Full wwPDB/EMDataBank EM Map/Model Validation Report (i)

Feb 20, 2018 – 09:35 pm GMT

PDB ID	:	6BPQ
EMDB ID:	:	EMD-7127
Title	:	Structure of the cold- and menthol-sensing ion channel TRPM8
Authors	:	Yin, Y.; Wu, M.; Zubcevic, L.; Borschel, W.F.; Lander, G.C.; Lee, S.-Y.
Deposited on	:	2017-11-25
Resolution	:	4.10 Å(reported)

This is a Full wwPDB/EMDataBank EM Map/Model Validation Report for a publicly released PDB/EMDB 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 (i) symbol.

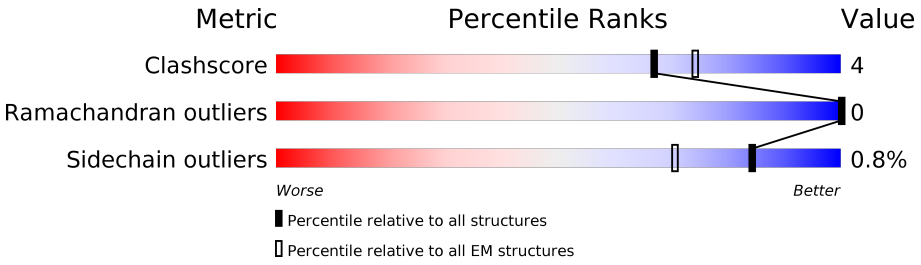
MolProbity	:	4.02b-467
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk30686

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 4.10 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	136279	1886
Ramachandran outliers	132675	1663
Sidechain outliers	132484	1531

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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 <=5%

Mol	Chain	Length	Quality of chain
1	A	950	80% 8% 12%
1	B	950	80% 7% 12%
1	C	950	80% 7% 12%
1	D	950	80% 8% 12%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 22404 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 Transient receptor potential cation channel subfamily M member 8.

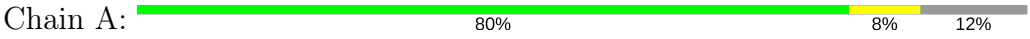
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	835	Total	C	N	O	S	0	0
			5601	3656	952	975	18		
1	B	835	Total	C	N	O	S	0	0
			5601	3656	952	975	18		
1	C	835	Total	C	N	O	S	0	0
			5601	3656	952	975	18		
1	D	835	Total	C	N	O	S	0	0
			5601	3656	952	975	18		

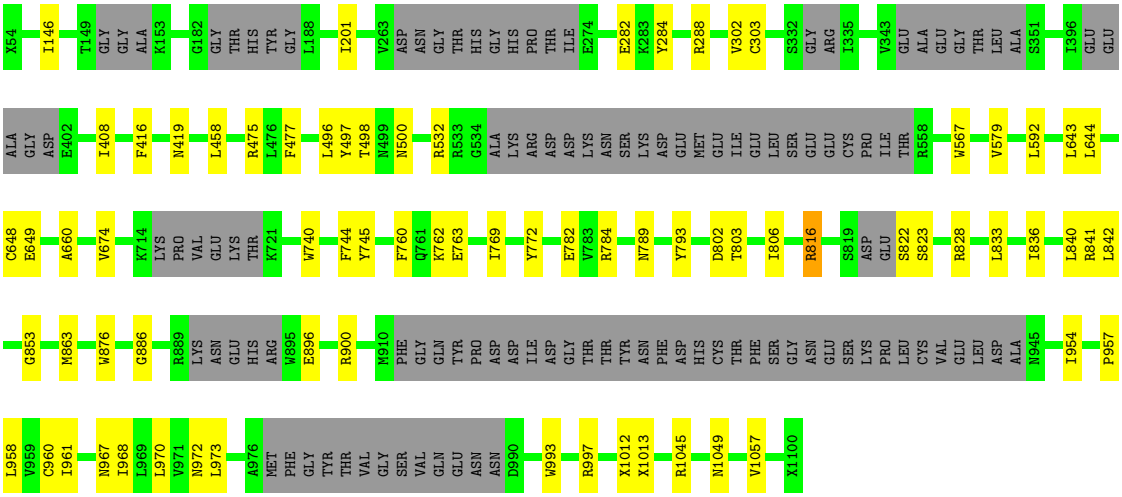
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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. 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. 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: Transient receptor potential cation channel subfamily M member 8

