



Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Sep 11, 2017 – 12:14 AM EDT

PDB ID : 5NV3
EMDB ID: : EMD-3699
Title : Structure of Rubisco from Rhodobacter sphaeroides in complex with CABP
Authors : Bracher, A.; Milicic, G.; Ciniawsky, S.; Wendler, P.; Hayer-Hartl, M.; Hartl, F.U.
Deposited on : unknown
Resolution : 3.39 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
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

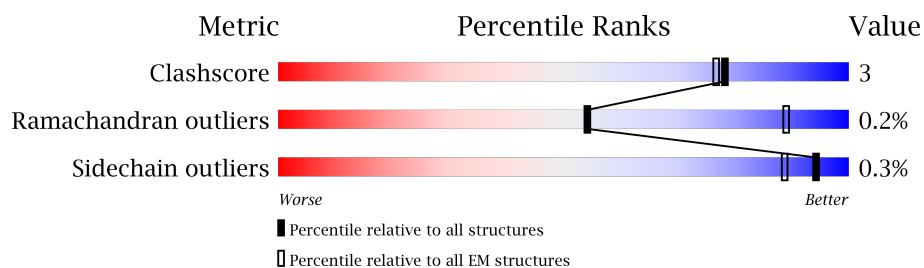
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.39 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	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	467	90% 10%
1	B	467	90% 10%
1	C	467	90% 10%
1	D	467	90% 10%
1	E	467	90% 10%
1	F	467	91% 9%
1	G	467	90% 10%
1	H	467	90% 10%
2	I	129	94% 5% •

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Mol	Chain	Length	Quality of chain
2	J	129	<div><div></div><div>94%</div><div>5%</div></div>
2	K	129	<div><div></div><div>94%</div><div>5%</div></div>
2	L	129	<div><div></div><div>93%</div><div>6%</div></div>
2	M	129	<div><div></div><div>93%</div><div>6%</div></div>
2	N	129	<div><div></div><div>94%</div><div>5%</div></div>
2	O	129	<div><div></div><div>92%</div><div>7%</div></div>
2	P	129	<div><div></div><div>93%</div><div>6%</div></div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 37816 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 Ribulose biphosphate carboxylase large chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	467	Total	C	N	O	S	0	0
			3642	2322	629	671	20		
1	B	467	Total	C	N	O	S	0	0
			3642	2322	629	671	20		
1	C	467	Total	C	N	O	S	0	0
			3642	2322	629	671	20		
1	D	467	Total	C	N	O	S	0	0
			3642	2322	629	671	20		
1	E	467	Total	C	N	O	S	0	0
			3642	2322	629	671	20		
1	F	467	Total	C	N	O	S	0	0
			3642	2322	629	671	20		
1	G	467	Total	C	N	O	S	0	0
			3642	2322	629	671	20		
1	H	467	Total	C	N	O	S	0	0
			3642	2322	629	671	20		

- Molecule 2 is a protein called Ribulose biphosphate carboxylase small chain 1.

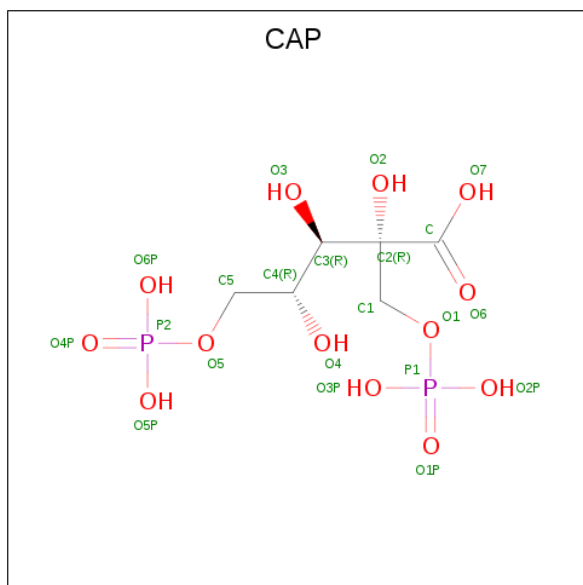
Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	129	Total	C	N	O	S	0	0
			1063	667	189	197	10		
2	J	129	Total	C	N	O	S	0	0
			1063	667	189	197	10		
2	K	129	Total	C	N	O	S	0	0
			1063	667	189	197	10		
2	L	129	Total	C	N	O	S	0	0
			1063	667	189	197	10		
2	M	129	Total	C	N	O	S	0	0
			1063	667	189	197	10		
2	N	129	Total	C	N	O	S	0	0
			1063	667	189	197	10		
2	O	129	Total	C	N	O	S	0	0
			1063	667	189	197	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	P	129	Total	C	N	O	S	0	0
			1063	667	189	197	10		

- Molecule 3 is 2-CARBOXYARABINITOL-1,5-DIPHOSPHATE (three-letter code: CAP) (formula: $C_6H_{14}O_{13}P_2$).



Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	O	P	0
			21	6	13	2	
3	B	1	Total	C	O	P	0
			21	6	13	2	
3	C	1	Total	C	O	P	0
			21	6	13	2	
3	D	1	Total	C	O	P	0
			21	6	13	2	
3	E	1	Total	C	O	P	0
			21	6	13	2	
3	F	1	Total	C	O	P	0
			21	6	13	2	
3	G	1	Total	C	O	P	0
			21	6	13	2	
3	H	1	Total	C	O	P	0
			21	6	13	2	

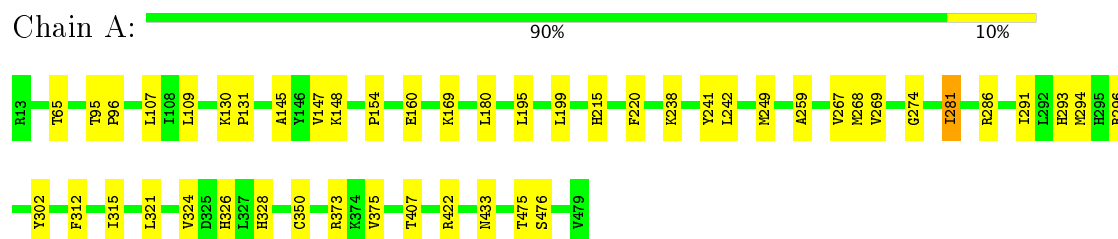
- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
4	G	1	Total 1	Mg 1	0
4	D	1	Total 1	Mg 1	0
4	E	1	Total 1	Mg 1	0
4	H	1	Total 1	Mg 1	0
4	B	1	Total 1	Mg 1	0
4	C	1	Total 1	Mg 1	0
4	A	1	Total 1	Mg 1	0
4	F	1	Total 1	Mg 1	0

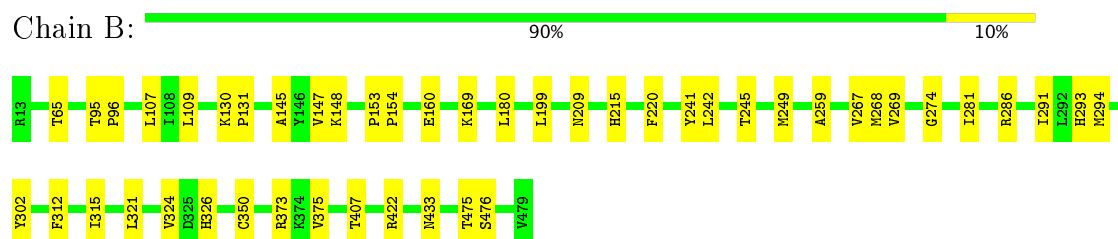
3 Residue-property plots

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.

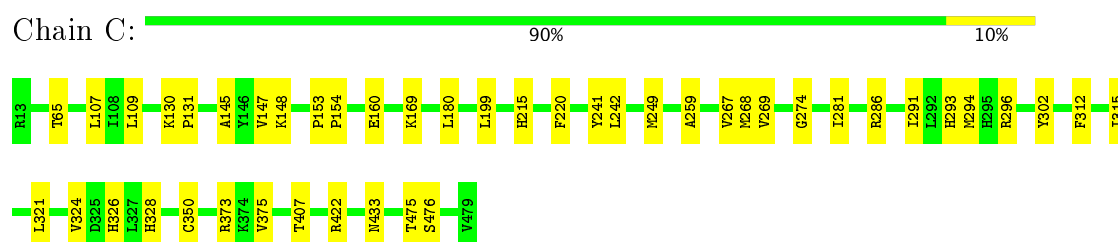
- Molecule 1: Ribulose biphosphate carboxylase large chain



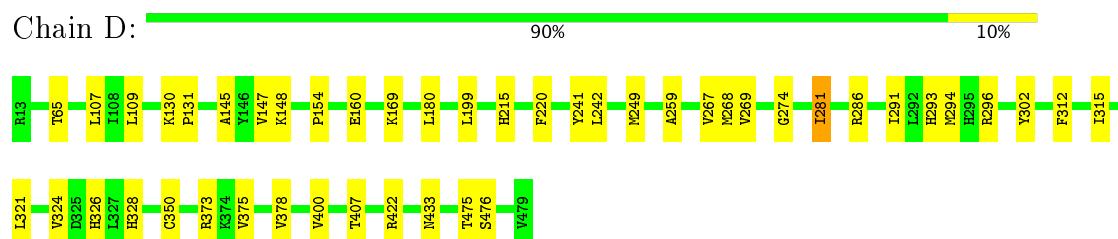
- Molecule 1: Ribulose bisphosphate carboxylase large chain



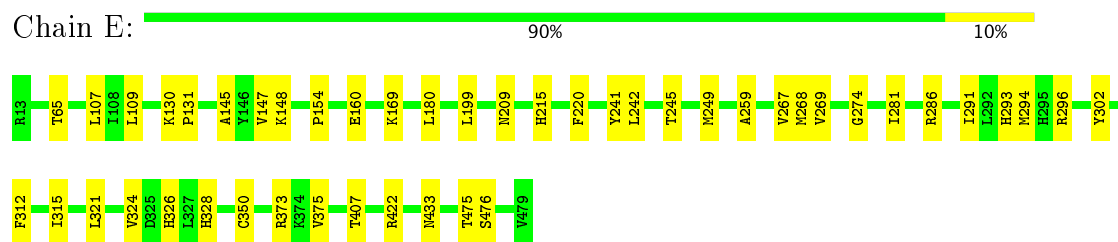
- Molecule 1: Ribulose bisphosphate carboxylase large chain



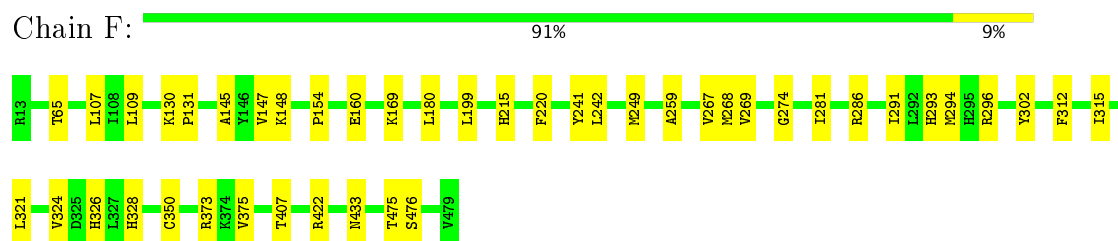
- Molecule 1: Ribulose bisphosphate carboxylase large chain



