



Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Oct 10, 2017 – 06:06 PM EDT

PDB ID : 6B45
EMDB ID: : EMD-7049
Title : Cryo-EM structure of Type I-F CRISPR crRNA-guided Csy surveillance complex
Authors : Guo, T.W.; Bartesaghi, A.; Yang, H.; Falconieri, V.; Rao, P.; Merk, A.; Fox, T.; Earl, L.; Patel, D.J.; Subramaniam, S.
Deposited on : unknown
Resolution : 3.50 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
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-20030345

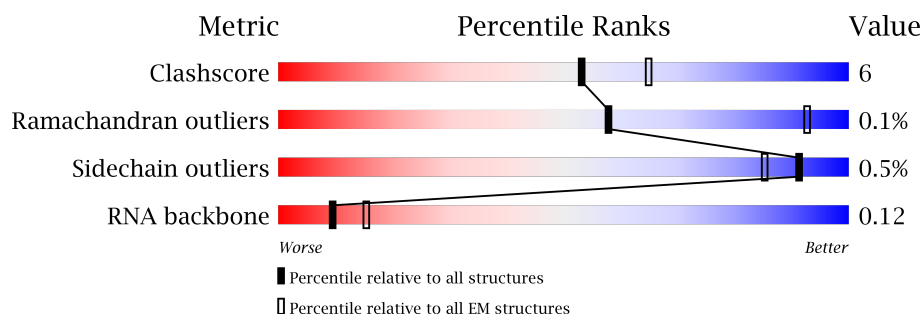
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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	436	91% 6% .
2	B	329	71% 21% 7%
3	C	344	68% 17% 15%
3	D	344	77% 19% .
3	E	344	82% 15% .
3	F	344	83% 13% . .
3	G	344	82% 15% .
3	H	344	81% 16% .

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Mol	Chain	Length	Quality of chain
4	L	189	<div><div></div><div>97%</div><div></div></div>
5	M	60	<div><div></div><div>20%</div><div>60%</div><div>20%</div></div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 21547 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 CRISPR-associated protein Csy1.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	424	Total	C	N	O	0	0
			2079	1145	473	461		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q02ML9
A	0	SER	-	expression tag	UNP Q02ML9

- Molecule 2 is a protein called CRISPR-associated protein Csy2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	305	Total	C	N	O	S	0	0
			2374	1504	440	425	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	MET	-	initiating methionine	UNP Q02MM0
B	0	ALA	-	expression tag	UNP Q02MM0

- Molecule 3 is a protein called CRISPR-associated protein Csy3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	293	Total	C	N	O	S	0	0
			2272	1430	409	431	2		
3	D	333	Total	C	N	O	S	0	0
			2554	1603	466	483	2		
3	E	334	Total	C	N	O	S	0	0
			2561	1611	466	482	2		
3	F	335	Total	C	N	O	S	0	0
			2566	1614	467	483	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	333	Total	C	N	O	S	0	0
			2557	1608	466	481	2		
3	H	333	Total	C	N	O	S	0	0
			2554	1603	466	483	2		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	MET	-	initiating methionine	UNP Q02MM1
C	0	ALA	-	expression tag	UNP Q02MM1
D	-1	MET	-	initiating methionine	UNP Q02MM1
D	0	ALA	-	expression tag	UNP Q02MM1
E	-1	MET	-	initiating methionine	UNP Q02MM1
E	0	ALA	-	expression tag	UNP Q02MM1
F	-1	MET	-	initiating methionine	UNP Q02MM1
F	0	ALA	-	expression tag	UNP Q02MM1
G	-1	MET	-	initiating methionine	UNP Q02MM1
G	0	ALA	-	expression tag	UNP Q02MM1
H	-1	MET	-	initiating methionine	UNP Q02MM1
H	0	ALA	-	expression tag	UNP Q02MM1

- Molecule 4 is a protein called CRISPR-associated endonuclease Cas6/Csy4.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	L	189	Total	C	N	O	0	0
			758	380	189	189		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	-1	MET	-	initiating methionine	UNP Q02MM2
L	0	ALA	-	expression tag	UNP Q02MM2

- Molecule 5 is a RNA chain called Pseudomonas aeruginosa strain SMC4485 CRISPR repeat sequence.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	60	Total	C	N	O	P	0	0
			1272	569	223	421	59		

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.