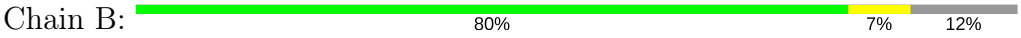
Chain A:

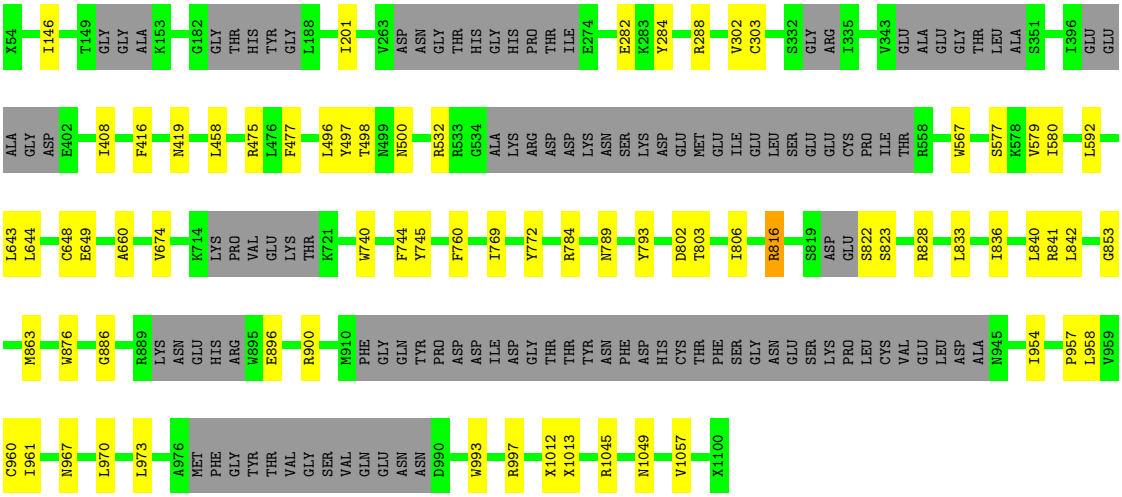




• Molecule 1: Transient receptor potential cation channel subfamily M member 8

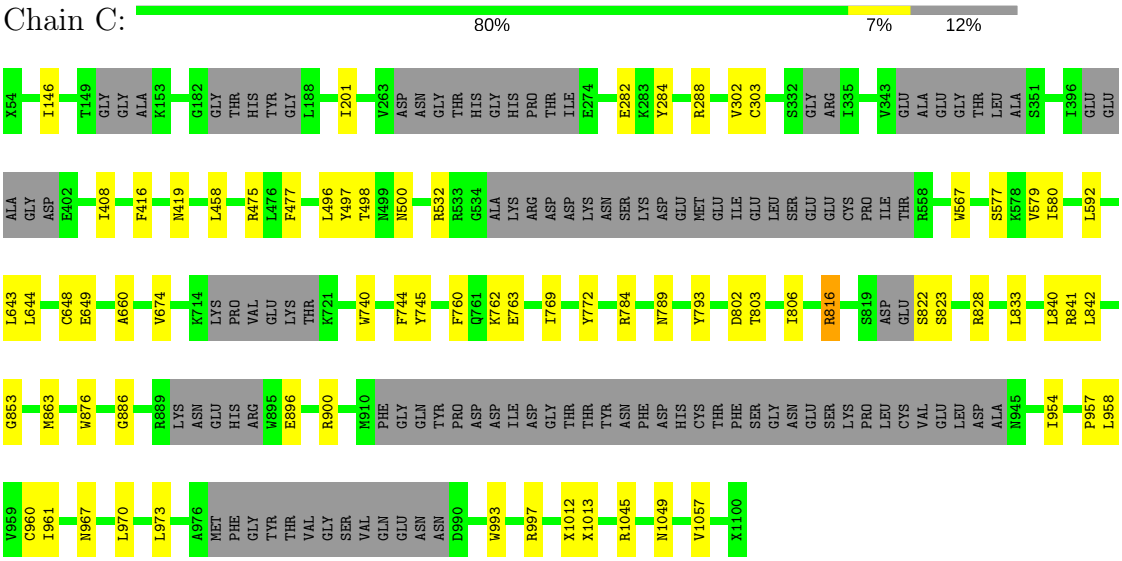
Chain B:





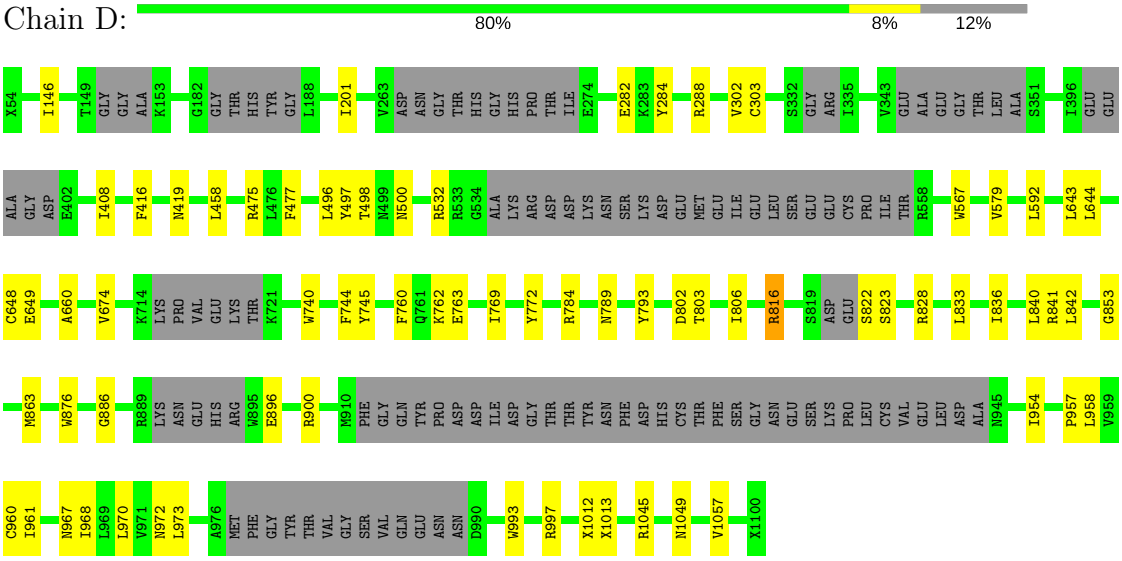
• Molecule 1: Transient receptor potential cation channel subfamily M member 8

Chain C:



• Molecule 1: Transient receptor potential cation channel subfamily M member 8

Chain D:



4 Experimental information (i)

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	19740	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 ($e^-/Å^2$)	56	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	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	$\#\|Z\| > 2$	RMSZ	$\#\|Z\| > 2$
1	A	0.38	0/5386	0.53	1/7394 (0.0%)
1	B	0.38	0/5386	0.53	1/7394 (0.0%)
1	C	0.38	0/5386	0.53	1/7394 (0.0%)
1	D	0.38	0/5386	0.53	1/7394 (0.0%)
All	All	0.38	0/21544	0.53	4/29576 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	643	LEU	CA-CB-CG	5.24	127.36	115.30
1	D	643	LEU	CA-CB-CG	5.24	127.36	115.30
1	A	643	LEU	CA-CB-CG	5.24	127.35	115.30
1	B	643	LEU	CA-CB-CG	5.23	127.33	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5601	0	4447	50	0
1	B	5601	0	4447	49	0
1	C	5601	0	4447	49	0
1	D	5601	0	4447	50	0
All	All	22404	0	17788	171	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 4.