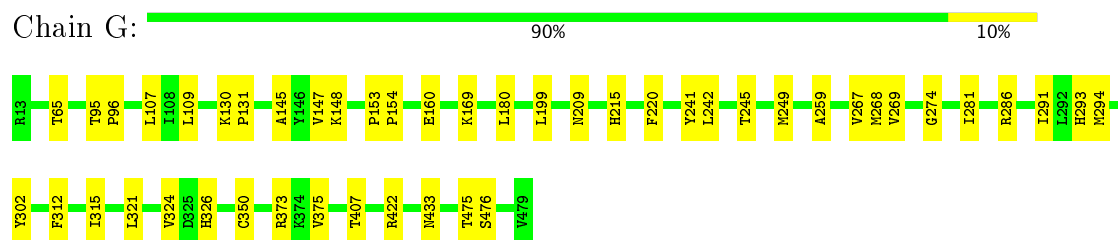
- Molecule 1: Ribulose bisphosphate carboxylase large chain



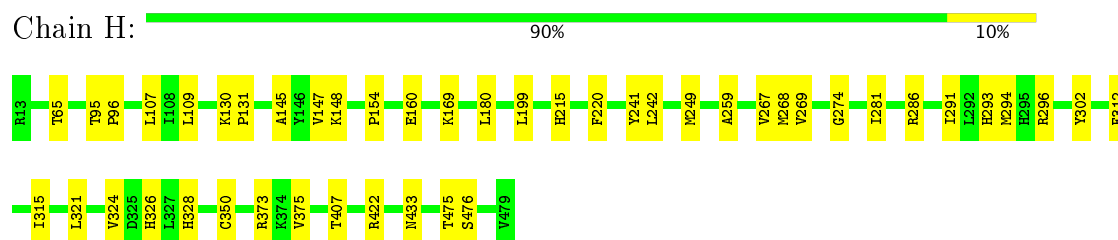
- Molecule 1: Ribulose biphosphate carboxylase large chain



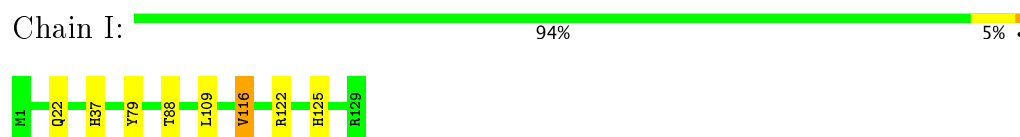
- Molecule 1: Ribulose biphosphate carboxylase large chain



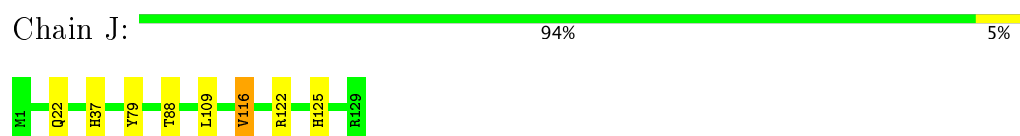
- Molecule 1: Ribulose bisphosphate carboxylase large chain



- Molecule 2: Ribulose bisphosphate carboxylase small chain 1



- Molecule 2: Ribulose bisphosphate carboxylase small chain 1



- Molecule 2: Ribulose biphosphate carboxylase small chain 1

Chain K:  94% 5% .



- Molecule 2: Ribulose biphosphate carboxylase small chain 1

Chain L:  93% 6% .



- Molecule 2: Ribulose biphosphate carboxylase small chain 1

Chain M:  93% 6% .



- Molecule 2: Ribulose biphosphate carboxylase small chain 1

Chain N:  94% 5% .



- Molecule 2: Ribulose biphosphate carboxylase small chain 1

Chain O:  92% 7% .



- Molecule 2: Ribulose biphosphate carboxylase small chain 1

Chain P:  93% 6% .



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D4	Depositor
Number of particles used	333122	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.37	0/3717	0.54	0/5041
1	B	0.37	0/3717	0.54	0/5041
1	C	0.37	0/3717	0.54	0/5041
1	D	0.37	0/3717	0.54	0/5041
1	E	0.37	0/3717	0.54	0/5041
1	F	0.37	0/3717	0.53	0/5041
1	G	0.37	0/3717	0.54	0/5041
1	H	0.37	0/3717	0.54	0/5041
2	I	0.39	0/1091	0.56	0/1476
2	J	0.39	0/1091	0.56	0/1476
2	K	0.39	0/1091	0.55	0/1476
2	L	0.39	0/1091	0.55	0/1476
2	M	0.39	0/1091	0.56	0/1476
2	N	0.39	0/1091	0.56	0/1476
2	O	0.39	0/1091	0.55	0/1476
2	P	0.39	0/1091	0.55	0/1476
All	All	0.37	0/38464	0.54	0/52136

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 [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3642	0	3580	34	0
1	B	3642	0	3580	34	0
1	C	3642	0	3580	33	0
1	D	3642	0	3580	33	0
1	E	3642	0	3580	33	0
1	F	3642	0	3580	32	0
1	G	3642	0	3580	34	0
1	H	3642	0	3580	33	0
2	I	1063	0	1021	4	0
2	J	1063	0	1021	4	0
2	K	1063	0	1021	4	0
2	L	1063	0	1021	4	0
2	M	1063	0	1021	5	0
2	N	1063	0	1021	4	0
2	O	1063	0	1021	5	0
2	P	1063	0	1021	4	0
3	A	21	0	9	0	0
3	B	21	0	9	0	0
3	C	21	0	9	0	0
3	D	21	0	9	0	0
3	E	21	0	9	0	0
3	F	21	0	9	0	0
3	G	21	0	9	0	0
3	H	21	0	9	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
All	All	37816	0	36880	244	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 3.