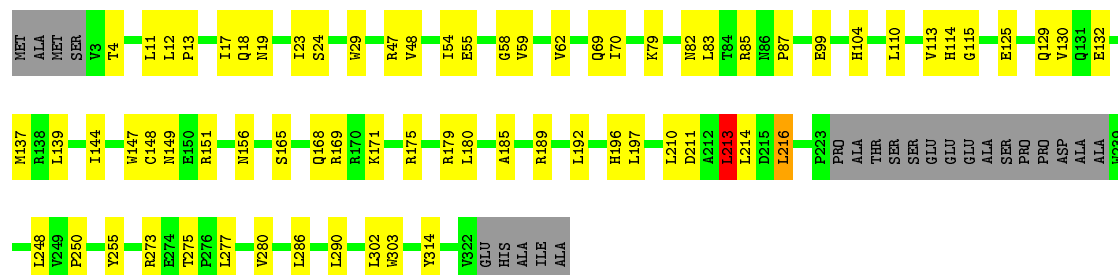
• Molecule 1: CRISPR-associated protein Csy1

Chain A: 



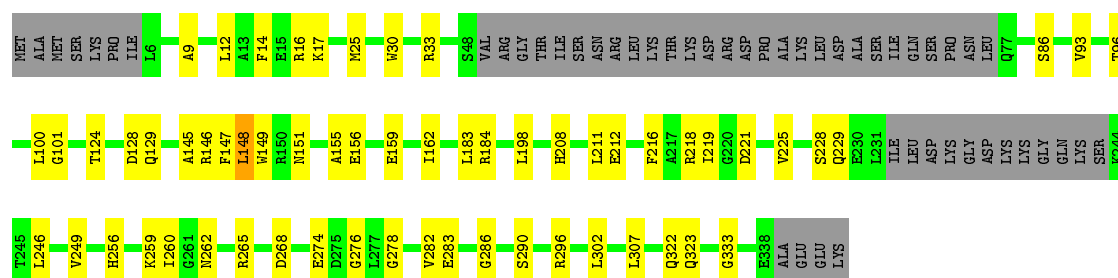
• Molecule 2: CRISPR-associated protein Csy2

Chain B: 



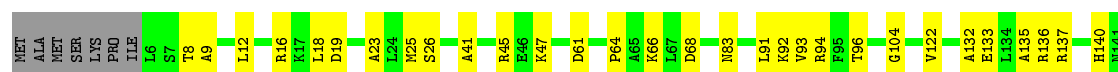
• Molecule 3: CRISPR-associated protein Csy3

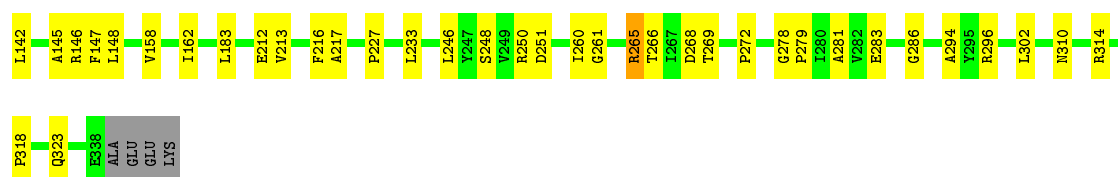
Chain C: 



• Molecule 3: CRISPR-associated protein Csy3

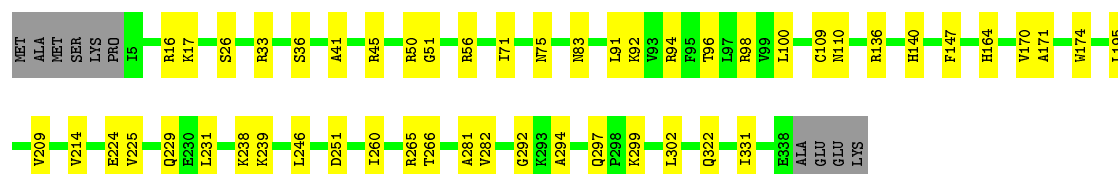
Chain D: 





