:HE1	1:C:599:CYS:HB2	1.80	0.45
2:E:54:ASN:HB2	2:E:58:ASP:HB2	1.98	0.45
1:A:683:LYS:O	1:A:686:GLU:HG2	2.16	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:348:ARG:NH2	1:D:351:ASN:O	2.50	0.45
1:D:955:ILE:HD12	1:D:956:PRO:CD	2.44	0.45
1:A:46:VAL:HA	1:A:216:ILE:HG22	1.99	0.45
1:A:785:LYS:HE2	1:A:785:LYS:HB2	1.80	0.45
1:D:838:LEU:HB3	1:D:853:LEU:HD11	1.98	0.45
2:E:64:ILE:HG12	2:E:110:PHE:CE1	2.52	0.45
1:A:636:PHE:CZ	1:B:956:PRO:HG3	2.51	0.45
1:B:218:TYR:CG	1:B:225:ILE:HD11	2.52	0.45
1:B:960:LYS:HD2	1:B:996:TYR:HE1	1.81	0.45
1:C:998:GLU:O	1:C:1002:ASN:HB2	2.17	0.45
2:E:100:LEU:O	2:E:101:HIS:C	2.55	0.45
1:A:407:ILE:HG12	1:A:589:TYR:HB3	1.99	0.45
1:A:673:ILE:H	1:A:673:ILE:HG13	1.46	0.45
1:A:412:LEU:HD22	1:A:441:PHE:CZ	2.52	0.45
1:A:914:SER:O	1:A:918:ILE:HD13	2.17	0.45
1:B:655:ILE:O	1:B:659:PHE:HB2	2.17	0.45
1:C:99:ALA:O	1:C:103:ILE:HG12	2.17	0.45
1:C:462:SER:O	1:C:462:SER:OG	2.25	0.45
1:C:834:GLN:O	1:C:838:LEU:HD12	2.16	0.45
1:A:867:ASN:HD21	2:E:76:GLU:C	2.20	0.44
1:B:576:PHE:HB2	2:E:14:LEU:HD11	1.99	0.44
1:A:14:LYS:HB2	1:A:14:LYS:HE3	1.73	0.44
1:A:723:ALA:O	1:A:726:VAL:HG22	2.17	0.44
1:A:951:TYR:OH	1:A:976:MET:SD	2.69	0.44
1:A:977:LYS:HE2	1:A:981:ILE:HD11	1.99	0.44
1:B:368:ASP:C	1:B:370:ARG:N	2.68	0.44
1:D:86:ARG:O	1:D:90:ILE:HG12	2.17	0.44
1:D:480:ARG:HD2	1:D:605:PHE:HE2	1.81	0.44
1:D:642:LYS:HD3	1:D:642:LYS:HA	1.79	0.44
1:A:370:ARG:HB3	1:A:378:TYR:HE1	1.82	0.44
1:C:236:GLN:HB2	1:C:239:SER:HB3	2.00	0.44
1:C:829:GLN:HA	1:C:835:ILE:HD11	1.99	0.44
1:A:717:LYS:HD2	1:A:757:TRP:HH2	1.81	0.44
1:C:641:LYS:HB2	1:C:641:LYS:HE2	1.74	0.44
1:D:784:GLU:C	1:D:786:HIS:H	2.21	0.44
1:A:345:THR:HB	1:A:397:ALA:HA	2.00	0.44
1:A:817:SER:CB	1:A:820:LEU:HB3	2.48	0.44
1:B:545:LEU:HD13	1:B:600:LEU:HD21	1.99	0.44
1:A:675:LYS:HB3	1:A:675:LYS:HE3	1.40	0.44
1:A:692:ALA:O	1:A:695:ILE:HG22	2.16	0.44
1:A:772:ILE:HD13	1:A:812:GLU:HG3	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:960:LYS:HE3	1:D:996:TYR:CZ	2.52	0.44
2:E:20:ILE:O	2:E:22:THR:HG23	2.18	0.44
1:B:326:ARG:HG3	1:B:329:ASP:HB2	2.00	0.44
1:C:531:MET:HG2	1:C:535:PHE:CD2	2.53	0.44
1:D:763:LYS:HD2	1:D:764:CYS:HB2	2.00	0.44
2:F:43:TYR:CE1	2:F:67:PHE:HB2	2.53	0.44
1:A:979:HIS:HA	1:A:982:GLU:HG3	1.98	0.44
1:B:499:THR:O	1:B:500:PHE:HB2	2.18	0.44
1:B:557:LYS:HB2	1:B:557:LYS:HE2	1.70	0.44
1:C:150:SER:HG	1:C:163:SER:HG	1.59	0.44
1:C:293:LEU:HD23	1:C:293:LEU:HA	1.87	0.44
1:C:422:LYS:O	1:C:425:ILE:HG22	2.17	0.44
1:C:480:ARG:HD2	1:C:605:PHE:HZ	1.83	0.44
1:C:772:ILE:HA	1:C:775:ILE:HD11	2.00	0.44
1:D:320:PHE:HE1	1:D:387:PHE:HB2	1.82	0.44
1:A:99:ALA:O	1:A:103:ILE:HG12	2.17	0.43
1:A:329:ASP:O	1:A:333:VAL:HG23	2.18	0.43
1:B:326:ARG:H	1:B:326:ARG:HG2	1.68	0.43
1:D:325:ILE:HD12	1:D:326:ARG:H	1.83	0.43
2:F:24:VAL:HA	2:F:113:VAL:O	2.18	0.43
1:A:476:ILE:HD13	1:A:524:ILE:HD11	2.00	0.43
1:A:718:ALA:O	1:A:721:TYR:N	2.51	0.43
1:B:22:LEU:HD12	1:B:22:LEU:HA	1.90	0.43
1:B:155:GLU:OE1	1:B:199:LEU:HB2	2.18	0.43
1:C:772:ILE:O	1:C:775:ILE:HD12	2.17	0.43
1:C:949:PHE:HZ	1:C:954:PHE:HB2	1.83	0.43
1:D:169:LYS:HD2	1:D:173:ASP:HB2	2.00	0.43
1:D:374:SER:O	1:D:376:LYS:N	2.49	0.43
1:D:376:LYS:HZ2	1:D:377:GLN:HE21	1.65	0.43
2:E:44:PHE:HB3	2:E:64:ILE:HD11	2.00	0.43
1:C:589:TYR:OH	1:C:651:ASP:OD2	2.37	0.43
1:C:950:ASP:HB3	1:C:953:LYS:NZ	2.32	0.43
1:D:866:MET:O	1:D:869:ILE:HG13	2.18	0.43
1:A:827:LEU:HD21	1:A:835:ILE:HG13	2.00	0.43
1:B:454:LEU:HA	1:B:457:ASN:HD22	1.83	0.43
1:B:881:HIS:HA	1:B:884:LEU:HD12	2.01	0.43
1:D:784:GLU:O	1:D:786:HIS:N	2.52	0.43
2:E:64:ILE:HG12	2:E:110:PHE:CZ	2.54	0.43
1:C:642:LYS:HE2	1:C:642:LYS:HB3	1.80	0.43
1:B:540:LYS:HE2	1:B:540:LYS:HB2	1.74	0.43
1:C:477:ASN:ND2	1:C:601:TRP:H	2.16	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:TYR:CG	1:B:532:PRO:HD3	2.53	0.43
1:A:418:TYR:O	1:A:421:MET:HB3	2.19	0.43
1:D:502:ARG:NH1	1:D:503:HIS:HB2	2.33	0.43
1:D:816:ILE:HD13	1:D:816:ILE:HA	1.88	0.43
2:F:30:ASP:HB2	2:F:41:LYS:HZ2	1.83	0.43
2:F:86:ALA:HB3	2:F:96:THR:HA	2.00	0.43
1:A:868:GLY:HA3	1:A:874:ILE:HD12	2.00	0.43
1:A:931:GLU:C	1:A:933:PHE:N	2.71	0.43
1:C:532:PRO:HG3	1:D:148:TYR:CZ	2.53	0.43
1:D:612:ILE:HG21	1:D:658:HIS:CD2	2.53	0.43
1:D:980:VAL:HA	1:D:983:VAL:HG12	2.00	0.43
