wwPDB EM Map/Model Validation Report (i)

Apr 10, 2016 – 01:54 PM BST

PDB ID	:	3JCF
EMDB ID:	:	EMD-6551
Title	:	Cryo-EM structure of the magnesium channel CorA in the closed symmetric magnesium-bound state
Authors	:	Matthies, D.; Perozo, E.; Subramaniam, S.
Deposited on	:	2015-12-11
Resolution	:	3.80 Å(reported)
Based on PDB ID	:	4I0U

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could
stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/EMValidationReportHelp

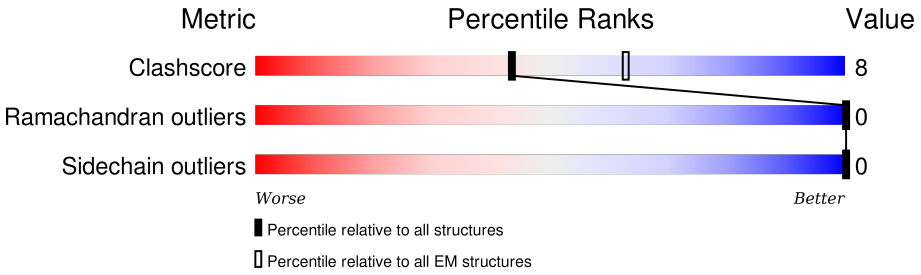
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk27241

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 3.80 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	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

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	351	77% 23%
1	B	351	77% 22%
1	C	351	77% 23%
1	D	351	77% 22%
1	E	351	77% 22%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14228 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 Magnesium transport protein CorA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	349	Total	C	N	O	S	0	0
			2843	1850	461	524	8		
1	B	349	Total	C	N	O	S	0	0
			2843	1850	461	524	8		
1	C	349	Total	C	N	O	S	0	0
			2843	1850	461	524	8		
1	D	349	Total	C	N	O	S	0	0
			2843	1850	461	524	8		
1	E	349	Total	C	N	O	S	0	0
			2843	1850	461	524	8		

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

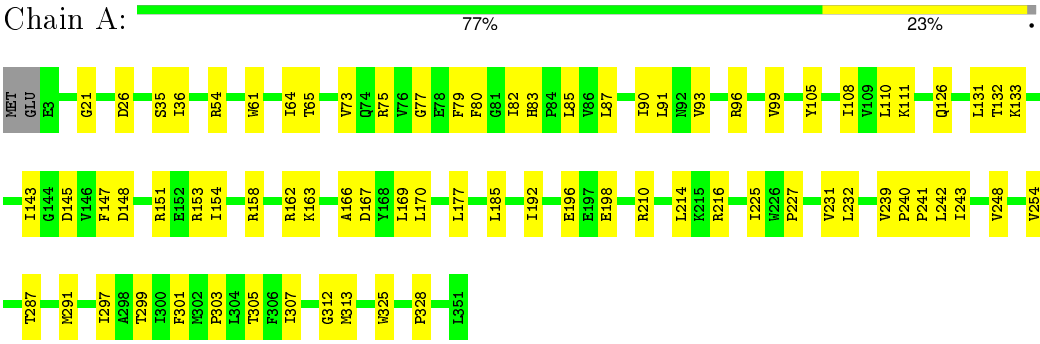
Mol	Chain	Residues	Atoms		AltConf
2	B	2	Total	Mg	0
			2	2	
2	A	2	Total	Mg	0
			2	2	
2	D	2	Total	Mg	0
			2	2	
2	C	2	Total	Mg	0
			2	2	
2	E	5	Total	Mg	0
			5	5	

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 errors 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.