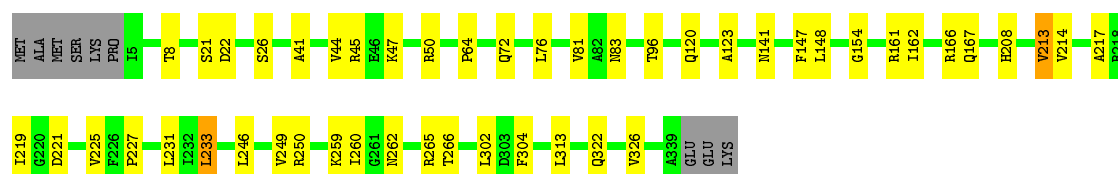
- Molecule 3: CRISPR-associated protein Csy3

Chain E: 82% 15% •



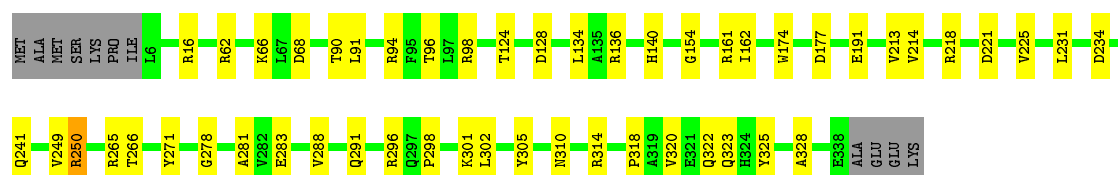
- Molecule 3: CRISPR-associated protein Csy3

Chain F: 83% 13% • •



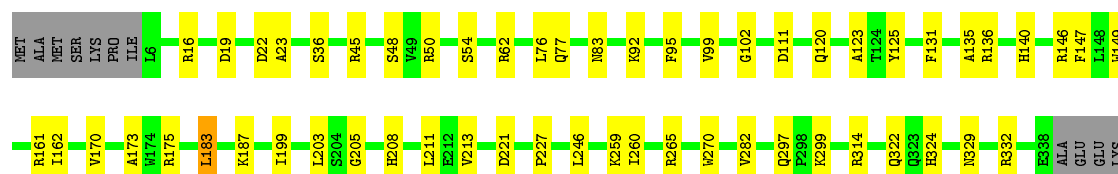
- Molecule 3: CRISPR-associated protein Csy3

Chain G: 82% 15% •



- Molecule 3: CRISPR-associated protein Csy3

Chain H: 81% 16% •

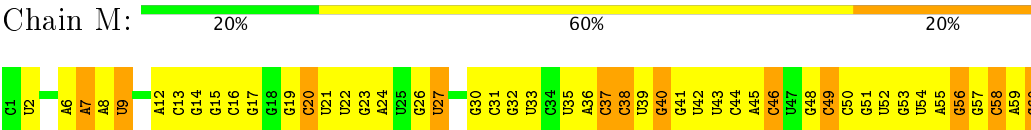


- Molecule 4: CRISPR-associated endonuclease Cas6/Csy4

Chain L: 97% •



- Molecule 5: Pseudomonas aeruginosa strain SMC4485 CRISPR repeat sequence



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	31488	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	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	0.26	0/2104	0.56	3/2715 (0.1%)
2	B	0.31	0/2431	0.63	2/3310 (0.1%)
3	C	0.30	0/2315	0.65	3/3143 (0.1%)
3	D	0.33	0/2601	0.63	1/3532 (0.0%)
3	E	0.34	0/2608	0.62	1/3540 (0.0%)
3	F	0.35	0/2613	0.63	1/3547 (0.0%)
3	G	0.34	0/2604	0.60	0/3533
3	H	0.32	0/2601	0.61	1/3532 (0.0%)
4	L	0.24	0/757	0.51	0/946
5	M	0.49	0/1420	1.14	14/2212 (0.6%)
All	All	0.33	0/22054	0.67	26/30010 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
2	B	0	1
3	C	0	1
3	G	0	1
All	All	0	5

There are no bond length outliers.