1:D:987:ARG:HA	1:D:987:ARG:NH1	2.34	0.43
2:F:46:LYS:HB3	2:F:116:VAL:HG12	2.00	0.43
1:A:208:ILE:HD13	1:A:228:LEU:HD11	1.99	0.43
1:B:237:LYS:NZ	1:B:238:ASP:OD1	2.51	0.43
1:D:422:LYS:HB2	1:D:422:LYS:HE3	1.90	0.43
1:D:544:PHE:HD2	1:D:550:PHE:HB2	1.84	0.43
1:C:294:ILE:O	1:C:297:GLN:HG2	2.19	0.42
1:A:693:GLU:O	1:A:696:THR:HG22	2.19	0.42
1:C:762:THR:HA	1:C:765:ASN:HB2	2.01	0.42
1:C:998:GLU:HA	1:C:1001:MET:SD	2.59	0.42
1:D:237:LYS:HZ2	1:D:238:ASP:HB2	1.84	0.42
1:D:291:ASP:O	1:D:295:GLU:HG2	2.18	0.42
1:D:984:LEU:HD11	1:D:1000:LEU:HB2	2.01	0.42
1:D:994:LYS:HD3	1:D:994:LYS:HA	1.80	0.42
1:A:554:ASP:OD2	1:A:591:ASN:ND2	2.51	0.42
1:B:759:GLU:HA	1:B:762:THR:HG22	2.01	0.42
1:B:811:PHE:CD1	1:B:811:PHE:N	2.87	0.42
1:C:326:ARG:NH1	1:C:328:ILE:HD11	2.34	0.42
1:C:767:LEU:HD22	1:C:771:ILE:HB	2.01	0.42
2:E:33:LEU:HA	2:E:80:ASN:CB	2.49	0.42
2:E:114:LYS:HA	2:E:114:LYS:HD2	1.85	0.42
1:A:816:ILE:HD13	1:A:846:SER:N	2.35	0.42
1:B:585:LEU:HD13	1:B:619:LEU:HD21	2.02	0.42
1:C:755:TYR:HB2	1:C:804:TYR:CE1	2.54	0.42
1:C:839:PHE:CZ	1:C:864:ASP:HA	2.54	0.42
1:C:869:ILE:HG13	1:C:870:ARG:N	2.35	0.42
2:F:106:ILE:HD12	2:F:106:ILE:HA	1.88	0.42
1:A:308:VAL:O	1:A:312:ILE:HG22	2.18	0.42
1:A:328:ILE:HD11	1:A:587:ARG:HD2	2.01	0.42
1:A:423:LYS:HE3	1:A:423:LYS:HA	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:666:ASN:HA	1:A:669:ARG:HG3	1.99	0.42
1:D:214:VAL:HG22	1:D:244:PHE:HB2	2.01	0.42
1:D:693:GLU:O	1:D:696:THR:HG22	2.18	0.42
1:D:713:ILE:HD12	1:D:713:ILE:HA	1.83	0.42
1:A:361:PHE:CE2	1:A:395:CYS:HA	2.55	0.42
1:A:655:ILE:O	1:A:659:PHE:HB2	2.19	0.42
1:B:492:PHE:CZ	1:B:503:HIS:HB3	2.54	0.42
1:B:776:ASP:HA	1:B:779:LEU:HG	2.02	0.42
1:C:213:ILE:HG23	1:C:243:PRO:HB3	2.02	0.42
1:D:639:PHE:HE1	1:D:641:LYS:HA	1.84	0.42
1:A:442:LEU:HD21	1:A:447:ARG:HB2	2.02	0.42
1:A:526:ASP:OD1	1:A:526:ASP:N	2.53	0.42
1:B:553:ASP:OD1	1:B:554:ASP:N	2.52	0.42
1:B:553:ASP:O	1:B:556:VAL:HG12	2.19	0.42
1:B:699:PHE:HB2	1:B:743:TYR:HB3	2.01	0.42
1:C:768:PRO:HD2	1:C:771:ILE:HD13	2.02	0.42
1:C:836:ASP:O	1:C:840:LYS:HG2	2.19	0.42
1:D:75:LYS:O	1:D:76:LYS:HG2	2.20	0.42
1:B:363:LEU:HD22	1:B:369:GLU:HB3	2.02	0.42
1:C:755:TYR:HB2	1:C:804:TYR:HE1	1.85	0.42
1:C:861:ASN:HA	1:C:888:TYR:OH	2.20	0.42
1:D:117:ILE:HD13	1:D:117:ILE:HA	1.91	0.42
1:D:414:TYR:O	1:D:657:ARG:NH2	2.53	0.42
1:D:628:THR:HA	1:D:631:ILE:HG22	2.02	0.42
1:D:738:LYS:O	1:D:742:PHE:HB2	2.20	0.42
1:D:783:ALA:HA	1:D:786:HIS:HD2	1.84	0.42
1:B:142:CYS:O	1:B:145:ARG:N	2.53	0.42
1:B:486:THR:O	1:B:489:VAL:HG12	2.19	0.42
1:B:805:GLY:O	1:B:807:LEU:N	2.53	0.42
1:C:278:ASN:OD1	1:C:281:ASP:HB2	2.20	0.42
1:C:467:ASN:OD1	1:C:468:GLY:N	2.53	0.42
1:C:479:TYR:HB2	1:C:522:PHE:HE2	1.84	0.42
1:C:629:ARG:NH1	1:C:643:SER:OG	2.52	0.42
1:C:981:ILE:HD13	1:C:981:ILE:HA	1.93	0.42
1:D:627:ARG:HH12	1:D:675:LYS:HG3	1.84	0.42
1:A:442:LEU:CD2	1:A:447:ARG:HB2	2.49	0.41
1:C:206:THR:HG21	1:D:206:THR:HG21	2.01	0.41
1:D:151:VAL:HA	1:D:167:LEU:HB3	2.02	0.41
1:D:227:MET:HE2	1:D:227:MET:HB2	1.96	0.41
1:A:699:PHE:CD2	1:A:743:TYR:HB3	2.55	0.41
1:B:661:ILE:HG12	1:B:717:LYS:NZ	2.35	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:663:ASP:OD1	1:B:664:ILE:N	2.52	0.41
1:B:742:PHE:HE1	1:B:778:PHE:HB2	1.84	0.41
1:C:122:LEU:HD23	1:C:122:LEU:HA	1.86	0.41
1:C:921:PHE:O	1:C:969:LYS:NZ	2.53	0.41
1:C:937:ASP:HB3	1:C:939:GLN:HG3	2.03	0.41
1:C:973:ASN:HB3	1:C:975:HIS:CE1	2.56	0.41
1:D:147:LYS:HA	1:D:147:LYS:HD3	1.91	0.41
1:D:958:TRP:HA	1:D:961:ASN:HD21	1.86	0.41
1:D:993:ASP:HB2	1:D:996:TYR:HD2	1.84	0.41
2:E:20:ILE:HD11	2:E:118:TYR:CE1	2.55	0.41
1:A:345:THR:HB	1:A:397:ALA:CA	2.50	0.41
1:A:348:ARG:NH2	1:A:353:GLY:O	2.53	0.41
1:A:405:THR:HG21	1:A:586:LEU:HD21	2.02	0.41
1:A:637:SER:O	1:A:638:PHE:C	2.58	0.41
1:A:678:PHE:HB3	1:A:681:GLN:NE2	2.33	0.41
1:A:738:LYS:O	1:A:739:ALA:HB3	2.20	0.41
1:B:461:ASN:OD1	1:B:462:SER:N	2.54	0.41
1:C:624:GLU:HG3	1:C:671:CYS:SG	2.60	0.41
1:D:432:ILE:HD13	1:D:432:ILE:HA	1.88	0.41
1:D:682:GLU:OE1	1:D:682:GLU:N	2.45	0.41
1:D:841:LEU:HD12	1:D:841:LEU:HA	1.93	0.41
2:F:28:GLU:HG3	2:F:41:LYS:CE	2.51	0.41
1:A:322:LEU:HD12	1:A:325:ILE:HD11	2.03	0.41
1:A:767:LEU:HD23	1:A:767:LEU:HA	1.86	0.41