All (244) 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:C:294:MET:HB2	1:C:324:VAL:HG11	1.64	0.80
1:A:294:MET:HB2	1:A:324:VAL:HG11	1.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:294:MET:HB2	1:F:324:VAL:HG11	1.65	0.79
1:B:294:MET:HB2	1:B:324:VAL:HG11	1.64	0.79
1:H:294:MET:HB2	1:H:324:VAL:HG11	1.66	0.78
1:E:294:MET:HB2	1:E:324:VAL:HG11	1.65	0.78
1:G:294:MET:HB2	1:G:324:VAL:HG11	1.65	0.78
1:D:294:MET:HB2	1:D:324:VAL:HG11	1.65	0.78
1:F:475:THR:HG22	1:F:476:SER:N	2.06	0.70
1:C:475:THR:HG22	1:C:476:SER:N	2.07	0.69
1:E:475:THR:HG22	1:E:476:SER:N	2.07	0.69
1:A:475:THR:HG22	1:A:476:SER:N	2.07	0.69
1:H:475:THR:HG22	1:H:476:SER:N	2.07	0.69
1:D:475:THR:HG22	1:D:476:SER:N	2.07	0.69
1:G:475:THR:HG22	1:G:476:SER:N	2.07	0.68
1:B:475:THR:HG22	1:B:476:SER:N	2.07	0.68
1:F:350:CYS:HB2	1:F:375:VAL:HB	1.80	0.64
1:E:350:CYS:HB2	1:E:375:VAL:HB	1.80	0.63
1:C:350:CYS:HB2	1:C:375:VAL:HB	1.81	0.63
1:H:154:PRO:HA	1:H:286:ARG:HE	1.62	0.63
1:G:350:CYS:HB2	1:G:375:VAL:HB	1.80	0.63
1:E:154:PRO:HA	1:E:286:ARG:HE	1.63	0.62
1:F:154:PRO:HA	1:F:286:ARG:HE	1.63	0.62
1:A:350:CYS:HB2	1:A:375:VAL:HB	1.81	0.62
1:B:350:CYS:HB2	1:B:375:VAL:HB	1.81	0.62
1:D:350:CYS:HB2	1:D:375:VAL:HB	1.82	0.62
1:A:154:PRO:HA	1:A:286:ARG:HE	1.63	0.62
1:H:350:CYS:HB2	1:H:375:VAL:HB	1.80	0.62
1:C:154:PRO:HA	1:C:286:ARG:HE	1.64	0.62
1:G:154:PRO:HA	1:G:286:ARG:HE	1.63	0.62
1:D:154:PRO:HA	1:D:286:ARG:HE	1.64	0.61
1:B:154:PRO:HA	1:B:286:ARG:HE	1.64	0.60
1:C:433:ASN:HD22	2:K:22:GLN:HE22	1.51	0.59
1:E:433:ASN:HD22	2:M:22:GLN:HE22	1.51	0.59
1:E:199:LEU:HD11	1:E:407:THR:HG21	1.84	0.59
1:D:199:LEU:HD11	1:D:407:THR:HG21	1.85	0.58
1:B:199:LEU:HD11	1:B:407:THR:HG21	1.84	0.58
1:C:199:LEU:HD11	1:C:407:THR:HG21	1.84	0.58
1:F:433:ASN:HD22	2:N:22:GLN:HE22	1.52	0.58
1:D:433:ASN:HD22	2:L:22:GLN:HE22	1.52	0.58
1:F:199:LEU:HD11	1:F:407:THR:HG21	1.85	0.58
1:A:199:LEU:HD11	1:A:407:THR:HG21	1.85	0.57
1:G:199:LEU:HD11	1:G:407:THR:HG21	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:199:LEU:HD11	1:H:407:THR:HG21	1.86	0.57
1:A:433:ASN:HD22	2:I:22:GLN:HE22	1.51	0.57
1:H:433:ASN:HD22	2:P:22:GLN:HE22	1.52	0.56
1:G:433:ASN:HD22	2:O:22:GLN:HE22	1.51	0.56
1:B:312:PHE:HA	1:B:315:ILE:HD12	1.88	0.56
1:B:433:ASN:HD22	2:J:22:GLN:HE22	1.52	0.56
1:D:145:ALA:HA	1:E:145:ALA:HA	1.88	0.56
1:G:312:PHE:HA	1:G:315:ILE:HD12	1.88	0.55
1:E:312:PHE:HA	1:E:315:ILE:HD12	1.88	0.55
1:D:312:PHE:HA	1:D:315:ILE:HD12	1.88	0.55
1:C:145:ALA:HA	1:H:145:ALA:HA	1.88	0.55
1:B:145:ALA:HA	1:G:145:ALA:HA	1.88	0.55
1:F:312:PHE:HA	1:F:315:ILE:HD12	1.88	0.54
1:C:312:PHE:HA	1:C:315:ILE:HD12	1.88	0.54
1:A:145:ALA:HA	1:F:145:ALA:HA	1.89	0.54
1:F:475:THR:CG2	1:F:476:SER:N	2.71	0.54
1:C:475:THR:CG2	1:C:476:SER:N	2.71	0.53
1:H:475:THR:CG2	1:H:476:SER:N	2.71	0.53
1:A:312:PHE:HA	1:A:315:ILE:HD12	1.88	0.53
1:A:475:THR:CG2	1:A:476:SER:N	2.71	0.53
1:H:312:PHE:HA	1:H:315:ILE:HD12	1.89	0.53
1:E:475:THR:CG2	1:E:476:SER:N	2.71	0.53
1:A:107:LEU:HD23	1:F:148:LYS:HE2	1.91	0.52
1:D:475:THR:CG2	1:D:476:SER:N	2.71	0.52
1:H:475:THR:HG22	1:H:476:SER:H	1.74	0.52
1:A:475:THR:HG22	1:A:476:SER:H	1.75	0.52
1:G:475:THR:CG2	1:G:476:SER:N	2.71	0.52
1:B:475:THR:CG2	1:B:476:SER:N	2.72	0.52
1:B:475:THR:HG22	1:B:476:SER:H	1.75	0.52
1:G:475:THR:HG22	1:G:476:SER:H	1.75	0.52
1:A:148:LYS:HE2	1:F:107:LEU:HD23	1.92	0.51
1:B:148:LYS:HE2	1:G:107:LEU:HD23	1.91	0.51
1:C:107:LEU:HD23	1:H:148:LYS:HE2	1.91	0.51
1:B:107:LEU:HD23	1:G:148:LYS:HE2	1.92	0.51
1:C:148:LYS:HE2	1:H:107:LEU:HD23	1.92	0.51
1:D:107:LEU:HD23	1:E:148:LYS:HE2	1.92	0.51
1:F:475:THR:HG22	1:F:476:SER:H	1.74	0.51
1:D:169:LYS:HZ1	1:D:422:ARG:HH21	1.58	0.50
1:D:148:LYS:HE2	1:E:107:LEU:HD23	1.92	0.50
1:E:169:LYS:HZ1	1:E:422:ARG:HH21	1.58	0.50
1:C:169:LYS:HZ1	1:C:422:ARG:HH21	1.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:249:MET:HG3	1:G:249:MET:HG3	1.93	0.50
1:C:475:THR:HG22	1:C:476:SER:H	1.74	0.50
1:D:475:THR:HG22	1:D:476:SER:H	1.74	0.50