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	M	58	C	N1-C2-O2	9.05	124.33	118.90
5	M	58	C	C2-N1-C1'	8.86	128.54	118.80
5	M	58	C	C6-N1-C2	-7.23	117.41	120.30
5	M	58	C	N3-C2-O2	-7.20	116.86	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	M	46	C	C6-N1-C2	-7.05	117.48	120.30
3	D	18	LEU	CA-CB-CG	6.80	130.95	115.30
5	M	60	G	C4-N9-C1'	6.44	134.88	126.50
1	A	189	LEU	CA-CB-CG	6.30	129.80	115.30
1	A	264	LEU	CA-CB-CG	6.09	129.30	115.30
5	M	46	C	C5-C6-N1	6.08	124.04	121.00
5	M	58	C	C5-C6-N1	5.96	123.98	121.00
5	M	46	C	N1-C2-O2	5.92	122.45	118.90
5	M	58	C	C6-N1-C1'	-5.73	113.92	120.80
3	E	251	ASP	CB-CG-OD1	5.71	123.44	118.30
3	C	198	LEU	CA-CB-CG	5.56	128.08	115.30
5	M	60	G	N3-C4-C5	-5.54	125.83	128.60
5	M	60	G	N3-C4-N9	5.53	129.32	126.00
3	F	233	LEU	CA-CB-CG	5.50	127.94	115.30
3	H	183	LEU	CA-CB-CG	5.48	127.91	115.30
2	B	213	LEU	CA-CB-CG	5.41	127.75	115.30
5	M	60	G	C8-N9-C1'	-5.25	120.18	127.00
5	M	46	C	C2-N1-C1'	5.20	124.52	118.80
3	C	148	LEU	CA-CB-CG	5.15	127.14	115.30
2	B	277	LEU	CA-CB-CG	5.08	126.99	115.30
3	C	307	LEU	CA-CB-CG	5.04	126.88	115.30
1	A	254	LEU	CA-CB-CG	5.00	126.81	115.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	227	SER	Peptide
1	A	263	TRP	Peptide
2	B	12	LEU	Peptide
3	C	249	VAL	Peptide
3	G	301	LYS	Peptide

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	2079	0	1094	17	0
2	B	2374	0	2345	53	0
3	C	2272	0	2232	39	0
3	D	2554	0	2522	40	0
3	E	2561	0	2542	35	0
3	F	2566	0	2547	31	0
3	G	2557	0	2542	31	0
3	H	2554	0	2522	38	0
4	L	758	0	209	5	0
5	M	1272	0	644	24	0
All	All	21547	0	19199	261	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 6.