1:D:634:LEU:HB2	1:D:638:PHE:CE2	2.55	0.41
1:D:638:PHE:CD1	1:D:638:PHE:C	2.93	0.41
1:D:668:GLU:OE2	1:D:760:ARG:NH2	2.53	0.41
1:A:118:HIS:O	1:A:121:ILE:HG22	2.21	0.41
1:A:374:SER:OG	1:A:375:LYS:N	2.53	0.41
1:A:681:GLN:H	1:A:681:GLN:HG2	1.71	0.41
1:A:941:ASP:OD1	1:A:945:ASP:HB3	2.20	0.41
1:B:256:GLU:CD	1:B:256:GLU:H	2.23	0.41
1:B:811:PHE:N	1:B:811:PHE:HD1	2.19	0.41
1:B:843:PRO:HD3	1:B:871:ILE:HD13	2.03	0.41
1:C:304:LYS:HG2	1:C:305:ASP:H	1.85	0.41
1:C:402:THR:HG23	1:C:402:THR:O	2.21	0.41
1:C:831:LYS:HA	1:C:831:LYS:HD2	1.88	0.41
1:C:866:MET:SD	1:C:867:ASN:N	2.93	0.41
1:D:697:LYS:HB3	1:D:697:LYS:HE2	1.62	0.41
1:D:938:ASP:OD1	1:D:938:ASP:N	2.53	0.41
1:D:979:HIS:O	1:D:983:VAL:HG12	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:TYR:HD1	1:A:11:TYR:HA	1.74	0.41
1:A:89:GLN:HE22	1:A:188:ASP:CG	2.24	0.41
1:B:721:TYR:O	1:B:760:ARG:NH1	2.43	0.41
2:E:68:SER:O	2:E:69:GLU:C	2.59	0.41
1:A:37:SER:HB2	1:A:42:LEU:HD22	2.02	0.41
1:A:728:LEU:HD12	1:A:733:LEU:HD23	2.03	0.41
1:A:755:TYR:O	1:A:758:LEU:HG	2.21	0.41
1:A:817:SER:O	1:A:818:LYS:C	2.59	0.41
1:D:104:LEU:HD12	1:D:104:LEU:HA	1.95	0.41
1:D:787:ILE:HG12	1:D:834:GLN:OE1	2.21	0.41
1:D:987:ARG:NH1	1:D:990:ASN:HD22	2.19	0.41
1:B:781:LEU:O	1:B:785:LYS:HG3	2.20	0.41
1:C:495:LEU:O	1:C:499:THR:HG22	2.20	0.41
1:D:780:VAL:HG12	1:D:820:LEU:HD21	2.02	0.41
1:A:73:SER:N	1:A:74:PRO:HD3	2.36	0.41
1:A:179:LYS:HE2	1:A:179:LYS:HB2	1.89	0.41
1:A:412:LEU:HD11	1:A:420:VAL:HB	2.03	0.41
1:A:867:ASN:ND2	2:E:76:GLU:HA	2.35	0.41
1:B:78:ASN:O	1:B:79:TYR:HD1	2.03	0.41
1:B:185:LEU:HD23	1:B:185:LEU:HA	1.85	0.41
1:B:293:LEU:HD23	1:B:293:LEU:HA	1.93	0.41
1:B:889:LEU:HD23	1:B:889:LEU:HA	1.78	0.41
1:C:720:LEU:HD13	1:C:720:LEU:HA	1.93	0.41
1:C:732:GLY:O	1:C:736:ILE:HG12	2.20	0.41
1:C:889:LEU:HD11	1:C:933:PHE:CG	2.55	0.41
1:D:661:ILE:HD13	1:D:661:ILE:HA	1.83	0.41
1:D:940:TYR:O	1:D:944:VAL:HB	2.20	0.41
2:F:85:LYS:HA	2:F:85:LYS:HD3	1.87	0.41
1:A:168:LEU:HD12	1:A:168:LEU:HA	1.86	0.41
1:B:873:LEU:HD23	1:B:873:LEU:HA	1.91	0.41
1:B:1000:LEU:HD23	1:B:1000:LEU:HA	1.88	0.41
1:C:423:LYS:HE3	1:C:423:LYS:HB3	1.98	0.41
1:C:592:LEU:HA	1:C:592:LEU:HD23	1.85	0.41
1:A:738:LYS:HE3	1:A:738:LYS:HB3	1.97	0.40
1:A:910:ASN:HD22	2:E:79:PHE:N	2.19	0.40
1:A:1000:LEU:HD12	1:A:1005:ILE:HD11	2.03	0.40
1:B:952:LYS:HA	1:B:952:LYS:HD3	1.97	0.40
1:C:254:GLU:OE1	1:C:254:GLU:N	2.54	0.40
1:C:1005:ILE:HD12	1:C:1005:ILE:HA	1.96	0.40
1:D:15:LEU:O	1:D:18:VAL:HG12	2.21	0.40
2:E:11:THR:HB	2:E:14:LEU:HD22	2.02	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:32:VAL:HB	2:E:82:LYS:CB	2.51	0.40
1:A:105:LYS:O	1:A:109:GLN:HB2	2.20	0.40
1:B:130:ILE:HD11	1:B:207:ILE:HG21	2.03	0.40
1:C:678:PHE:HB3	1:C:681:GLN:HE22	1.86	0.40
1:D:288:ALA:O	1:D:292:LEU:HB2	2.21	0.40
1:D:330:LEU:HD23	1:D:330:LEU:HA	1.88	0.40
1:D:809:LYS:HD3	1:D:809:LYS:HA	1.80	0.40
1:D:987:ARG:HA	1:D:987:ARG:HH11	1.86	0.40
1:A:502:ARG:O	1:A:504:TYR:CD2	2.74	0.40
1:A:836:ASP:O	1:A:840:LYS:HG3	2.21	0.40
1:B:959:LEU:HA	1:B:962:TYR:CD2	2.57	0.40
1:C:987:ARG:NE	1:C:987:ARG:HA	2.37	0.40
1:D:62:LEU:HA	1:D:62:LEU:HD23	1.83	0.40
1:D:152:ILE:HB	1:D:168:LEU:HD12	2.03	0.40
1:D:701:ALA:O	1:D:702:ASN:ND2	2.55	0.40
1:B:865:LEU:HD21	1:B:881:HIS:HB3	2.04	0.40
1:C:114:THR:HG22	1:C:115:ASN:N	2.36	0.40
1:C:220:LEU:HD21	1:C:268:ILE:HD11	2.03	0.40
1:C:1002:ASN:HB3	1:C:1003:TYR:HD1	1.87	0.40
1:D:978:HIS:O	1:D:981:ILE:HG22	2.21	0.40
2:E:54:ASN:CB	2:E:58:ASP:HB2	2.51	0.40
1:B:419:ASP:OD1	1:B:420:VAL:HG23	2.20	0.40
1:B:544:PHE:HD1	1:B:549:GLN:HE21	1.70	0.40
1:B:987:ARG:HD3	1:B:996:TYR:CE2	2.56	0.40
1:C:744:PHE:CD1	1:C:749:LEU:HD23	2.57	0.40
1:D:29:CYS:O	1:D:33:ILE:HG22	2.22	0.40
1:D:859:VAL:HG11	1:D:881:HIS:HE2	1.85	0.40
2:E:35:ASP:HB2	2:E:37:LYS:HE3	2.04	0.40
2:E:95:VAL:O	2:E:96:THR:C	2.59	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	A	963/1005 (96%)	900 (94%)	57 (6%)	6 (1%)	25	64
1	B	964/1005 (96%)	924 (96%)	40 (4%)	0	100	100
1	C	964/1005 (96%)	939 (97%)	25 (3%)	0	100	100
1	D	963/1005 (96%)	928 (96%)	34 (4%)	1 (0%)	51	83
2	E	109/120 (91%)	87 (80%)	19 (17%)	3 (3%)	5	34
2	F	109/120 (91%)	100 (92%)	8 (7%)	1 (1%)	17	57
All	All	4072/4260 (96%)	3878 (95%)	183 (4%)	11 (0%)	44	75