All (171) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:498:THR:HA	1:B:532:ARG:HH12	1.51	0.76
1:C:498:THR:HA	1:C:532:ARG:HH12	1.51	0.76
1:A:498:THR:HA	1:A:532:ARG:HH12	1.51	0.75
1:D:498:THR:HA	1:D:532:ARG:HH12	1.51	0.75
1:A:973:LEU:HD13	1:D:970:LEU:HD22	1.78	0.66
1:B:967:ASN:ND2	1:C:863:MET:SD	2.72	0.62
1:A:954:ILE:HG21	1:B:833:LEU:HD13	1.81	0.61
1:C:967:ASN:ND2	1:D:863:MET:SD	2.72	0.61
1:D:498:THR:HA	1:D:532:ARG:NH1	2.15	0.60
1:B:954:ILE:HA	1:B:957:PRO:HD2	1.83	0.60
1:B:498:THR:HA	1:B:532:ARG:NH1	2.15	0.60
1:C:498:THR:HA	1:C:532:ARG:NH1	2.15	0.60
1:B:970:LEU:HD22	1:C:973:LEU:HD13	1.83	0.60
1:D:954:ILE:HA	1:D:957:PRO:HD2	1.83	0.60
1:C:970:LEU:HD22	1:D:973:LEU:HD13	1.83	0.60
1:A:954:ILE:HA	1:A:957:PRO:HD2	1.83	0.59
1:C:954:ILE:HA	1:C:957:PRO:HD2	1.83	0.59
1:A:863:MET:SD	1:D:967:ASN:ND2	2.76	0.59
1:A:498:THR:HA	1:A:532:ARG:NH1	2.15	0.59
1:A:896:GLU:O	1:A:900:ARG:HB2	2.03	0.59
1:B:896:GLU:O	1:B:900:ARG:HB2	2.03	0.59
1:B:284:TYR:OH	1:B:288:ARG:NH2	2.36	0.59
1:C:896:GLU:O	1:C:900:ARG:HB2	2.03	0.59
1:B:146:ILE:HG23	1:B:303:CYS:HA	1.86	0.58
1:D:146:ILE:HG23	1:D:303:CYS:HA	1.86	0.58
1:C:284:TYR:OH	1:C:288:ARG:NH2	2.36	0.58
1:D:896:GLU:O	1:D:900:ARG:HB2	2.03	0.58
1:A:967:ASN:ND2	1:B:863:MET:SD	2.77	0.58
1:C:146:ILE:HG23	1:C:303:CYS:HA	1.86	0.58
1:A:146:ILE:HG23	1:A:303:CYS:HA	1.86	0.58
1:D:760:PHE:O	1:D:816:ARG:NH2	2.37	0.58
1:A:760:PHE:O	1:A:816:ARG:NH2	2.37	0.58
1:D:284:TYR:OH	1:D:288:ARG:NH2	2.36	0.58
1:B:760:PHE:O	1:B:816:ARG:NH2	2.37	0.58
1:C:853:GLY:O	1:C:993:TRP:NE1	2.37	0.58
1:D:853:GLY:O	1:D:993:TRP:NE1	2.37	0.57
1:C:760:PHE:O	1:C:816:ARG:NH2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1057:VAL:HG21	1:D:201:ILE:HD11	1.86	0.57
1:A:284:TYR:OH	1:A:288:ARG:NH2	2.36	0.57
1:A:853:GLY:O	1:A:993:TRP:NE1	2.37	0.57
1:B:592:LEU:HD21	1:B:660:ALA:HB2	1.86	0.57
1:D:592:LEU:HD21	1:D:660:ALA:HB2	1.86	0.57
1:B:853:GLY:O	1:B:993:TRP:NE1	2.37	0.56
1:C:201:ILE:HD11	1:D:1057:VAL:HG21	1.88	0.56
1:B:201:ILE:HD11	1:C:1057:VAL:HG21	1.88	0.56
1:C:592:LEU:HD21	1:C:660:ALA:HB2	1.86	0.56
1:A:592:LEU:HD21	1:A:660:ALA:HB2	1.86	0.56
1:A:970:LEU:HD22	1:B:973:LEU:HD13	1.88	0.55
1:A:886:GLY:O	1:B:828:ARG:NE	2.40	0.55
1:B:954:ILE:HG21	1:C:833:LEU:HD13	1.89	0.55
1:A:961:ILE:HG12	1:B:840:LEU:HD21	1.90	0.54
1:B:958:LEU:O	1:B:961:ILE:HB	2.08	0.54
1:A:958:LEU:O	1:A:961:ILE:HB	2.08	0.54
1:C:954:ILE:HG21	1:D:833:LEU:HD13	1.89	0.54
1:C:302:VAL:HG21	1:C:408:ILE:HG23	1.90	0.54
1:C:958:LEU:O	1:C:961:ILE:HB	2.08	0.53
1:D:302:VAL:HG21	1:D:408:ILE:HG23	1.90	0.53
1:B:146:ILE:HG21	1:B:282:GLU:OE2	2.09	0.53
1:C:146:ILE:HG21	1:C:282:GLU:OE2	2.09	0.53
1:A:146:ILE:HG21	1:A:282:GLU:OE2	2.09	0.53
1:D:958:LEU:O	1:D:961:ILE:HB	2.08	0.53