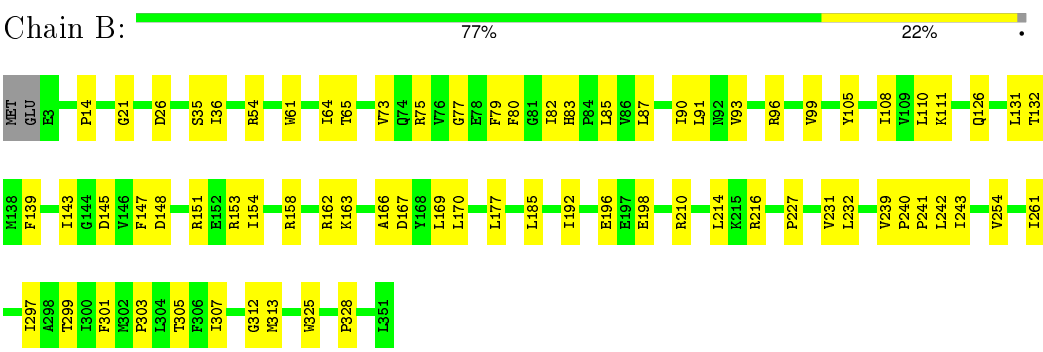
- Molecule 1: Magnesium transport protein CorA

Chain A:



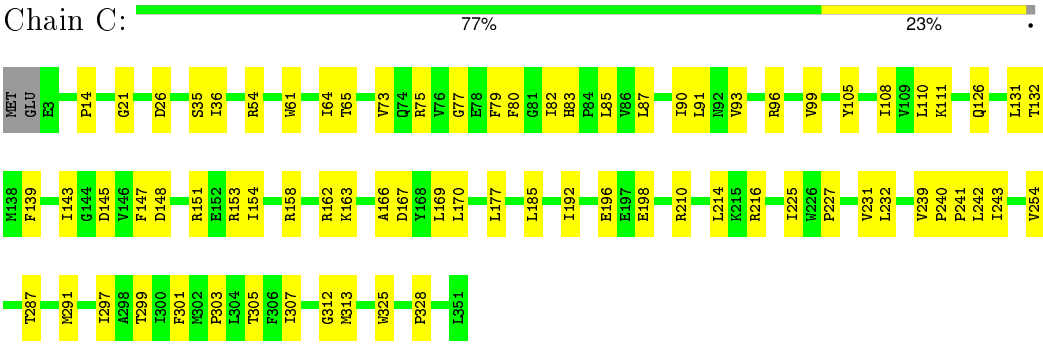
- Molecule 1: Magnesium transport protein CorA

Chain B:



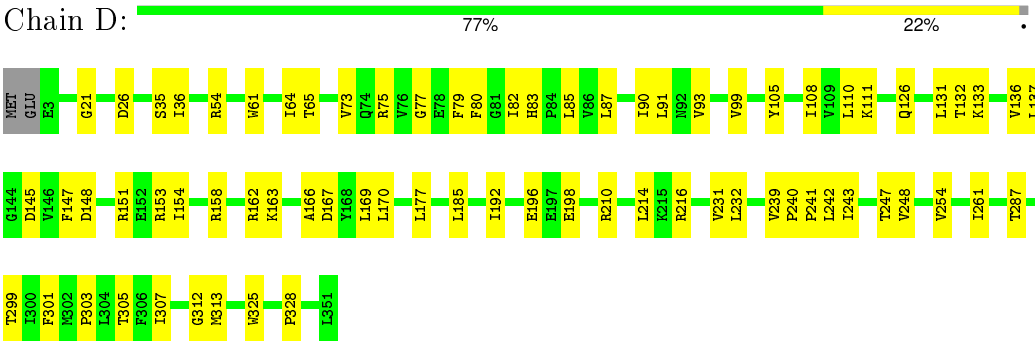
- Molecule 1: Magnesium transport protein CorA

Chain C:



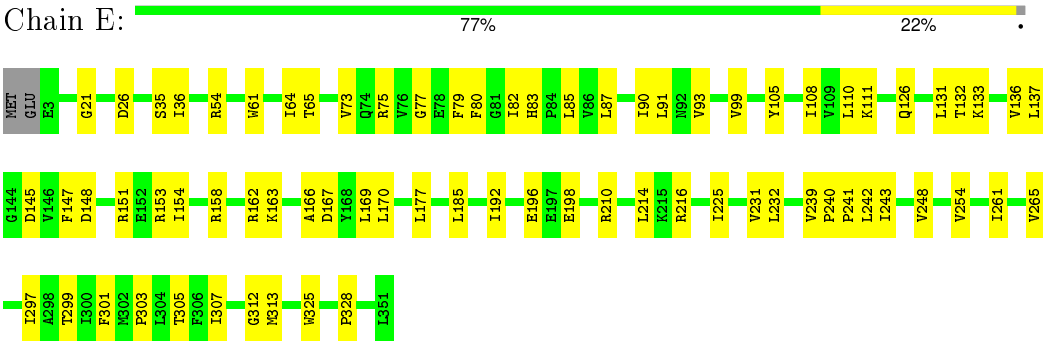
- Molecule 1: Magnesium transport protein CorA

Chain D:



- Molecule 1: Magnesium transport protein CorA

Chain E:



4 Experimental information (i)

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	46206	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	CTF parameters obtained from whole micrograph	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	860	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.21	0/2905	0.38	0/3946
1	B	0.21	0/2905	0.38	0/3946
1	C	0.21	0/2905	0.38	0/3946
1	D	0.21	0/2905	0.38	0/3946
1	E	0.21	0/2905	0.38	0/3946
All	All	0.21	0/14525	0.38	0/19730

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	2843	0	2837	53	0
1	B	2843	0	2837	53	0
1	C	2843	0	2837	52	0
1	D	2843	0	2837	51	0
1	E	2843	0	2837	52	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	2	0	0	0	0
2	E	5	0	0	0	0
All	All	14228	0	14185	241	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 8.