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	83	ILE
1	A	680	GLU
2	E	54	ASN
1	A	403	LEU
1	A	495	LEU
1	A	672	SER
1	A	492	PHE
2	E	78	GLU
1	A	675	LYS
1	D	507	PHE
2	E	83	ILE

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	A	885/923 (96%)	823 (93%)	62 (7%)	15	48
1	B	885/923 (96%)	843 (95%)	42 (5%)	26	61
1	C	892/923 (97%)	856 (96%)	36 (4%)	31	65
1	D	893/923 (97%)	846 (95%)	47 (5%)	22	58
2	E	92/113 (81%)	82 (89%)	10 (11%)	6	32
2	F	92/113 (81%)	86 (94%)	6 (6%)	17	51

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3739/3918 (95%)	3536 (95%)	203 (5%)	26 57

All (203) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ARG
1	A	11	TYR
1	A	14	LYS
1	A	19	PHE
1	A	21	MET
1	A	23	ASP
1	A	76	LYS
1	A	80	SER
1	A	84	TYR
1	A	124	MET
1	A	134	TYR
1	A	142	CYS
1	A	160	ASN
1	A	190	TYR
1	A	227	MET
1	A	276	ASP
1	A	366	SER
1	A	368	ASP
1	A	396	MET
1	A	441	PHE
1	A	444	CYS
1	A	449	GLU
1	A	493	ASN
1	A	495	LEU
1	A	520	THR
1	A	525	ASP
1	A	526	ASP
1	A	527	LEU
1	A	547	ASP
1	A	596	TYR
1	A	647	MET
1	A	649	TYR
1	A	662	ASP
1	A	670	SER
1	A	673	ILE
1	A	675	LYS
1	A	678	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	680	GLU
1	A	697	LYS
1	A	717	LYS
1	A	722	PHE
1	A	741	LEU
1	A	744	PHE
1	A	753	LYS
1	A	765	ASN
1	A	769	LYS
1	A	795	SER
1	A	815	PHE
1	A	816	ILE
1	A	837	PHE
1	A	844	LEU
1	A	889	LEU
1	A	895	ASN
1	A	911	ASP
1	A	913	MET
1	A	926	ASN
1	A	929	LYS
1	A	931	GLU
1	A	932	GLU
1	A	940	TYR
1	A	958	TRP
1	A	991	SER
1	B	31	LYS
1	B	107	PHE
1	B	124	MET
1	B	134	TYR
1	B	149	PHE
1	B	190	TYR
1	B	276	ASP
1	B	282	TYR
1	B	306	ASP
1	B	326	ARG
1	B	328	ILE
1	B	356	TYR
1	B	368	ASP
1	B	375	LYS
1	B	376	LYS
1	B	378	TYR
1	B	396	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	404	ASN
1	B	467	ASN
1	B	469	CYS
1	B	475	GLN
1	B	495	LEU
1	B	497	LEU
1	B	499	THR
1	B	511	PHE
1	B	636	PHE
1	B	646	PHE
1	B	647	MET
1	B	656	SER
1	B	708	PHE
1	B	712	PHE
1	B	717	LYS
1	B	744	PHE
1	B	803	ASP
1	B	815	PHE
1	B	888	TYR
1	B	916	PHE
1	B	920	TYR
1	B	921	PHE
1	B	934	ILE
1	B	961	ASN
1	B	976	MET
1	C	81	SER
1	C	110	VAL
1	C	131	THR
1	C	149	PHE
1	C	160	ASN
1	C	186	LYS
1	C	279	GLU
1	C	317	SER
1	C	388	PHE
1	C	435	ASP
1	C	504	TYR
1	C	573	SER
1	C	578	MET
1	C	638	PHE
1	C	646	PHE
1	C	662	ASP
1	C	704	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	709	TYR
1	C	721	TYR
1	C	722	PHE
1	C	744	PHE
1	C	747	ARG
1	C	755	TYR
1	C	810	HIS
1	C	811	PHE
1	C	813	LYS
1	C	822	GLU
1	C	839	PHE
1	C	841	LEU
1	C	866	MET
1	C	877	PHE
1	C	913	MET
1	C	955	ILE
1	C	987	ARG
1	C	993	ASP
1	C	1001	MET
1	D	43	VAL
1	D	131	THR
1	D	134	TYR
1	D	145	ARG
1	D	157	ASP
1	D	183	VAL
1	D	190	TYR
1	D	194	ASP
1	D	240	PHE
1	D	317	SER
1	D	396	MET
1	D	419	ASP
1	D	430	VAL
1	D	449	GLU
1	D	469	CYS
1	D	495	LEU
1	D	500	PHE
1	D	508	THR
1	D	533	PHE
1	D	621	GLU
1	D	636	PHE
1	D	638	PHE
1	D	641	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	649	TYR
1	D	651	ASP
1	D	662	ASP
1	D	677	ARG
1	D	678	PHE
1	D	697	LYS
1	D	704	MET
1	D	709	TYR
1	D	728	LEU
1	D	744	PHE
1	D	763	LYS
1	D	832	GLN
1	D	846	SER
1	D	850	LYS
1	D	871	ILE
1	D	877	PHE
1	D	913	MET
1	D	916	PHE
1	D	929	LYS
1	D	930	MET
1	D	936	MET
1	D	939	GLN
1	D	943	PHE
1	D	974	LYS
2	E	11	THR
2	E	14	LEU
2	E	20	ILE
2	E	42	CYS
2	E	44	PHE
2	E	49	ASN
2	E	59	PHE
2	E	88	HIS
2	E	100	LEU
2	E	112	ILE
2	F	18	SER
2	F	39	LEU
2	F	43	TYR
2	F	62	SER
2	F	65	ASP
2	F	101	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (47) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	GLN
1	A	93	ASN
1	A	109	GLN
1	A	160	ASN
1	A	477	ASN
1	A	491	GLN
1	A	503	HIS
1	A	521	ASN
1	A	786	HIS
1	A	867	ASN
1	A	910	ASN
1	B	182	ASN
1	B	297	GLN
1	B	404	ASN
1	B	457	ASN
1	B	493	ASN
1	B	549	GLN
1	B	789	GLN
1	B	978	HIS
1	C	89	GLN
1	C	93	ASN
1	C	297	GLN
1	C	382	ASN
1	C	477	ASN
1	C	503	HIS
1	C	666	ASN
1	C	681	GLN
1	C	782	GLN
1	C	834	GLN
1	C	848	ASN
1	C	990	ASN
1	D	89	GLN
1	D	93	ASN
1	D	118	HIS
1	D	125	ASN
1	D	192	ASN
1	D	211	HIS
1	D	332	HIS
1	D	339	HIS
1	D	391	ASN
1	D	477	ASN
1	D	702	ASN
1	D	786	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	810	HIS
1	D	939	GLN
1	D	961	ASN
2	E	49	ASN

5.3.3 RNA [i](#)

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

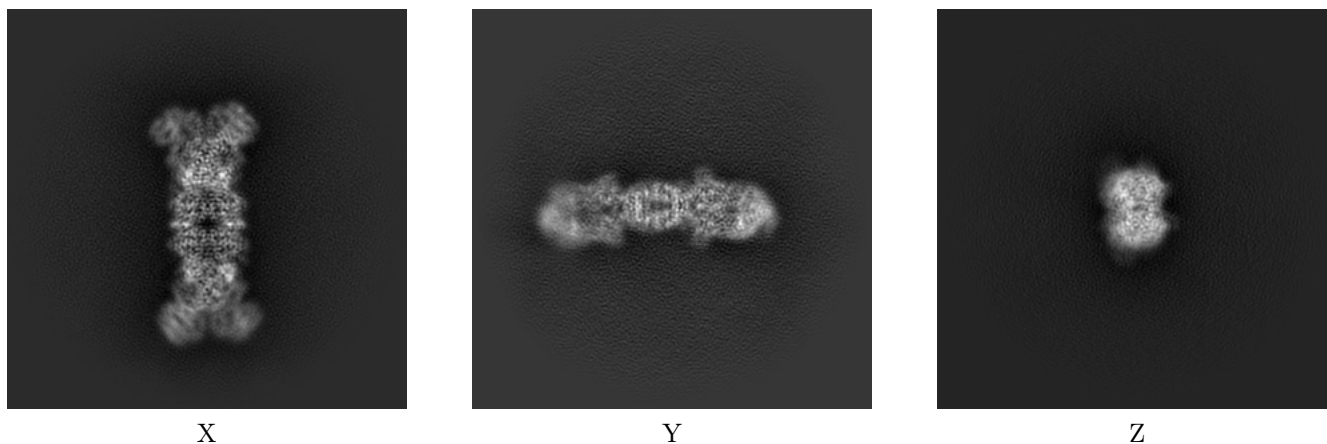
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37272. These allow visual inspection of the internal detail of the map and identification of artifacts.

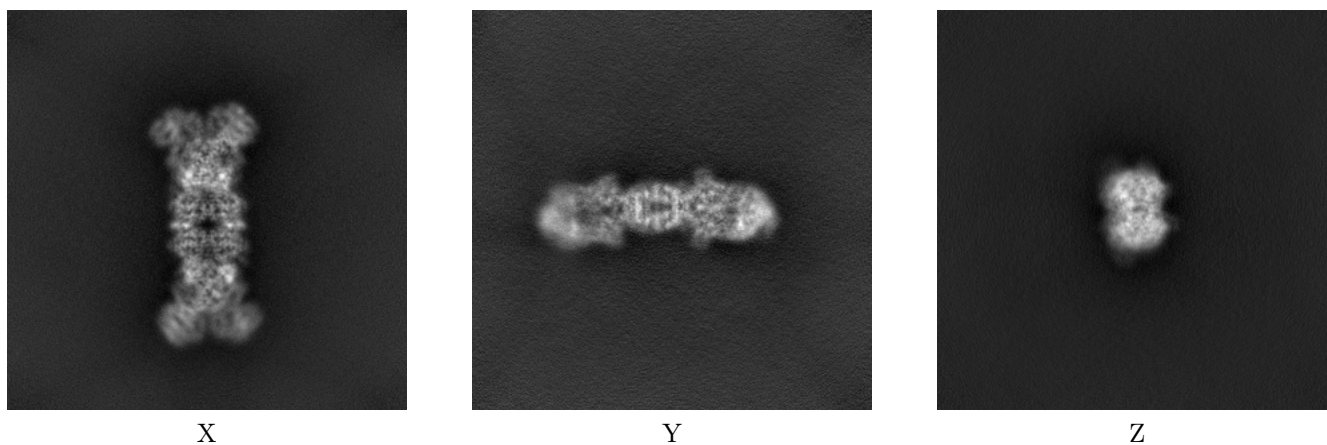
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



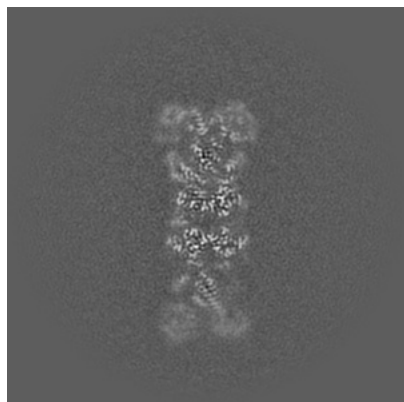
6.1.2 Raw map



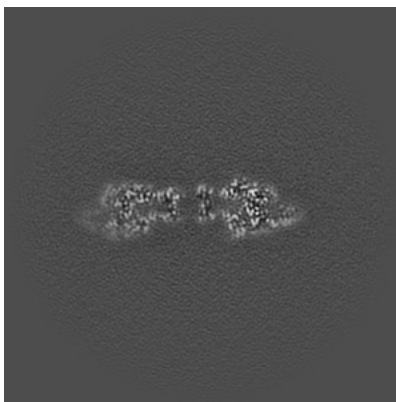
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