1:B:886:GLY:O	1:C:828:ARG:NE	2.42	0.53
1:B:302:VAL:HG21	1:B:408:ILE:HG23	1.90	0.53
1:A:201:ILE:HD11	1:B:1057:VAL:HG21	1.91	0.53
1:C:886:GLY:O	1:D:828:ARG:NE	2.42	0.53
1:B:1045:ARG:O	1:B:1049:ASN:ND2	2.43	0.52
1:D:1045:ARG:O	1:D:1049:ASN:ND2	2.43	0.52
1:A:1045:ARG:O	1:A:1049:ASN:ND2	2.43	0.52
1:C:1045:ARG:O	1:C:1049:ASN:ND2	2.43	0.52
1:A:302:VAL:HG21	1:A:408:ILE:HG23	1.90	0.52
1:D:146:ILE:HG21	1:D:282:GLU:OE2	2.09	0.52
1:D:769:ILE:HA	1:D:772:TYR:HD2	1.76	0.51
1:C:769:ILE:HA	1:C:772:TYR:HD2	1.76	0.51
1:A:822:SER:OG	1:A:823:SER:N	2.45	0.50
1:B:475:ARG:HD3	1:B:579:VAL:HG22	1.94	0.50
1:C:475:ARG:HD3	1:C:579:VAL:HG22	1.94	0.50
1:A:833:LEU:HD13	1:D:954:ILE:HG21	1.92	0.50
1:D:475:ARG:HD3	1:D:579:VAL:HG22	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:475:ARG:HD3	1:A:579:VAL:HG22	1.93	0.50
1:A:769:ILE:HA	1:A:772:TYR:HD2	1.76	0.50
1:D:822:SER:OG	1:D:823:SER:N	2.44	0.50
1:D:648:CYS:SG	1:D:649:GLU:N	2.85	0.50
1:B:769:ILE:HA	1:B:772:TYR:HD2	1.76	0.49
1:B:961:ILE:HG12	1:C:840:LEU:HD21	1.94	0.49
1:A:648:CYS:SG	1:A:649:GLU:N	2.85	0.49
1:C:648:CYS:SG	1:C:649:GLU:N	2.85	0.49
1:B:822:SER:OG	1:B:823:SER:N	2.44	0.49
1:B:648:CYS:SG	1:B:649:GLU:N	2.85	0.49
1:C:822:SER:OG	1:C:823:SER:N	2.44	0.49
1:C:961:ILE:HG12	1:D:840:LEU:HD21	1.94	0.48
1:A:789:ASN:HB2	1:A:793:TYR:HB2	1.95	0.48
1:C:789:ASN:HB2	1:C:793:TYR:HB2	1.95	0.48
1:B:789:ASN:HB2	1:B:793:TYR:HB2	1.95	0.47
1:A:496:LEU:HD12	1:A:500:ASN:HB2	1.96	0.47
1:C:416:PHE:HD1	1:C:419:ASN:HD22	1.62	0.47
1:C:496:LEU:HD12	1:C:500:ASN:HB2	1.96	0.47
1:D:416:PHE:HD1	1:D:419:ASN:HD22	1.62	0.47
1:D:496:LEU:HD12	1:D:500:ASN:HB2	1.96	0.47
1:D:957:PRO:O	1:D:960:CYS:HB3	2.14	0.47
1:A:416:PHE:HD1	1:A:419:ASN:HD22	1.62	0.47
1:A:957:PRO:O	1:A:960:CYS:HB3	2.14	0.47
1:C:957:PRO:O	1:C:960:CYS:HB3	2.14	0.47
1:D:789:ASN:HB2	1:D:793:TYR:HB2	1.95	0.47
1:B:496:LEU:HD12	1:B:500:ASN:HB2	1.96	0.47
1:A:958:LEU:HD12	1:A:961:ILE:HD12	1.97	0.47
1:D:958:LEU:HD12	1:D:961:ILE:HD12	1.97	0.46
1:B:958:LEU:HD12	1:B:961:ILE:HD12	1.97	0.46
1:B:957:PRO:O	1:B:960:CYS:HB3	2.14	0.46
1:C:958:LEU:HD12	1:C:961:ILE:HD12	1.97	0.46
1:A:840:LEU:HD21	1:D:961:ILE:HG12	1.97	0.46
1:A:876:TRP:HE1	1:A:961:ILE:HD13	1.81	0.45
1:B:416:PHE:HD1	1:B:419:ASN:HD22	1.62	0.45
1:D:876:TRP:HE1	1:D:961:ILE:HD13	1.82	0.45
1:A:802:ASP:OD2	1:A:841:ARG:NH1	2.49	0.45
1:C:497:TYR:HE1	1:C:567:TRP:HB2	1.81	0.45
1:C:876:TRP:HE1	1:C:961:ILE:HD13	1.81	0.45
1:B:876:TRP:HE1	1:B:961:ILE:HD13	1.81	0.45
1:C:762:LYS:HB3	1:C:763:GLU:H	1.56	0.45
1:B:497:TYR:HE1	1:B:567:TRP:HB2	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:740:TRP:CD1	1:C:1012:UNK:CB	3.00	0.44
1:A:740:TRP:CD1	1:A:1012:UNK:CB	3.01	0.44
1:C:802:ASP:OD2	1:C:841:ARG:NH1	2.49	0.44