1:B:249:MET:HG3	1:F:249:MET:HG3	1.93	0.50
1:H:169:LYS:HZ1	1:H:422:ARG:HH21	1.58	0.50
1:D:249:MET:HG3	1:H:249:MET:HG3	1.92	0.50
1:E:475:THR:HG22	1:E:476:SER:H	1.74	0.50
1:A:249:MET:HG3	1:E:249:MET:HG3	1.93	0.49
1:B:109:LEU:HD22	1:F:180:LEU:HD13	1.95	0.49
1:G:169:LYS:HZ1	1:G:422:ARG:HH21	1.61	0.49
1:A:169:LYS:HZ1	1:A:422:ARG:HH21	1.58	0.48
1:B:180:LEU:HD13	1:F:109:LEU:HD22	1.95	0.48
1:D:109:LEU:HD22	1:H:180:LEU:HD13	1.95	0.48
1:G:293:HIS:HA	1:G:326:HIS:HB2	1.96	0.48
1:B:293:HIS:HA	1:B:326:HIS:HB2	1.96	0.48
1:G:160:GLU:HG3	1:G:291:ILE:HD13	1.95	0.48
1:B:160:GLU:HG3	1:B:291:ILE:HD13	1.96	0.47
1:F:293:HIS:HA	1:F:326:HIS:HB2	1.96	0.47
1:D:160:GLU:HG3	1:D:291:ILE:HD13	1.95	0.47
1:A:293:HIS:HA	1:A:326:HIS:HB2	1.96	0.47
1:C:109:LEU:HD22	1:G:180:LEU:HD13	1.96	0.47
1:B:169:LYS:HZ1	1:B:422:ARG:HH21	1.62	0.47
1:C:293:HIS:HA	1:C:326:HIS:HB2	1.97	0.47
2:J:116:VAL:HG21	2:J:122:ARG:HG2	1.96	0.47
2:P:116:VAL:HG21	2:P:122:ARG:HG2	1.97	0.47
1:D:180:LEU:HD13	1:H:109:LEU:HD22	1.95	0.47
1:H:293:HIS:HA	1:H:326:HIS:HB2	1.97	0.47
2:I:116:VAL:HG21	2:I:122:ARG:HG2	1.97	0.47
1:C:242:LEU:HB2	1:C:267:VAL:HG12	1.96	0.46
1:A:180:LEU:HD13	1:E:109:LEU:HD22	1.97	0.46
2:L:116:VAL:HG21	2:L:122:ARG:HG2	1.97	0.46
1:D:293:HIS:HA	1:D:326:HIS:HB2	1.96	0.46
1:E:147:VAL:HG12	1:E:321:LEU:HD21	1.97	0.46
1:G:242:LEU:HB2	1:G:267:VAL:HG12	1.97	0.46
1:F:169:LYS:HZ1	1:F:422:ARG:HH21	1.64	0.46
2:K:116:VAL:HG21	2:K:122:ARG:HG2	1.96	0.46
1:A:160:GLU:HG3	1:A:291:ILE:HD13	1.96	0.46
1:E:160:GLU:HG3	1:E:291:ILE:HD13	1.97	0.46
2:N:116:VAL:HG21	2:N:122:ARG:HG2	1.96	0.46
1:A:109:LEU:HD22	1:E:180:LEU:HD13	1.97	0.46
1:E:475:THR:CG2	1:E:476:SER:H	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:475:THR:CG2	1:D:476:SER:H	2.29	0.46
1:G:220:PHE:HE2	1:G:259:ALA:HB2	1.81	0.46
1:G:475:THR:CG2	1:G:476:SER:H	2.29	0.46
1:A:242:LEU:HB2	1:A:267:VAL:HG12	1.96	0.46
1:B:475:THR:CG2	1:B:476:SER:H	2.29	0.46
1:C:220:PHE:HE2	1:C:259:ALA:HB2	1.81	0.45
1:E:293:HIS:HA	1:E:326:HIS:HB2	1.97	0.45
1:F:475:THR:CG2	1:F:476:SER:H	2.28	0.45
1:A:220:PHE:HE2	1:A:259:ALA:HB2	1.81	0.45
1:C:302:TYR:HB3	1:G:302:TYR:HB3	1.98	0.45
1:H:220:PHE:HE2	1:H:259:ALA:HB2	1.81	0.45
1:B:302:TYR:HB3	1:F:302:TYR:HB3	1.98	0.45
1:F:220:PHE:HE2	1:F:259:ALA:HB2	1.81	0.45
1:H:475:THR:CG2	1:H:476:SER:H	2.29	0.45
1:B:242:LEU:HB2	1:B:267:VAL:HG12	1.98	0.45
1:C:180:LEU:HD13	1:G:109:LEU:HD22	1.97	0.45
1:D:302:TYR:HB3	1:H:302:TYR:HB3	1.98	0.45
1:B:220:PHE:HE2	1:B:259:ALA:HB2	1.81	0.45
1:H:160:GLU:HG3	1:H:291:ILE:HD13	1.97	0.45
1:C:160:GLU:HG3	1:C:291:ILE:HD13	1.98	0.45
1:C:475:THR:CG2	1:C:476:SER:H	2.29	0.45
1:E:242:LEU:HB2	1:E:267:VAL:HG12	1.97	0.45
1:F:160:GLU:HG3	1:F:291:ILE:HD13	1.98	0.45
1:D:220:PHE:HE2	1:D:259:ALA:HB2	1.81	0.45
1:E:220:PHE:HE2	1:E:259:ALA:HB2	1.81	0.45
1:F:242:LEU:HB2	1:F:267:VAL:HG12	1.98	0.45
2:M:116:VAL:HG21	2:M:122:ARG:HG2	1.99	0.45
2:O:116:VAL:HG21	2:O:122:ARG:HG2	1.99	0.44
1:D:269:VAL:HG21	1:D:281:ILE:HD13	1.99	0.44
1:D:242:LEU:HB2	1:D:267:VAL:HG12	1.98	0.44
1:A:274:GLY:HA3	1:E:274:GLY:HA3	1.99	0.44
1:G:147:VAL:HG12	1:G:321:LEU:HD21	1.99	0.44
1:A:302:TYR:HB3	1:E:302:TYR:HB3	2.00	0.44
1:H:242:LEU:HB2	1:H:267:VAL:HG12	1.98	0.44
2:O:116:VAL:HG12	2:O:117:ASP:H	1.83	0.44
1:H:147:VAL:HG12	1:H:321:LEU:HD21	2.00	0.44
2:M:109:LEU:HD23	2:M:125:HIS:HB3	2.00	0.44
1:C:274:GLY:HA3	1:G:274:GLY:HA3	1.98	0.43
1:D:274:GLY:HA3	1:H:274:GLY:HA3	1.99	0.43
1:B:274:GLY:HA3	1:F:274:GLY:HA3	1.99	0.43
1:D:147:VAL:HG12	1:D:321:LEU:HD21	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:215:HIS:HB2	1:F:373:ARG:HH22	1.82	0.43
1:B:269:VAL:HG21	1:B:281:ILE:HD13	1.99	0.43
1:B:373:ARG:HH22	1:C:215:HIS:HB2	1.82	0.43
2:J:109:LEU:HD23	2:J:125:HIS:HB3	2.00	0.43
2:L:109:LEU:HD23	2:L:125:HIS:HB3	2.01	0.43
2:N:109:LEU:HD23	2:N:125:HIS:HB3	2.01	0.43
1:E:269:VAL:HG21	1:E:281:ILE:HD13	2.01	0.43
2:O:109:LEU:HD23	2:O:125:HIS:HB3	2.01	0.43
1:G:153:PRO:HA	1:G:154:PRO:HD3	1.95	0.43