All (241) 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:154:ILE:O	1:A:162:ARG:NH2	2.24	0.70
1:E:154:ILE:O	1:E:162:ARG:NH2	2.24	0.69
1:C:154:ILE:O	1:C:162:ARG:NH2	2.24	0.69
1:B:154:ILE:O	1:B:162:ARG:NH2	2.24	0.68
1:D:154:ILE:O	1:D:162:ARG:NH2	2.24	0.67
1:B:99:VAL:HG22	1:B:108:ILE:HG12	1.80	0.64
1:A:99:VAL:HG22	1:A:108:ILE:HG12	1.80	0.63
1:E:99:VAL:HG22	1:E:108:ILE:HG12	1.80	0.62
1:D:73:VAL:HG21	1:D:91:LEU:HD21	1.81	0.62
1:D:99:VAL:HG22	1:D:108:ILE:HG12	1.80	0.62
1:C:73:VAL:HG21	1:C:91:LEU:HD21	1.81	0.62
1:A:299:THR:HG22	1:B:297:ILE:HG13	1.81	0.62
1:C:99:VAL:HG22	1:C:108:ILE:HG12	1.80	0.62
1:E:73:VAL:HG21	1:E:91:LEU:HD21	1.81	0.62
1:A:73:VAL:HG21	1:A:91:LEU:HD21	1.81	0.62
1:B:73:VAL:HG21	1:B:91:LEU:HD21	1.81	0.61
1:B:299:THR:HG22	1:C:297:ILE:HG13	1.83	0.60
1:C:299:THR:HG22	1:D:297:ILE:HG13	1.84	0.60
1:B:75:ARG:HH12	1:B:79:PHE:HB2	1.68	0.59
1:B:99:VAL:HG23	1:B:231:VAL:HG13	1.84	0.59
1:C:75:ARG:HH12	1:C:79:PHE:HB2	1.68	0.59
1:C:99:VAL:HG23	1:C:231:VAL:HG13	1.84	0.59
1:C:145:ASP:OD2	1:C:151:ARG:NH2	2.34	0.59
1:A:99:VAL:HG23	1:A:231:VAL:HG13	1.84	0.58
1:D:145:ASP:OD2	1:D:151:ARG:NH2	2.33	0.58
1:A:75:ARG:HH12	1:A:79:PHE:HB2	1.67	0.58
1:D:99:VAL:HG23	1:D:231:VAL:HG13	1.84	0.58
1:B:313:MET:HA	1:C:312:GLY:HA2	1.85	0.58
1:A:291:MET:HG3	1:B:287:THR:HG23	1.86	0.58
1:D:75:ARG:HH12	1:D:79:PHE:HB2	1.68	0.58
1:A:297:ILE:HG13	1:E:299:THR:HG22	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:75:ARG:HH12	1:E:79:PHE:HB2	1.68	0.58
1:E:99:VAL:HG23	1:E:231:VAL:HG13	1.84	0.57
1:D:299:THR:HG22	1:E:297:ILE:HG13	1.87	0.56
1:B:145:ASP:OD2	1:B:151:ARG:NH2	2.34	0.56
1:C:291:MET:HG3	1:D:287:THR:HG23	1.87	0.56
1:A:239:VAL:HG12	1:A:242:LEU:HD12	1.88	0.56
1:B:239:VAL:HG12	1:B:242:LEU:HD12	1.88	0.56
1:C:111:LYS:HZ3	1:C:126:GLN:HB2	1.71	0.55
1:C:239:VAL:HG12	1:C:242:LEU:HD12	1.88	0.55
1:E:239:VAL:HG12	1:E:242:LEU:HD12	1.88	0.55
1:D:111:LYS:HZ3	1:D:126:GLN:HB2	1.72	0.55
1:A:145:ASP:OD2	1:A:151:ARG:NH2	2.34	0.55
1:E:301:PHE:O	1:E:305:THR:N	2.36	0.55
1:D:65:THR:HG21	1:D:143:ILE:HD13	1.89	0.54
1:D:313:MET:HA	1:E:312:GLY:HA2	1.89	0.54
1:B:111:LYS:NZ	1:B:126:GLN:HB2	2.23	0.54
1:D:239:VAL:HG12	1:D:242:LEU:HD12	1.88	0.54
1:C:111:LYS:NZ	1:C:126:GLN:HB2	2.23	0.54
1:C:65:THR:HG21	1:C:143:ILE:HD13	1.89	0.54
1:A:312:GLY:HA2	1:E:313:MET:HA	1.89	0.54