1:D:740:TRP:CD1	1:D:1012:UNK:CB	3.00	0.44
1:A:828:ARG:NE	1:D:886:GLY:O	2.51	0.44
1:B:740:TRP:CD1	1:B:1012:UNK:CB	3.00	0.44
1:B:802:ASP:OD2	1:B:841:ARG:NH1	2.49	0.44
1:D:497:TYR:HE1	1:D:567:TRP:HB2	1.81	0.44
1:D:802:ASP:OD2	1:D:841:ARG:NH1	2.49	0.44
1:A:497:TYR:HE1	1:A:567:TRP:HB2	1.81	0.44
1:C:973:LEU:HD23	1:D:973:LEU:HD11	1.99	0.44
1:A:744:PHE:CD2	1:A:1013:UNK:CB	3.01	0.44
1:C:744:PHE:CD2	1:C:1013:UNK:CB	3.01	0.44
1:B:973:LEU:HD23	1:C:973:LEU:HD11	1.99	0.43
1:C:458:LEU:HD22	1:C:477:PHE:HE1	1.83	0.43
1:B:744:PHE:CD2	1:B:1013:UNK:CB	3.02	0.43
1:D:458:LEU:HD22	1:D:477:PHE:HE1	1.83	0.43
1:D:744:PHE:CD2	1:D:1013:UNK:CB	3.01	0.43
1:B:458:LEU:HD22	1:B:477:PHE:HE1	1.83	0.43
1:A:458:LEU:HD22	1:A:477:PHE:HE1	1.83	0.42
1:B:803:THR:HA	1:B:806:ILE:HG22	2.02	0.42
1:A:803:THR:HA	1:A:806:ILE:HG22	2.02	0.42
1:A:762:LYS:HB3	1:A:763:GLU:H	1.56	0.42
1:C:745:TYR:HD2	1:C:842:LEU:HD13	1.85	0.42
1:C:803:THR:HA	1:C:806:ILE:HG22	2.02	0.42
1:D:803:THR:HA	1:D:806:ILE:HG22	2.02	0.42
1:A:968:ILE:O	1:A:972:ASN:N	2.48	0.42
1:D:644:LEU:HD11	1:D:674:VAL:HG12	2.02	0.42
1:D:745:TYR:HD2	1:D:842:LEU:HD13	1.85	0.42
1:D:958:LEU:HA	1:D:961:ILE:HD12	2.02	0.42
1:C:958:LEU:HA	1:C:961:ILE:HD12	2.02	0.41
1:A:958:LEU:HA	1:A:961:ILE:HD12	2.02	0.41
1:A:745:TYR:HD2	1:A:842:LEU:HD13	1.85	0.41
1:A:644:LEU:HD11	1:A:674:VAL:HG12	2.02	0.41
1:A:782:GLU:OE1	1:A:793:TYR:OH	2.37	0.41
1:A:973:LEU:HD11	1:D:973:LEU:HD23	2.01	0.41
1:B:745:TYR:HD2	1:B:842:LEU:HD13	1.85	0.41
1:B:644:LEU:HA	1:B:644:LEU:HD23	1.90	0.41
1:D:968:ILE:O	1:D:972:ASN:N	2.48	0.41
1:C:644:LEU:HD11	1:C:674:VAL:HG12	2.02	0.41
1:B:577:SER:HA	1:B:580:ILE:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:833:LEU:HD23	1:B:836:ILE:HD12	2.03	0.41
1:B:958:LEU:HA	1:B:961:ILE:HD12	2.02	0.40
1:C:577:SER:HA	1:C:580:ILE:HG22	2.03	0.40
1:C:896:GLU:O	1:C:900:ARG:CB	2.69	0.40
1:A:833:LEU:HD23	1:A:836:ILE:HD12	2.03	0.40
1:B:896:GLU:O	1:B:900:ARG:CB	2.69	0.40
1:D:833:LEU:HD23	1:D:836:ILE:HD12	2.03	0.40
1:D:896:GLU:O	1:D:900:ARG:CB	2.69	0.40
1:B:644:LEU:HD11	1:B:674:VAL:HG12	2.02	0.40
1:D:762:LYS:HB3	1:D:763:GLU:H	1.56	0.40
1:A:896:GLU:O	1:A:900:ARG:CB	2.69	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	740/950 (78%)	709 (96%)	31 (4%)	0	100	100
1	B	740/950 (78%)	709 (96%)	31 (4%)	0	100	100
1	C	740/950 (78%)	709 (96%)	31 (4%)	0	100	100
1	D	740/950 (78%)	709 (96%)	31 (4%)	0	100	100
All	All	2960/3800 (78%)	2836 (96%)	124 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	396/791 (50%)	393 (99%)	3 (1%)	83	91
1	B	396/791 (50%)	393 (99%)	3 (1%)	83	91
1	C	396/791 (50%)	393 (99%)	3 (1%)	83	91
1	D	396/791 (50%)	393 (99%)	3 (1%)	83	91
All	All	1584/3164 (50%)	1572 (99%)	12 (1%)	84	91