2:K:109:LEU:HD23	2:K:125:HIS:HB3	2.01	0.43
1:A:215:HIS:HB2	1:D:373:ARG:HH22	1.83	0.43
1:A:269:VAL:HG21	1:A:281:ILE:HD13	2.00	0.43
1:A:475:THR:CG2	1:A:476:SER:H	2.29	0.43
1:B:153:PRO:HA	1:B:154:PRO:HD3	1.95	0.43
2:I:109:LEU:HD23	2:I:125:HIS:HB3	2.01	0.43
2:P:109:LEU:HD23	2:P:125:HIS:HB3	2.01	0.43
1:B:95:THR:HA	1:B:96:PRO:HD3	1.91	0.42
1:C:180:LEU:H	1:G:65:THR:HG22	1.84	0.42
1:E:296:ARG:HG2	1:E:328:HIS:HB2	2.01	0.42
1:F:269:VAL:HG21	1:F:281:ILE:HD13	2.00	0.42
1:B:147:VAL:HG12	1:B:321:LEU:HD21	2.01	0.42
1:F:147:VAL:HG12	1:F:321:LEU:HD21	2.01	0.42
1:G:269:VAL:HG21	1:G:281:ILE:HD13	2.00	0.42
2:M:116:VAL:HG12	2:M:117:ASP:H	1.83	0.42
2:P:37:HIS:HA	2:P:79:TYR:O	2.20	0.42
1:F:241:TYR:HB3	1:F:268:MET:HB3	2.02	0.42
1:H:269:VAL:HG21	1:H:281:ILE:HD13	2.01	0.42
1:G:215:HIS:HB2	1:H:373:ARG:HH22	1.83	0.42
1:C:241:TYR:HB3	1:C:268:MET:HB3	2.02	0.42
2:I:37:HIS:HA	2:I:79:TYR:O	2.20	0.42
2:M:37:HIS:HA	2:M:79:TYR:O	2.20	0.42
2:O:37:HIS:HA	2:O:79:TYR:O	2.20	0.42
1:C:269:VAL:HG21	1:C:281:ILE:HD13	2.01	0.42
1:C:373:ARG:HH22	1:D:215:HIS:HB2	1.83	0.42
1:D:296:ARG:HG2	1:D:328:HIS:HB2	2.02	0.42
1:E:373:ARG:HH22	1:H:215:HIS:HB2	1.83	0.42
1:C:296:ARG:HG2	1:C:328:HIS:HB2	2.01	0.41
1:G:241:TYR:HB3	1:G:268:MET:HB3	2.02	0.41
2:K:37:HIS:HA	2:K:79:TYR:O	2.20	0.41
1:C:65:THR:HG22	1:G:180:LEU:H	1.85	0.41
2:N:37:HIS:HA	2:N:79:TYR:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:LYS:N	1:A:131:PRO:HD2	2.36	0.41
1:A:65:THR:HG22	1:E:180:LEU:H	1.85	0.41
1:B:130:LYS:N	1:B:131:PRO:HD2	2.36	0.41
1:F:215:HIS:HB2	1:G:373:ARG:HH22	1.83	0.41
2:L:37:HIS:HA	2:L:79:TYR:O	2.20	0.41
1:D:241:TYR:HB3	1:D:268:MET:HB3	2.02	0.41
2:J:37:HIS:HA	2:J:79:TYR:O	2.21	0.41
1:C:130:LYS:N	1:C:131:PRO:HD2	2.36	0.41
1:D:130:LYS:N	1:D:131:PRO:HD2	2.35	0.41
1:H:130:LYS:N	1:H:131:PRO:HD2	2.36	0.41
1:D:180:LEU:H	1:H:65:THR:HG22	1.86	0.41
1:E:209:ASN:HD21	1:E:245:THR:HB	1.86	0.41
1:G:130:LYS:N	1:G:131:PRO:HD2	2.36	0.41
1:G:95:THR:HA	1:G:96:PRO:HD3	1.93	0.41
1:B:180:LEU:H	1:F:65:THR:HG22	1.86	0.41
1:A:95:THR:HA	1:A:96:PRO:HD3	1.92	0.41
1:E:241:TYR:HB3	1:E:268:MET:HB3	2.02	0.41
1:F:296:ARG:HG2	1:F:328:HIS:HB2	2.02	0.41
1:H:296:ARG:HG2	1:H:328:HIS:HB2	2.02	0.41
1:A:180:LEU:H	1:E:65:THR:HG22	1.86	0.41
1:H:95:THR:HA	1:H:96:PRO:HD3	1.92	0.41
1:E:130:LYS:N	1:E:131:PRO:HD2	2.36	0.40
1:F:130:LYS:N	1:F:131:PRO:HD2	2.36	0.40
1:A:373:ARG:HH22	1:B:215:HIS:HB2	1.85	0.40
1:B:241:TYR:HB3	1:B:268:MET:HB3	2.02	0.40
1:C:153:PRO:HA	1:C:154:PRO:HD3	1.95	0.40
1:D:378:VAL:HG22	1:D:400:VAL:HB	2.03	0.40
1:H:241:TYR:HB3	1:H:268:MET:HB3	2.01	0.40
1:A:296:ARG:HG2	1:A:328:HIS:HB2	2.02	0.40
1:B:65:THR:HG22	1:F:180:LEU:H	1.87	0.40
1:D:65:THR:HG22	1:H:180:LEU:H	1.86	0.40
1:A:147:VAL:HG12	1:A:321:LEU:HD21	2.04	0.40
1:A:195:LEU:HD22	1:A:238:LYS:HB3	2.04	0.40
1:A:241:TYR:HB3	1:A:268:MET:HB3	2.02	0.40
1:B:209:ASN:HD21	1:B:245:THR:HB	1.87	0.40
1:C:147:VAL:HG12	1:C:321:LEU:HD21	2.02	0.40
1:G:209:ASN:HD21	1:G:245:THR:HB	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	464/467 (99%)	439 (95%)	25 (5%)	0	100	100
1	B	464/467 (99%)	439 (95%)	25 (5%)	0	100	100
1	C	464/467 (99%)	440 (95%)	24 (5%)	0	100	100
1	D	464/467 (99%)	439 (95%)	25 (5%)	0	100	100
1	E	464/467 (99%)	439 (95%)	25 (5%)	0	100	100
1	F	464/467 (99%)	440 (95%)	24 (5%)	0	100	100
1	G	464/467 (99%)	439 (95%)	25 (5%)	0	100	100
1	H	464/467 (99%)	440 (95%)	24 (5%)	0	100	100
2	I	127/129 (98%)	118 (93%)	8 (6%)	1 (1%)	22	62
2	J	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	22	62
2	K	127/129 (98%)	118 (93%)	8 (6%)	1 (1%)	22	62
2	L	127/129 (98%)	118 (93%)	8 (6%)	1 (1%)	22	62
2	M	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	22	62
2	N	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	22	62
2	O	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	22	62
2	P	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	22	62
All	All	4728/4768 (99%)	4454 (94%)	266 (6%)	8 (0%)	54	84