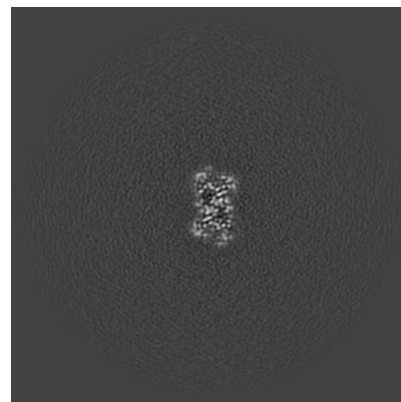
6.2.1 Primary map



X Index: 250

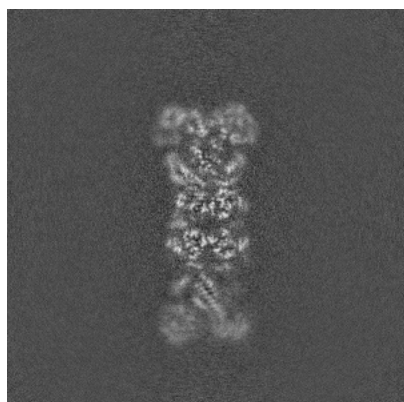


Y Index: 250

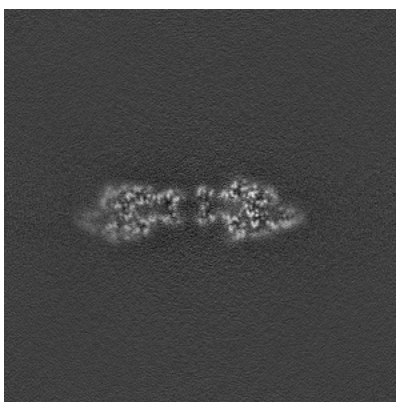


Z Index: 250

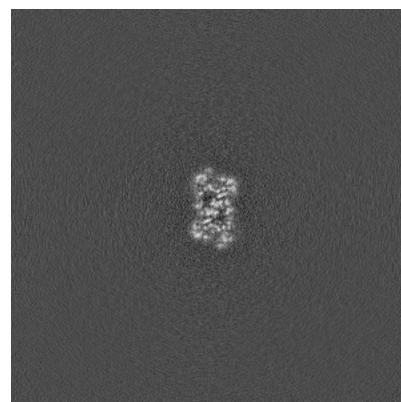
6.2.2 Raw map



X Index: 250



Y Index: 250

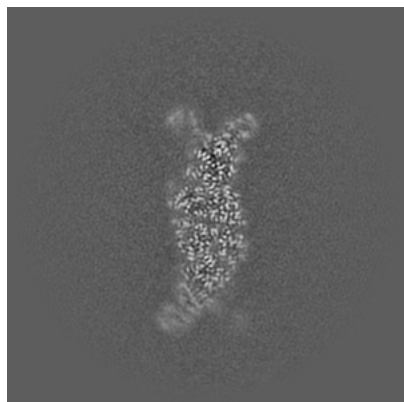


Z Index: 250

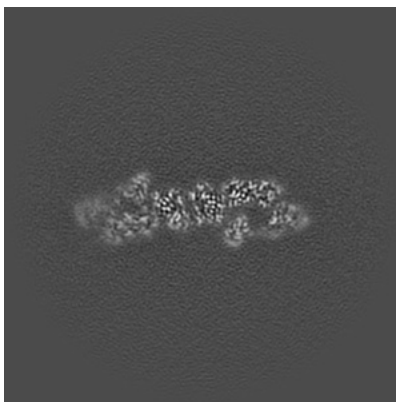
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

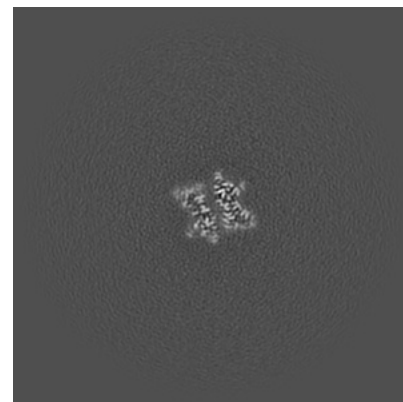
6.3.1 Primary map



X Index: 265

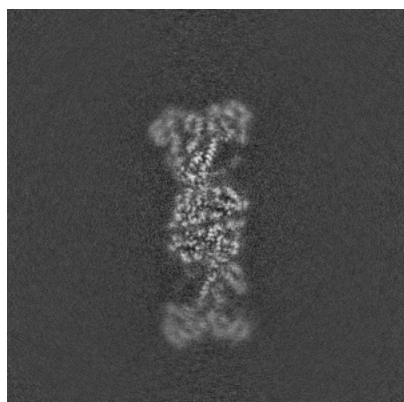


Y Index: 267

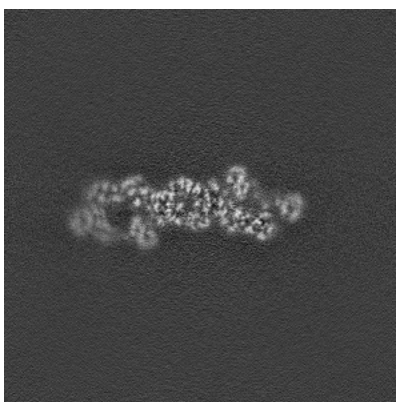


Z Index: 290

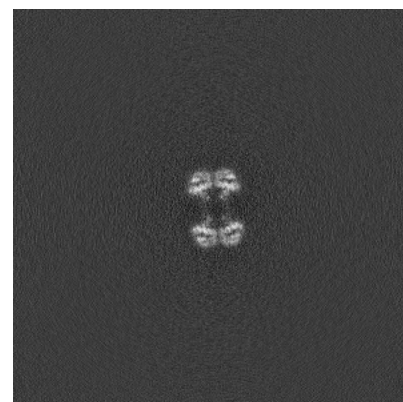
6.3.2 Raw map



X Index: 242



Y Index: 229

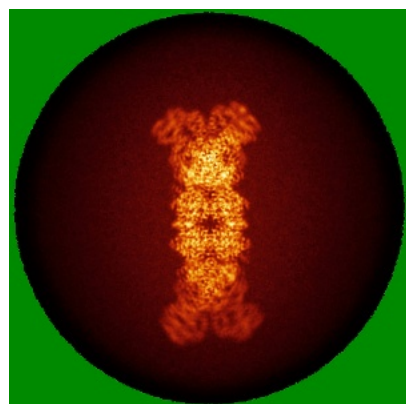


Z Index: 231

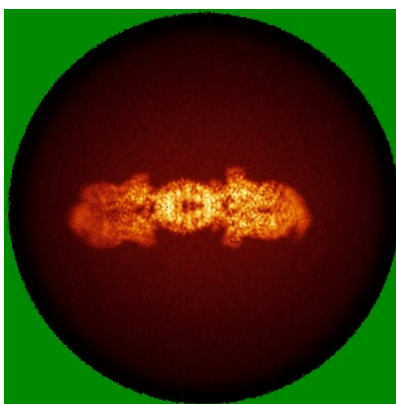
The images above show the largest variance slices of the map in three orthogonal directions.

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

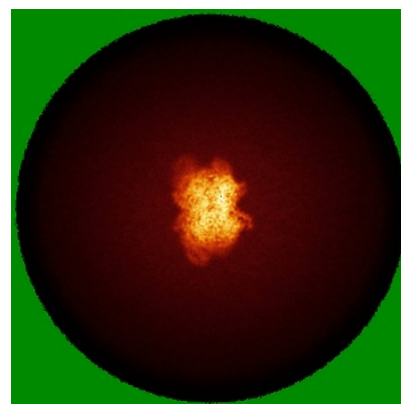
6.4.1 Primary map



X

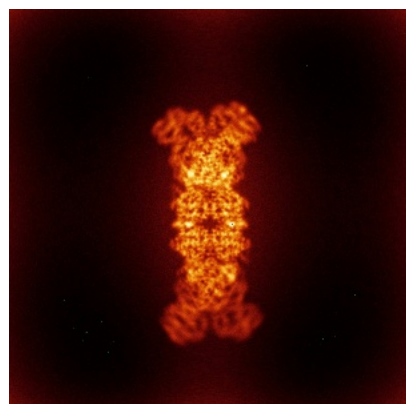


Y

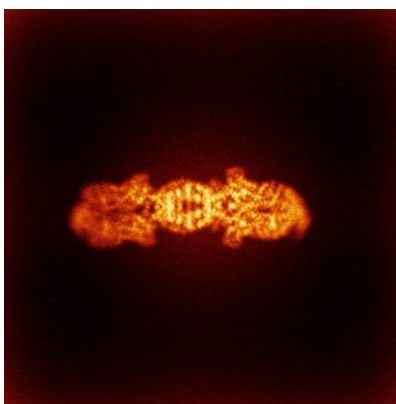


Z

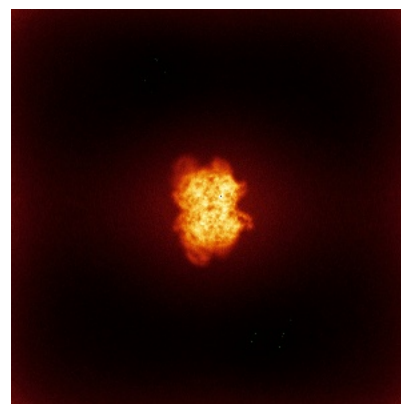
6.4.2 Raw map



X



Y

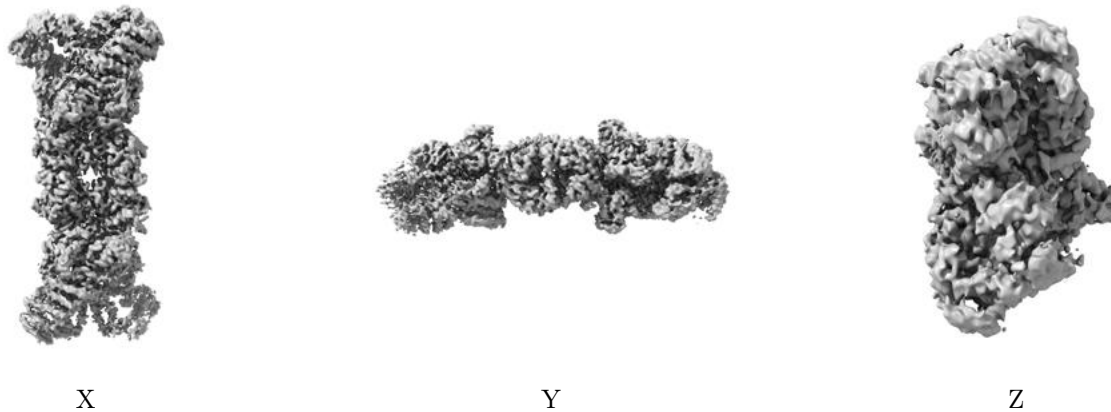


Z

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.