1:A:111:LYS:NZ	1:A:126:GLN:HB2	2.23	0.54
1:E:111:LYS:NZ	1:E:126:GLN:HB2	2.23	0.54
1:D:111:LYS:NZ	1:D:126:GLN:HB2	2.23	0.54
1:A:287:THR:HG23	1:E:291:MET:HG3	1.90	0.54
1:A:65:THR:HG21	1:A:143:ILE:HD13	1.89	0.54
1:C:301:PHE:O	1:C:305:THR:N	2.36	0.54
1:E:65:THR:HG21	1:E:143:ILE:HD13	1.89	0.53
1:E:145:ASP:OD2	1:E:151:ARG:NH2	2.33	0.53
1:B:301:PHE:O	1:B:305:THR:N	2.36	0.53
1:C:313:MET:HA	1:D:312:GLY:HA2	1.91	0.53
1:D:291:MET:HG3	1:E:287:THR:HG23	1.89	0.53
1:B:65:THR:HG21	1:B:143:ILE:HD13	1.89	0.53
1:C:232:LEU:HD13	1:C:254:VAL:HG12	1.91	0.52
1:B:232:LEU:HD13	1:B:254:VAL:HG12	1.91	0.52
1:A:301:PHE:O	1:A:305:THR:N	2.36	0.52
1:D:232:LEU:HD13	1:D:254:VAL:HG12	1.91	0.52
1:C:54:ARG:NH1	1:C:133:LYS:NZ	2.58	0.52
1:E:232:LEU:HD13	1:E:254:VAL:HG12	1.92	0.52
1:B:54:ARG:NH1	1:B:133:LYS:NZ	2.58	0.52
1:B:77:GLY:HA2	1:B:82:ILE:HD12	1.92	0.52
1:A:232:LEU:HD13	1:A:254:VAL:HG12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:77:GLY:HA2	1:C:82:ILE:HD12	1.92	0.51
1:E:111:LYS:HZ3	1:E:126:GLN:HB2	1.75	0.51
1:D:54:ARG:NH1	1:D:133:LYS:NZ	2.58	0.51
1:E:54:ARG:NH1	1:E:133:LYS:NZ	2.58	0.51
1:A:36:ILE:HG22	1:A:163:LYS:HA	1.93	0.51
1:C:36:ILE:HG22	1:C:163:LYS:HA	1.93	0.51
1:A:77:GLY:HA2	1:A:82:ILE:HD12	1.92	0.51
1:A:54:ARG:NH1	1:A:133:LYS:NZ	2.58	0.51
1:B:291:MET:HG3	1:C:287:THR:HG23	1.93	0.51
1:D:77:GLY:HA2	1:D:82:ILE:HD12	1.92	0.51
1:D:196:GLU:OE1	1:E:216:ARG:NH2	2.44	0.50
1:B:148:ASP:HA	1:B:151:ARG:HH11	1.75	0.50
1:D:148:ASP:HA	1:D:151:ARG:HH11	1.76	0.50
1:A:148:ASP:HA	1:A:151:ARG:HH11	1.76	0.50
1:D:36:ILE:HG22	1:D:163:LYS:HA	1.93	0.50
1:C:196:GLU:OE1	1:D:216:ARG:NH2	2.45	0.50
1:B:36:ILE:HG22	1:B:163:LYS:HA	1.93	0.50
1:E:148:ASP:HA	1:E:151:ARG:HH11	1.76	0.50
1:E:77:GLY:HA2	1:E:82:ILE:HD12	1.92	0.50
1:C:148:ASP:HA	1:C:151:ARG:HH11	1.77	0.49
1:A:216:ARG:NH2	1:E:196:GLU:OE1	2.45	0.49
1:D:301:PHE:O	1:D:305:THR:N	2.36	0.49
1:B:167:ASP:OD2	1:B:243:ILE:HG12	2.13	0.49
1:E:36:ILE:HG22	1:E:163:LYS:HA	1.93	0.49
1:E:167:ASP:OD2	1:E:243:ILE:HG12	2.13	0.49
1:E:35:SER:O	1:E:162:ARG:HD2	2.13	0.49
1:A:196:GLU:OE1	1:B:216:ARG:NH2	2.46	0.49
1:B:35:SER:O	1:B:162:ARG:HD2	2.13	0.48
1:D:35:SER:O	1:D:162:ARG:HD2	2.13	0.48
1:A:75:ARG:NH1	1:A:79:PHE:HB2	2.28	0.48
1:D:75:ARG:NH1	1:D:79:PHE:HB2	2.29	0.48
1:D:167:ASP:OD2	1:D:243:ILE:HG12	2.13	0.48
1:B:136:VAL:HG23	1:B:166:ALA:HB1	1.96	0.48