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	P	116	VAL
2	I	116	VAL
2	J	116	VAL
2	K	116	VAL
2	L	116	VAL
2	M	116	VAL

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Mol	Chain	Res	Type
2	N	116	VAL
2	O	116	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	375/375 (100%)	374 (100%)	1 (0%)	94	98
1	B	375/375 (100%)	375 (100%)	0	100	100
1	C	375/375 (100%)	375 (100%)	0	100	100
1	D	375/375 (100%)	374 (100%)	1 (0%)	94	98
1	E	375/375 (100%)	375 (100%)	0	100	100
1	F	375/375 (100%)	375 (100%)	0	100	100
1	G	375/375 (100%)	375 (100%)	0	100	100
1	H	375/375 (100%)	375 (100%)	0	100	100
2	I	117/117 (100%)	116 (99%)	1 (1%)	82	92
2	J	117/117 (100%)	116 (99%)	1 (1%)	82	92
2	K	117/117 (100%)	116 (99%)	1 (1%)	82	92
2	L	117/117 (100%)	115 (98%)	2 (2%)	66	86
2	M	117/117 (100%)	116 (99%)	1 (1%)	82	92
2	N	117/117 (100%)	116 (99%)	1 (1%)	82	92
2	O	117/117 (100%)	115 (98%)	2 (2%)	66	86
2	P	117/117 (100%)	115 (98%)	2 (2%)	66	86
All	All	3936/3936 (100%)	3923 (100%)	13 (0%)	94	98