All (261) 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)
3:H:199:ILE:O	3:H:203:LEU:HB2	1.85	0.77
3:C:148:LEU:HB2	3:C:151:ASN:HB3	1.68	0.75
3:C:124:THR:O	3:C:128:ASP:HB2	1.88	0.73
1:A:221:ALA:HB1	1:A:227:SER:HB2	1.71	0.72
4:L:-1:MET:CB	4:L:183:PHE:C	2.58	0.71
3:G:302:LEU:HB3	3:G:322:GLN:HE22	1.57	0.69
3:F:162:ILE:HG12	3:F:213:VAL:HG12	1.77	0.66
3:E:238:LYS:HG2	3:E:239:LYS:HG3	1.78	0.66
2:B:189:ARG:HB3	2:B:192:LEU:HB3	1.79	0.64
3:D:283:GLU:HB3	3:D:286:GLY:HA2	1.81	0.63
3:G:298:PRO:HB2	3:H:62:ARG:HD3	1.80	0.63
3:C:9:ALA:HB3	3:C:12:LEU:HD12	1.80	0.62
2:B:23:ILE:HA	2:B:29:TRP:HA	1.82	0.62
3:G:161:ARG:HB2	3:G:214:VAL:HB	1.80	0.62
3:C:296:ARG:HH12	3:C:322:GLN:HE22	1.47	0.61
3:D:310:ASN:OD1	3:D:314:ARG:NH2	2.34	0.61
3:G:265:ARG:NH2	5:M:14:G:OP2	2.33	0.60
3:D:16:ARG:HB2	5:M:30:G:H5"	1.82	0.60
3:G:90:THR:HA	3:G:218:ARG:HA	1.84	0.60
2:B:69:GLN:HB3	2:B:82:ASN:HB2	1.83	0.60
2:B:83:LEU:HD21	2:B:99:GLU:HG2	1.84	0.59
3:C:162:ILE:HD11	3:C:211:LEU:HB3	1.85	0.59
3:C:129:GLN:NE2	3:C:323:GLN:OE1	2.35	0.59
4:L:-1:MET:CB	4:L:183:PHE:CA	2.80	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:58:GLY:HA3	2:B:302:LEU:HB3	1.84	0.59
2:B:156:ASN:OD1	2:B:179:ARG:NH2	2.36	0.59
3:C:16:ARG:NH1	5:M:37:C:OP1	2.36	0.59
3:E:98:ARG:NH1	3:F:219:ILE:O	2.36	0.59
2:B:85:ARG:NH2	5:M:9:U:O2	2.36	0.58
3:E:17:LYS:HG3	3:E:100:LEU:HB2	1.84	0.58
3:H:136:ARG:O	3:H:140:HIS:ND1	2.33	0.58
3:D:146:ARG:NH2	3:D:183:LEU:O	2.37	0.58
3:E:16:ARG:HD3	5:M:24:A:H5'	1.85	0.57
2:B:11:LEU:O	2:B:156:ASN:ND2	2.37	0.57
2:B:197:LEU:HB2	2:B:210:LEU:HD22	1.85	0.57
3:E:96:THR:HG21	3:F:221:ASP:HB3	1.86	0.57
2:B:214:LEU:HD22	2:B:248:LEU:HD13	1.86	0.57
2:B:273:ARG:NH1	3:H:111:ASP:OD1	2.37	0.57
3:D:272:PRO:HD3	3:D:302:LEU:HD12	1.85	0.57
3:G:234:ASP:OD1	3:G:241:GLN:NE2	2.36	0.57
3:D:248:SER:O	3:E:45:ARG:NH2	2.38	0.57
3:C:25:MET:HG2	3:C:93:VAL:HG12	1.85	0.56
3:E:109:CYS:SG	3:E:110:ASN:N	2.77	0.56
3:C:14:PHE:HB2	3:C:333:GLY:HA2	1.86	0.56
1:A:218:ALA:HB2	1:A:232:PHE:HB2	1.87	0.56
2:B:59:VAL:HG22	2:B:303:TRP:HB2	1.88	0.56
3:D:266:THR:HA	3:D:281:ALA:HA	1.87	0.56
3:E:265:ARG:NH1	3:E:282:VAL:O	2.39	0.56
2:B:70:ILE:HD12	2:B:79:LYS:HD3	1.87	0.56
3:G:231:LEU:HD21	3:H:76:LEU:HB3	1.88	0.56
3:H:131:PHE:O	3:H:135:ALA:N	2.37	0.56
3:E:94:ARG:HG3	3:E:214:VAL:HG22	1.88	0.55
3:D:61:ASP:OD2	3:D:66:LYS:NZ	2.40	0.55
3:C:184:ARG:HD3	3:C:278:GLY:HA3	1.88	0.55
3:H:147:PHE:HB2	3:H:260:ILE:HG13	1.88	0.55
3:C:155:ALA:HA	3:C:219:ILE:HA	1.89	0.55
3:D:96:THR:HG22	3:D:212:GLU:HG2	1.89	0.55
2:B:148:CYS:SG	2:B:149:ASN:N	2.80	0.55
3:C:124:THR:O	3:C:128:ASP:CB	2.54	0.55