1:A:61:TRP:HB2	1:A:169:LEU:HD21	1.96	0.48
1:C:61:TRP:HB2	1:C:169:LEU:HD21	1.96	0.48
1:B:196:GLU:OE1	1:C:216:ARG:NH2	2.47	0.48
1:A:136:VAL:HG23	1:A:166:ALA:HB1	1.96	0.48
1:A:35:SER:O	1:A:162:ARG:HD2	2.13	0.48
1:E:61:TRP:HB2	1:E:169:LEU:HD21	1.96	0.48
1:D:136:VAL:HG23	1:D:166:ALA:HB1	1.96	0.48
1:A:167:ASP:OD2	1:A:243:ILE:HG12	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:61:TRP:HB2	1:D:169:LEU:HD21	1.96	0.48
1:C:35:SER:O	1:C:162:ARG:HD2	2.13	0.48
1:C:167:ASP:OD2	1:C:243:ILE:HG12	2.13	0.48
1:C:136:VAL:HG23	1:C:166:ALA:HB1	1.96	0.48
1:E:136:VAL:HG23	1:E:166:ALA:HB1	1.96	0.48
1:E:75:ARG:NH1	1:E:79:PHE:HB2	2.29	0.48
1:D:145:ASP:OD2	1:D:147:PHE:HB2	2.14	0.47
1:A:145:ASP:HB2	1:A:147:PHE:HD2	1.79	0.47
1:B:61:TRP:HB2	1:B:169:LEU:HD21	1.96	0.47
1:D:21:GLY:HA2	1:D:93:VAL:HG21	1.97	0.47
1:E:145:ASP:OD2	1:E:147:PHE:HB2	2.14	0.47
1:A:54:ARG:NH1	1:A:133:LYS:HZ2	2.12	0.47
1:C:75:ARG:NH1	1:C:79:PHE:HB2	2.29	0.47
1:A:185:LEU:HD11	1:A:261:ILE:HG23	1.97	0.47
1:C:145:ASP:HB2	1:C:147:PHE:HD2	1.79	0.47
1:D:145:ASP:HB2	1:D:147:PHE:HD2	1.79	0.47
1:B:145:ASP:OD2	1:B:147:PHE:HB2	2.14	0.47
1:A:145:ASP:OD2	1:A:147:PHE:HB2	2.14	0.47
1:E:145:ASP:HB2	1:E:147:PHE:HD2	1.79	0.47
1:D:185:LEU:HD11	1:D:261:ILE:HG23	1.97	0.47
1:B:75:ARG:NH1	1:B:79:PHE:HB2	2.28	0.47
1:B:145:ASP:HB2	1:B:147:PHE:HD2	1.79	0.47
1:A:313:MET:HA	1:B:312:GLY:HA2	1.97	0.47
1:A:21:GLY:HA2	1:A:93:VAL:HG21	1.97	0.47
1:B:185:LEU:HD11	1:B:261:ILE:HG23	1.97	0.47
1:E:185:LEU:HD11	1:E:261:ILE:HG23	1.97	0.47
1:C:185:LEU:HD11	1:C:261:ILE:HG23	1.97	0.47
1:E:26:ASP:OD2	1:E:143:ILE:HG12	2.15	0.47
1:B:26:ASP:OD2	1:B:143:ILE:HG12	2.15	0.46
1:A:54:ARG:HH11	1:A:133:LYS:HZ2	1.64	0.46
1:D:80:PHE:HE2	1:D:137:LEU:HD21	1.80	0.46
1:B:21:GLY:HA2	1:B:93:VAL:HG21	1.97	0.46
1:C:80:PHE:HE2	1:C:137:LEU:HD21	1.80	0.46
1:C:145:ASP:OD2	1:C:147:PHE:HB2	2.14	0.46
1:B:54:ARG:NH1	1:B:133:LYS:HZ2	2.14	0.46
1:E:80:PHE:HE2	1:E:137:LEU:HD21	1.80	0.46
1:A:80:PHE:HE2	1:A:137:LEU:HD21	1.80	0.46
1:C:21:GLY:HA2	1:C:93:VAL:HG21	1.97	0.46
1:E:192:ILE:HG12	1:E:214:LEU:HD21	1.98	0.46
1:E:21:GLY:HA2	1:E:93:VAL:HG21	1.97	0.46
1:B:80:PHE:HE2	1:B:137:LEU:HD21	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:26:ASP:OD2	1:C:143:ILE:HG12	2.15	0.46
1:B:153:ARG:HA	1:B:158:ARG:HB3	1.98	0.45
1:C:110:LEU:HD13	1:C:177:LEU:HD23	1.99	0.45