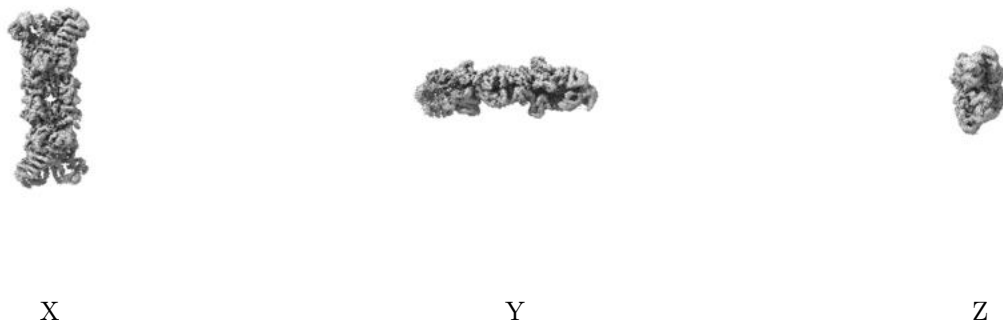
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.266. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

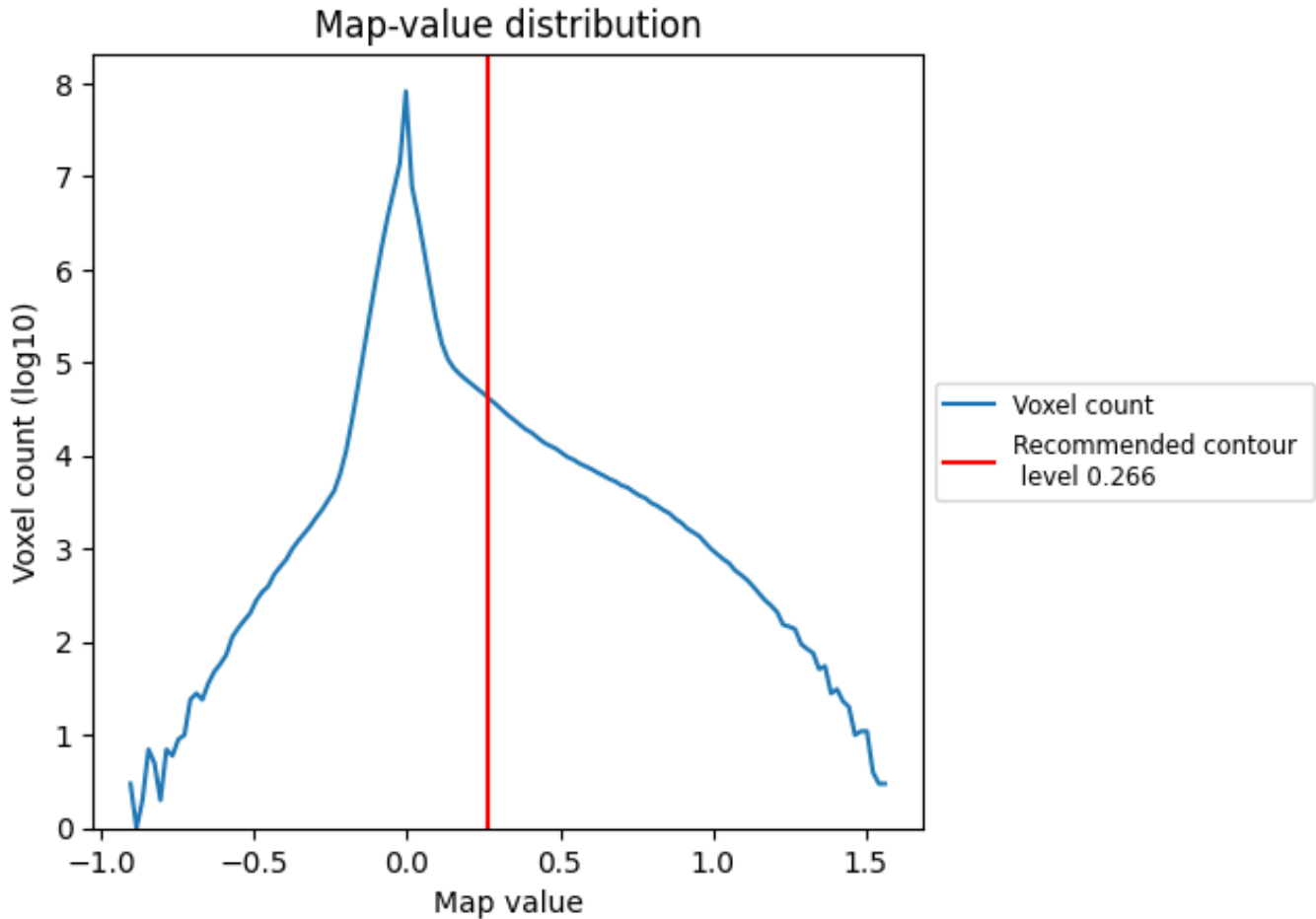
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

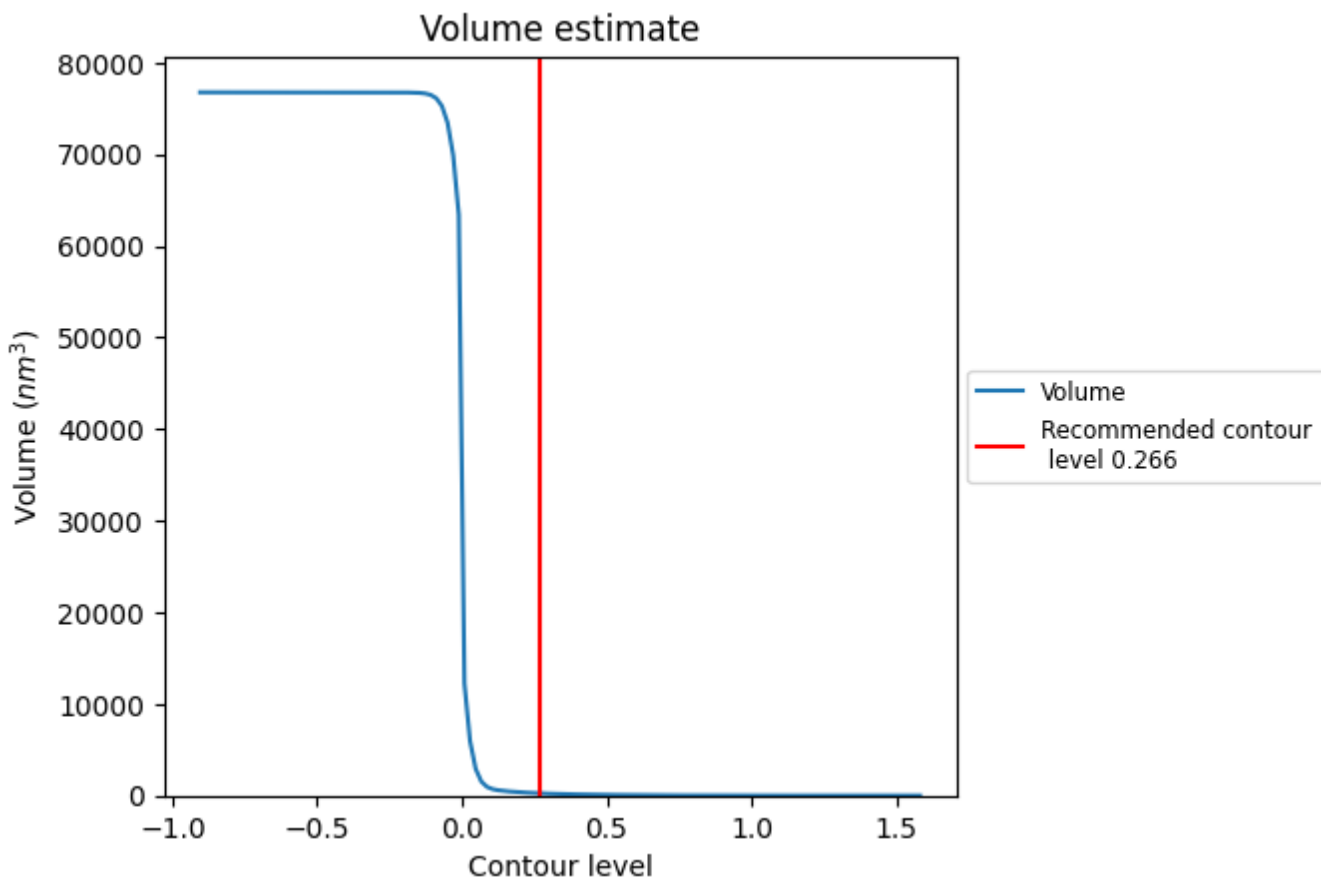
This section contains the results of statistical analysis of the map.