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	281	ILE
2	I	88	THR

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Mol	Chain	Res	Type
2	J	88	THR
2	K	88	THR
1	D	281	ILE
2	L	88	THR
2	L	100	VAL
2	M	88	THR
2	N	88	THR
2	O	88	THR
2	O	100	VAL
2	P	88	THR
2	P	100	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	233	GLN
1	A	387	GLN
2	I	18	GLN
2	I	22	GLN
1	B	233	GLN
1	B	387	GLN
2	J	18	GLN
2	J	22	GLN
1	C	233	GLN
1	C	387	GLN
2	K	18	GLN
2	K	22	GLN
1	D	233	GLN
1	D	387	GLN
2	L	18	GLN
2	L	22	GLN
1	E	233	GLN
2	M	18	GLN
2	M	22	GLN
1	F	233	GLN
2	N	18	GLN
2	N	22	GLN
1	G	233	GLN
2	O	18	GLN
2	O	22	GLN
1	H	233	GLN
2	P	18	GLN

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Mol	Chain	Res	Type
2	P	22	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

8 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	KCX	A	203	1,4	8,11,12	0.43	0	6,12,14	0.93	0
1	KCX	B	203	1,4	8,11,12	0.42	0	6,12,14	0.85	0
1	KCX	C	203	1,4	8,11,12	0.42	0	6,12,14	0.92	0
1	KCX	D	203	1,4	8,11,12	0.42	0	6,12,14	0.87	0
1	KCX	E	203	1,4	8,11,12	0.42	0	6,12,14	0.86	0
1	KCX	F	203	1,4	8,11,12	0.50	0	6,12,14	0.86	0
1	KCX	G	203	1,4	8,11,12	0.42	0	6,12,14	0.88	0
1	KCX	H	203	1,4	8,11,12	0.50	0	6,12,14	0.86	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	KCX	A	203	1,4	-	0/6/10/12	0/0/0/0
1	KCX	B	203	1,4	-	0/6/10/12	0/0/0/0
1	KCX	C	203	1,4	-	0/6/10/12	0/0/0/0
1	KCX	D	203	1,4	-	0/6/10/12	0/0/0/0
1	KCX	E	203	1,4	-	0/6/10/12	0/0/0/0
1	KCX	F	203	1,4	-	0/6/10/12	0/0/0/0
1	KCX	G	203	1,4	-	0/6/10/12	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	KCX	H	203	1,4	-	0/6/10/12	0/0/0/0

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.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	CAP	A	1001	4	14,20,20	0.61	0	17,31,31	1.05	0
3	CAP	B	1001	4	14,20,20	0.61	0	17,31,31	1.05	0
3	CAP	C	1001	4	14,20,20	0.61	0	17,31,31	1.05	0
3	CAP	D	1001	4	14,20,20	0.61	0	17,31,31	1.05	0
3	CAP	E	1001	4	14,20,20	0.61	0	17,31,31	1.05	0
3	CAP	F	1001	4	14,20,20	0.61	0	17,31,31	1.05	0
3	CAP	G	1001	4	14,20,20	0.61	0	17,31,31	1.04	0
3	CAP	H	1001	4	14,20,20	0.61	0	17,31,31	1.06	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CAP	A	1001	4	-	0/23/29/29	0/0/0/0
3	CAP	B	1001	4	-	0/23/29/29	0/0/0/0
3	CAP	C	1001	4	-	0/23/29/29	0/0/0/0
3	CAP	D	1001	4	-	0/23/29/29	0/0/0/0
3	CAP	E	1001	4	-	0/23/29/29	0/0/0/0
3	CAP	F	1001	4	-	0/23/29/29	0/0/0/0
3	CAP	G	1001	4	-	0/23/29/29	0/0/0/0
3	CAP	H	1001	4	-	0/23/29/29	0/0/0/0

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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.