1:B:192:ILE:HG12	1:B:214:LEU:HD21	1.98	0.45
1:A:26:ASP:OD2	1:A:143:ILE:HG12	2.15	0.45
1:D:153:ARG:HA	1:D:158:ARG:HB3	1.98	0.45
1:E:153:ARG:HA	1:E:158:ARG:HB3	1.98	0.45
1:A:192:ILE:HG12	1:A:214:LEU:HD21	1.98	0.45
1:D:26:ASP:OD2	1:D:143:ILE:HG12	2.15	0.45
1:B:110:LEU:HD13	1:B:177:LEU:HD23	1.99	0.45
1:D:110:LEU:HD13	1:D:177:LEU:HD23	1.99	0.45
1:C:153:ARG:HA	1:C:158:ARG:HB3	1.98	0.45
1:A:110:LEU:HD13	1:A:177:LEU:HD23	1.99	0.45
1:E:64:ILE:HD12	1:E:139:PHE:HE1	1.83	0.44
1:A:153:ARG:HA	1:A:158:ARG:HB3	1.98	0.44
1:C:192:ILE:HG12	1:C:214:LEU:HD21	1.98	0.44
1:C:64:ILE:HD12	1:C:139:PHE:HE1	1.83	0.44
1:B:111:LYS:HZ3	1:B:126:GLN:HB2	1.80	0.44
1:B:54:ARG:HH11	1:B:133:LYS:HZ2	1.66	0.44
1:A:64:ILE:HD12	1:A:139:PHE:HE1	1.83	0.44
1:D:192:ILE:HG12	1:D:214:LEU:HD21	1.98	0.44
1:D:64:ILE:HD12	1:D:139:PHE:HE1	1.83	0.44
1:E:110:LEU:HD13	1:E:177:LEU:HD23	1.99	0.44
1:B:64:ILE:HD12	1:B:139:PHE:HE1	1.83	0.44
1:D:105:TYR:HB3	1:D:132:THR:HB	2.00	0.44
1:E:105:TYR:HB3	1:E:132:THR:HB	2.00	0.43
1:A:111:LYS:HZ3	1:A:126:GLN:HB2	1.83	0.43
1:C:105:TYR:HB3	1:C:132:THR:HB	2.00	0.43
1:D:131:LEU:HD13	1:D:170:LEU:HD22	2.01	0.43
1:B:105:TYR:HB3	1:B:132:THR:HB	2.00	0.43
1:B:325:TRP:HE3	1:B:328:PRO:HG2	1.84	0.43
1:E:87:LEU:HA	1:E:90:ILE:HD12	2.01	0.43
1:E:131:LEU:HD13	1:E:170:LEU:HD22	2.01	0.43
1:A:325:TRP:HE3	1:A:328:PRO:HG2	1.84	0.43
1:C:131:LEU:HD13	1:C:170:LEU:HD22	2.01	0.43
1:C:325:TRP:HE3	1:C:328:PRO:HG2	1.84	0.42
1:D:325:TRP:HE3	1:D:328:PRO:HG2	1.84	0.42
1:A:105:TYR:HB3	1:A:132:THR:HB	2.00	0.42
1:D:111:LYS:HD2	1:D:126:GLN:HA	2.01	0.42
1:A:198:GLU:OE1	1:A:210:ARG:NH2	2.53	0.42
1:C:87:LEU:HA	1:C:90:ILE:HD12	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:240:PRO:HG2	1:D:241:PRO:HD3	2.02	0.42
1:E:111:LYS:HD2	1:E:126:GLN:HA	2.01	0.42
1:E:325:TRP:HE3	1:E:328:PRO:HG2	1.84	0.42
1:B:87:LEU:HA	1:B:90:ILE:HD12	2.01	0.42
1:A:83:HIS:HD2	1:A:85:LEU:HB2	1.85	0.42
1:A:131:LEU:HD13	1:A:170:LEU:HD22	2.01	0.42
1:D:83:HIS:HD2	1:D:85:LEU:HB2	1.85	0.42
1:C:198:GLU:OE1	1:C:210:ARG:NH2	2.53	0.42
1:B:111:LYS:HD2	1:B:126:GLN:HA	2.01	0.42
1:B:198:GLU:OE1	1:B:210:ARG:NH2	2.53	0.42
1:C:240:PRO:HG2	1:C:241:PRO:HD3	2.02	0.42
1:D:87:LEU:HA	1:D:90:ILE:HD12	2.01	0.42
1:A:87:LEU:HA	1:A:90:ILE:HD12	2.01	0.42
1:A:303:PRO:O	1:A:307:ILE:HG12	2.20	0.42
1:E:240:PRO:HG2	1:E:241:PRO:HD3	2.02	0.41