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	784	ARG
1	A	816	ARG
1	A	997	ARG
1	B	784	ARG
1	B	816	ARG
1	B	997	ARG
1	C	784	ARG
1	C	816	ARG
1	C	997	ARG
1	D	784	ARG
1	D	816	ARG
1	D	997	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	419	ASN
1	B	419	ASN
1	C	419	ASN
1	D	419	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 carbohydrates 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	6
1	A	6
1	D	6
1	C	6

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1027:UNK	C	1045:ARG	N	30.47
1	B	1027:UNK	C	1045:ARG	N	30.47
1	C	1027:UNK	C	1045:ARG	N	30.47
1	D	1027:UNK	C	1045:ARG	N	30.47
1	A	240:UNK	C	245:LEU	N	16.23
1	B	240:UNK	C	245:LEU	N	16.23
1	C	240:UNK	C	245:LEU	N	16.23
1	D	240:UNK	C	245:LEU	N	16.23
1	B	60:UNK	C	104:UNK	N	15.66
1	C	60:UNK	C	104:UNK	N	15.66
1	D	60:UNK	C	104:UNK	N	15.66
1	A	60:UNK	C	104:UNK	N	15.65
1	A	215:ALA	C	236:UNK	N	11.78
1	B	215:ALA	C	236:UNK	N	11.78
1	C	215:ALA	C	236:UNK	N	11.78
1	D	215:ALA	C	236:UNK	N	11.78
1	A	109:UNK	C	115:UNK	N	11.41

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	109:UNK	C	115:UNK	N	11.41
1	C	109:UNK	C	115:UNK	N	11.41
1	D	109:UNK	C	115:UNK	N	11.41
1	A	1068:THR	C	1077:UNK	N	10.53
1	B	1068:THR	C	1077:UNK	N	10.53
1	C	1068:THR	C	1077:UNK	N	10.53
1	D	1068:THR	C	1077:UNK	N	10.53