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.

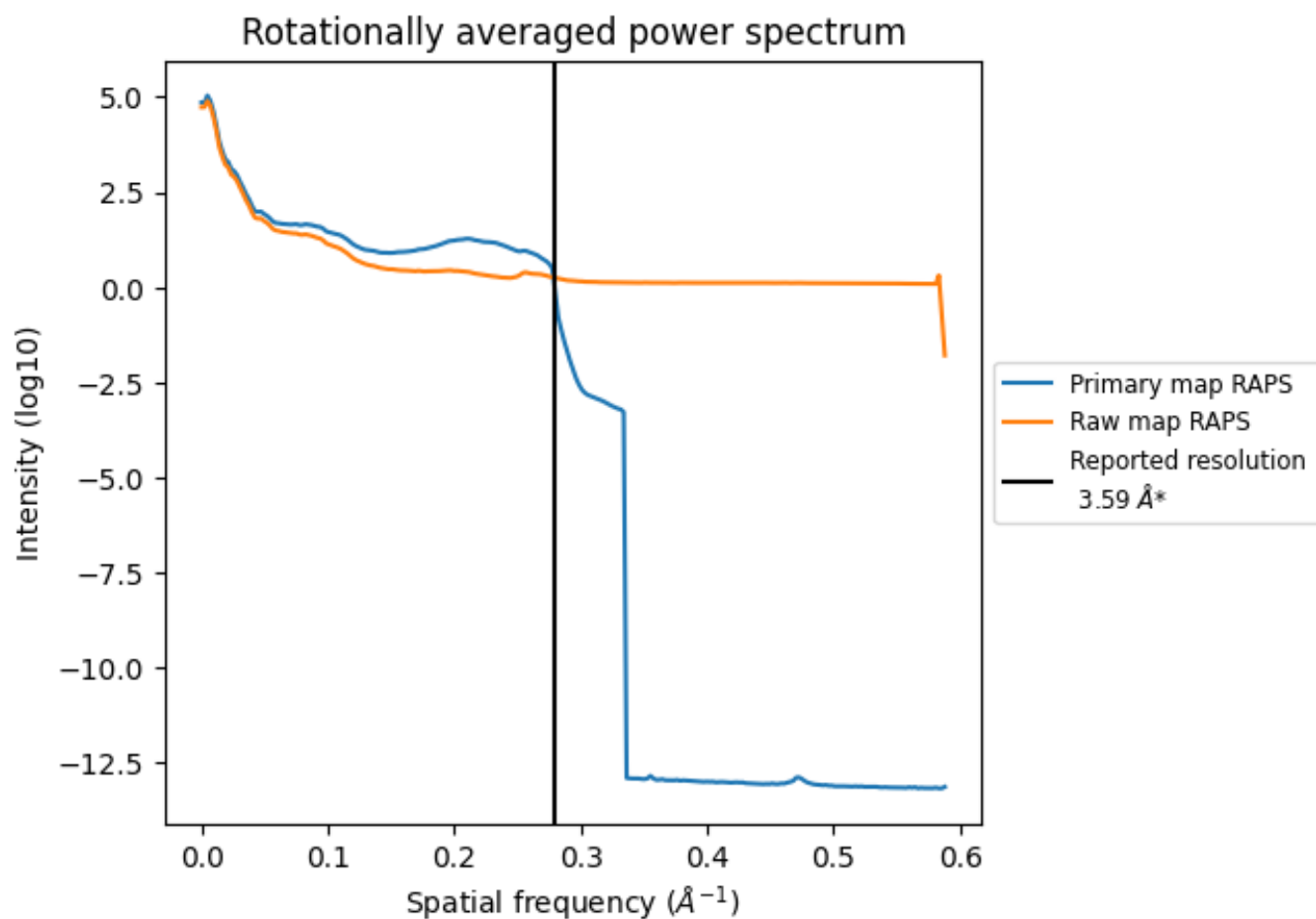
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 250 nm³; this corresponds to an approximate mass of 226 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](#)