1:C:303:PRO:O	1:C:307:ILE:HG12	2.20	0.41
1:C:111:LYS:HD2	1:C:126:GLN:HA	2.01	0.41
1:B:83:HIS:HD2	1:B:85:LEU:HB2	1.85	0.41
1:C:83:HIS:HD2	1:C:85:LEU:HB2	1.85	0.41
1:E:303:PRO:O	1:E:307:ILE:HG12	2.20	0.41
1:B:131:LEU:HD13	1:B:170:LEU:HD22	2.01	0.41
1:A:111:LYS:HD2	1:A:126:GLN:HA	2.01	0.41
1:E:54:ARG:NH1	1:E:133:LYS:HZ2	2.18	0.41
1:D:243:ILE:O	1:D:247:THR:OG1	2.28	0.41
1:B:240:PRO:HG2	1:B:241:PRO:HD3	2.01	0.41
1:D:148:ASP:OD1	1:D:151:ARG:NH1	2.54	0.41
1:E:83:HIS:HD2	1:E:85:LEU:HB2	1.85	0.41
1:E:198:GLU:OE1	1:E:210:ARG:NH2	2.53	0.41
1:D:198:GLU:OE1	1:D:210:ARG:NH2	2.53	0.41
1:B:303:PRO:O	1:B:307:ILE:HG12	2.20	0.41
1:A:240:PRO:HG2	1:A:241:PRO:HD3	2.02	0.41
1:C:225:ILE:HD12	1:C:265:VAL:HG21	2.03	0.41
1:B:148:ASP:OD1	1:B:151:ARG:NH1	2.54	0.40
1:E:225:ILE:HD12	1:E:265:VAL:HG21	2.03	0.40
1:C:148:ASP:OD1	1:C:151:ARG:NH1	2.54	0.40
1:E:239:VAL:HG21	1:E:248:VAL:HG22	2.04	0.40
1:A:96:ARG:HH11	1:A:227:PRO:CB	2.34	0.40
1:B:96:ARG:HH11	1:B:227:PRO:CB	2.34	0.40
1:A:239:VAL:HG21	1:A:248:VAL:HG22	2.04	0.40
1:B:14:PRO:HB2	1:B:85:LEU:HD21	2.03	0.40
1:D:303:PRO:O	1:D:307:ILE:HG12	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:225:ILE:HD12	1:A:265:VAL:HG21	2.03	0.40
1:C:96:ARG:HH11	1:C:227:PRO:CB	2.34	0.40
1:D:239:VAL:HG21	1:D:248:VAL:HG22	2.04	0.40
1:E:148:ASP:OD1	1:E:151:ARG:NH1	2.54	0.40
1:C:14:PRO:HB2	1:C:85:LEU:HD21	2.04	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	347/351 (99%)	331 (95%)	16 (5%)	0	100	100
1	B	347/351 (99%)	331 (95%)	16 (5%)	0	100	100
1	C	347/351 (99%)	331 (95%)	16 (5%)	0	100	100
1	D	347/351 (99%)	331 (95%)	16 (5%)	0	100	100
1	E	347/351 (99%)	331 (95%)	16 (5%)	0	100	100
All	All	1735/1755 (99%)	1655 (95%)	80 (5%)	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	314/330 (95%)	314 (100%)	0	100	100
1	B	314/330 (95%)	314 (100%)	0	100	100
1	C	314/330 (95%)	314 (100%)	0	100	100
1	D	314/330 (95%)	314 (100%)	0	100	100
1	E	314/330 (95%)	314 (100%)	0	100	100
All	All	1570/1650 (95%)	1570 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	140	GLN
1	A	314	ASN
1	B	140	GLN
1	B	314	ASN
1	C	140	GLN
1	C	314	ASN
1	D	140	GLN
1	D	314	ASN
1	E	140	GLN
1	E	314	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)

Of 13 ligands modelled in this entry, 13 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.