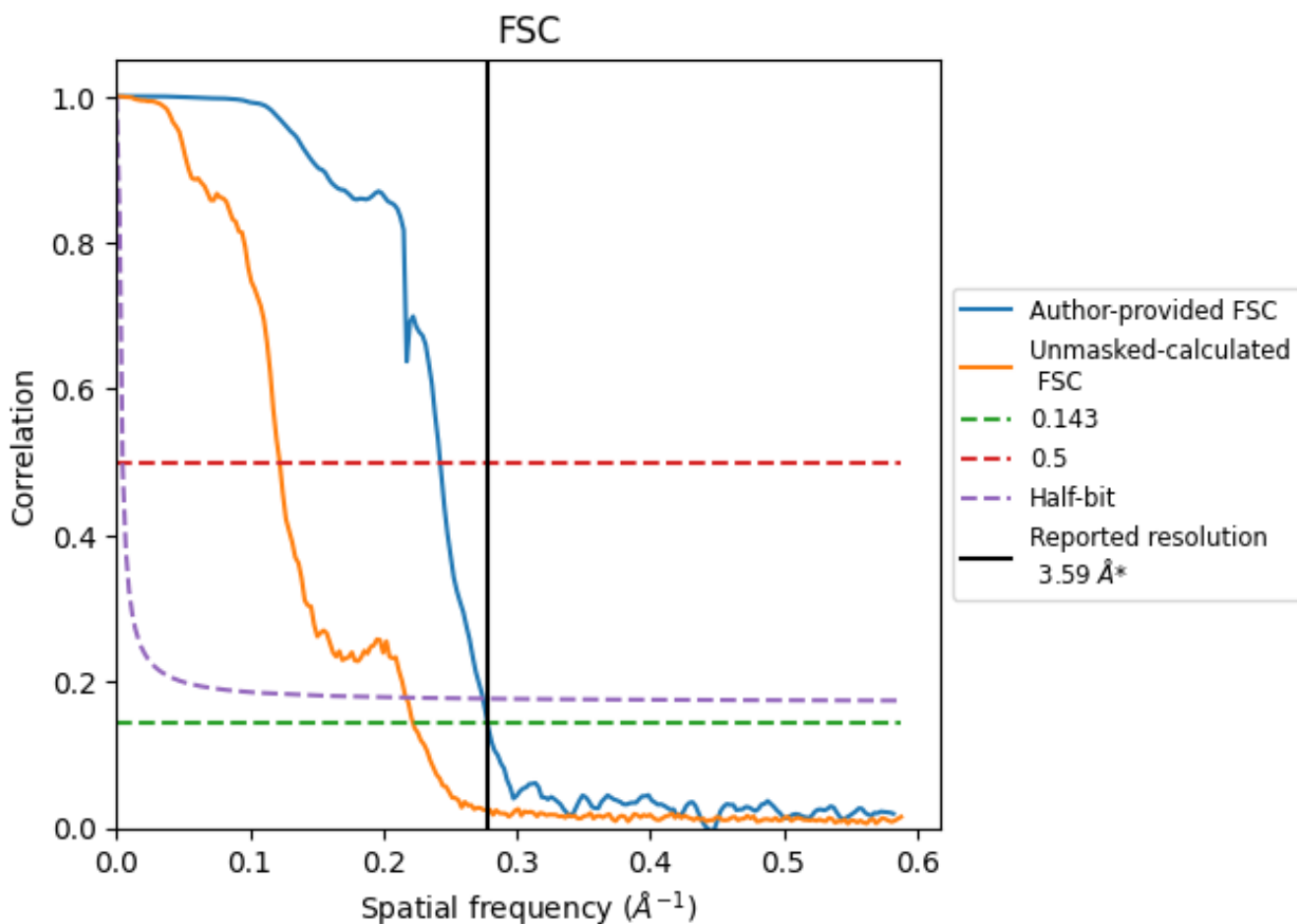


*Reported resolution corresponds to spatial frequency of 0.279 Å⁻¹

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 0.279 \AA^{-1}

8.2 Resolution estimates [i](#)

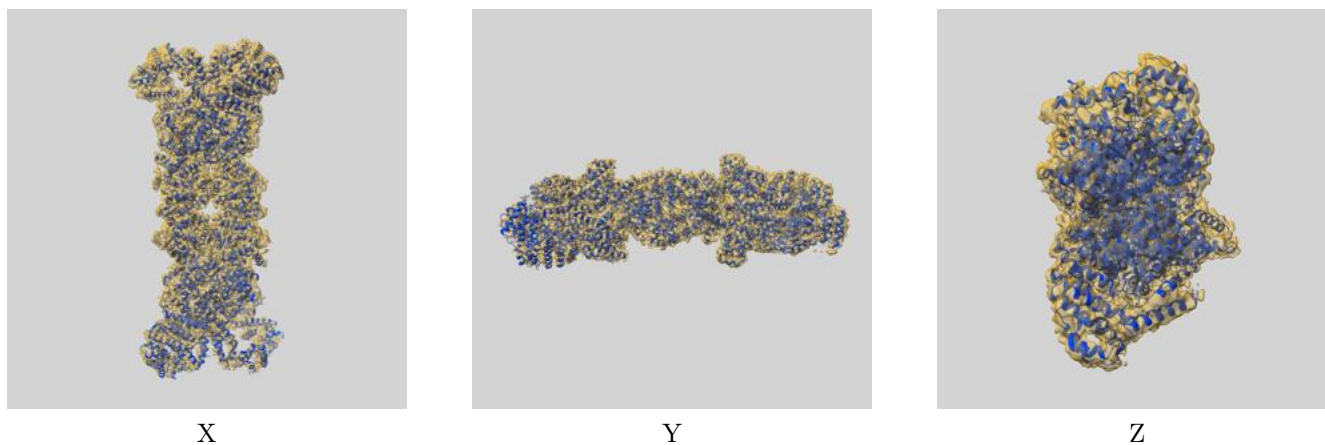
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.59	-	-
Author-provided FSC curve	3.59	4.12	3.64
Unmasked-calculated*	4.50	8.18	4.61

*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 4.50 differs from the reported value 3.59 by more than 10 %

9 Map-model fit [i](#)

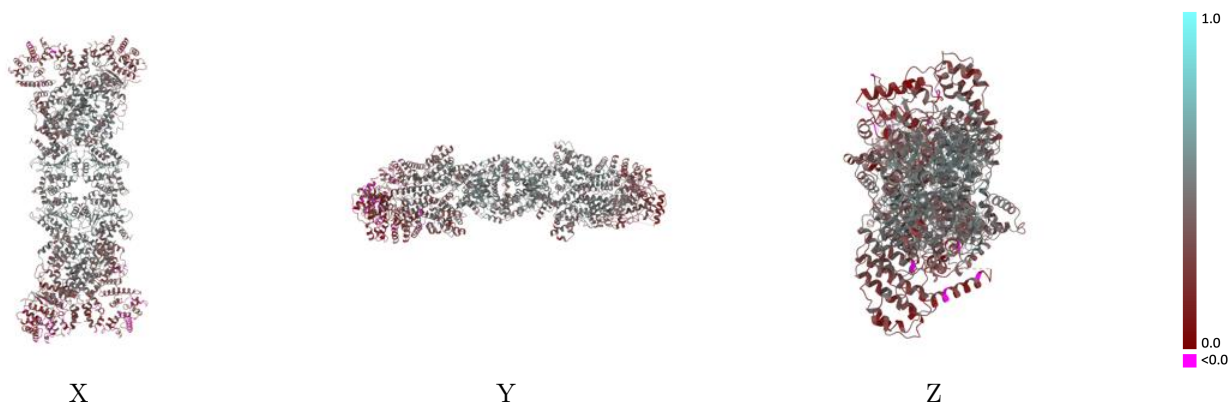
This section contains information regarding the fit between EMDB map EMD-37272 and PDB model 8W56. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)



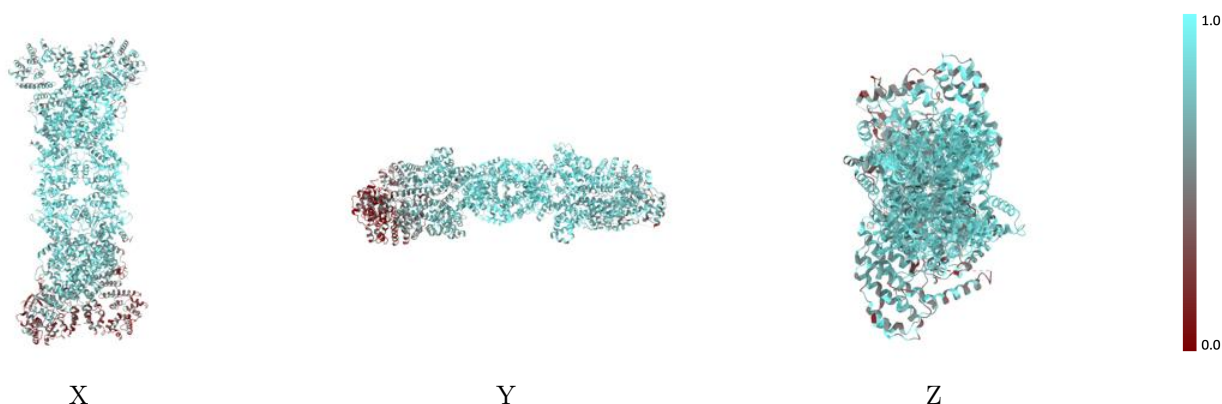
The images above show the 3D surface view of the map at the recommended contour level 0.266 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



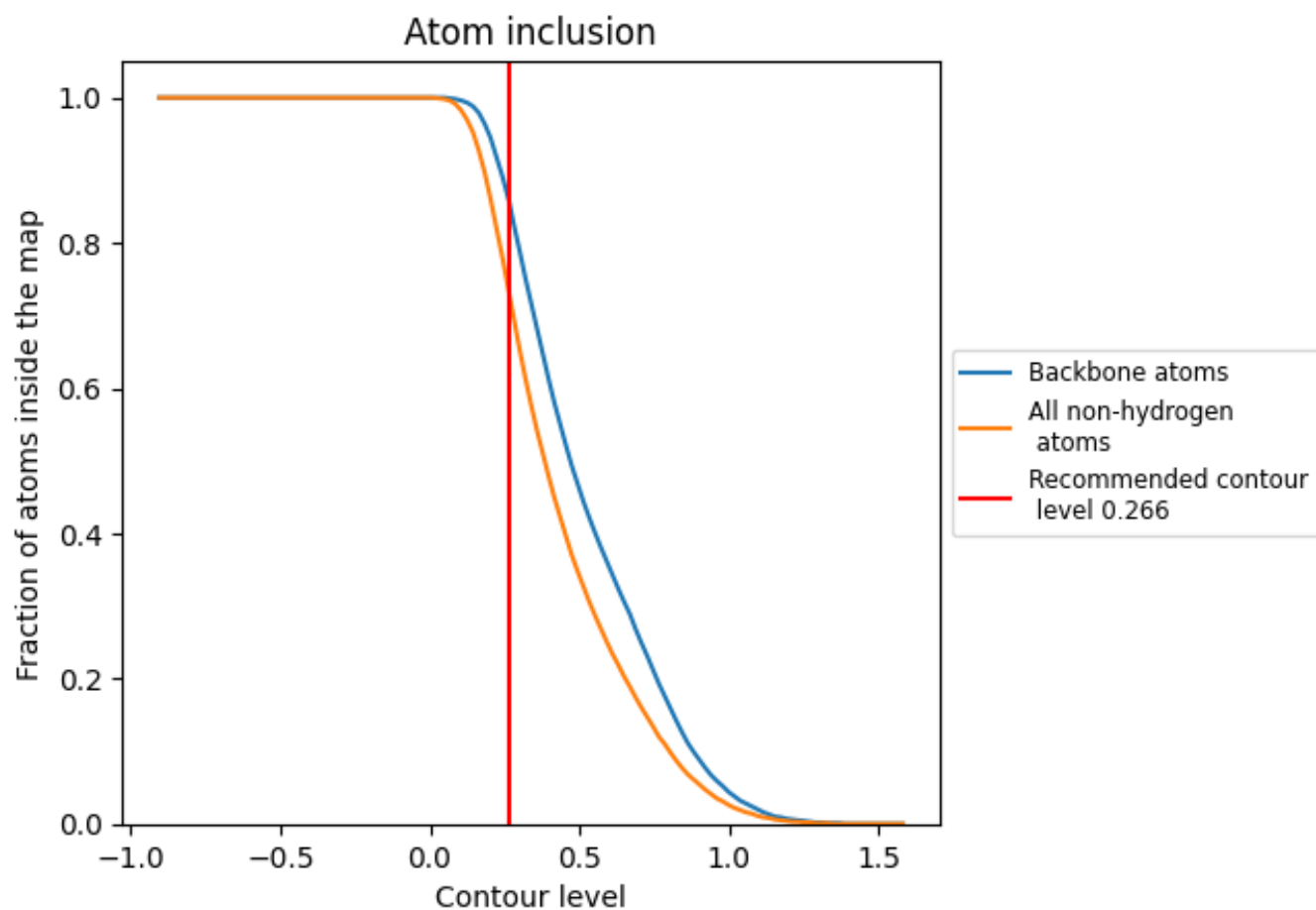
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.266).















9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 73% 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 (0.266) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7290	 0.3880
A	 0.6790	 0.3730
B	 0.6230	 0.3500
C	 0.8160	 0.4100
D	 0.8400	 0.4290
E	 0.3410	 0.3130
F	 0.7330	 0.3580