3:E:51:GLY:O	3:E:75:ASN:ND2	2.40	0.55
3:G:271:TYR:HB3	3:G:296:ARG:HE	1.72	0.55
2:B:165:SER:O	2:B:169:ARG:N	2.39	0.55
3:E:147:PHE:HB2	3:E:260:ILE:HG13	1.89	0.55
3:E:164:HIS:HD2	3:E:171:ALA:HB3	1.73	0.54
3:H:99:VAL:HG11	3:H:203:LEU:HA	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:171:LYS:O	2:B:175:ARG:HB2	2.07	0.54
1:A:216:LYS:NZ	1:A:220:GLU:OE1	2.37	0.53
2:B:11:LEU:HD23	2:B:110:LEU:HB3	1.90	0.53
3:F:47:LYS:HE2	3:F:81:VAL:HG21	1.89	0.53
3:C:265:ARG:HH22	5:M:37:C:H4'	1.73	0.53
1:A:195:PRO:HB2	1:A:198:LEU:HB2	1.89	0.53
3:H:162:ILE:HD11	3:H:211:LEU:HB3	1.91	0.53
3:D:132:ALA:HA	3:D:135:ALA:HB3	1.91	0.53
4:L:6:ASP:H	4:L:86:GLY:HA3	1.74	0.53
3:C:290:SER:OG	4:L:12:ASP:O	2.24	0.52
2:B:18:GLN:HE22	3:H:22:ASP:H	1.57	0.52
3:F:148:LEU:HD13	3:F:217:ALA:HB2	1.92	0.52
3:D:261:GLY:O	3:D:265:ARG:NE	2.41	0.52
3:F:96:THR:HG21	3:G:221:ASP:HB2	1.92	0.52
3:E:36:SER:O	3:E:92:LYS:NZ	2.32	0.52
3:H:146:ARG:NH2	3:H:183:LEU:O	2.42	0.52
3:H:162:ILE:HD13	3:H:213:VAL:HG22	1.91	0.52
3:C:151:ASN:HA	3:C:225:VAL:HB	1.92	0.52
3:E:231:LEU:HD11	3:F:76:LEU:HB3	1.92	0.52
2:B:125:GLU:OE2	2:B:129:GLN:NE2	2.43	0.52
3:H:297:GLN:HG2	3:H:299:LYS:H	1.75	0.51
3:E:292:GLY:O	3:F:72:GLN:NE2	2.43	0.51
3:F:208:HIS:NE2	3:G:154:GLY:O	2.43	0.51
3:H:36:SER:O	3:H:92:LYS:NZ	2.37	0.51
3:H:227:PRO:HG2	3:H:246:LEU:HD22	1.93	0.51
3:C:33:ARG:HB2	3:C:216:PHE:HZ	1.76	0.51
3:C:147:PHE:HB2	3:C:260:ILE:HG13	1.92	0.51
3:E:136:ARG:O	3:E:140:HIS:ND1	2.39	0.51
3:D:25:MET:HG2	3:D:93:VAL:HG22	1.93	0.50
3:G:124:THR:O	3:G:128:ASP:HB2	2.11	0.50
2:B:165:SER:HB3	2:B:168:GLN:HB2	1.92	0.50
3:C:274:GLU:OE1	3:C:276:GLY:N	2.44	0.50
3:C:283:GLU:HG2	3:C:286:GLY:HA2	1.94	0.49
3:D:294:ALA:HB2	3:E:71:ILE:HD11	1.93	0.49
2:B:17:ILE:HG22	2:B:144:ILE:HG12	1.95	0.49
2:B:189:ARG:HH21	2:B:290:LEU:HD21	1.77	0.49
3:F:45:ARG:NH2	3:F:83:ASN:OD1	2.45	0.49
3:C:256:HIS:HD2	3:D:47:LYS:HD2	1.76	0.49
3:G:231:LEU:HD13	3:H:48:SER:HB2	1.94	0.49
3:D:45:ARG:NH2	3:D:83:ASN:OD1	2.46	0.49
1:A:258:ARG:NH1	1:A:261:GLU:O	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:162:ILE:HG12	3:D:213:VAL:HG12	1.94	0.49
1:A:187:TYR:O	2:B:275:THR:OG1	2.31	0.48
2:B:192:LEU:O	2:B:196:HIS:CB	2.61	0.48
3:E:294:ALA:O	3:E:297:GLN:NE2	2.34	0.48
3:D:137:ARG:HH22	3:D:269:THR:HG23	1.78	0.48
2:B:13:PRO:HD3	2:B:156:ASN:HD21	1.78	0.48
3:E:299:LYS:HB2	3:F:64:PRO:HB3	1.95	0.48
3:E:83:ASN:HA	3:E:224:GLU:HA	1.95	0.48
3:E:91:LEU:HD13	3:E:225:VAL:HG11	1.96	0.48
3:H:125:TYR:HH	3:H:324:HIS:HD1	1.61	0.48
3:H:45:ARG:HH21	3:H:83:ASN:HB2	1.77	0.48
5:M:49:C:H2'	5:M:56:G:H22	1.77	0.48
2:B:185:ALA:N	2:B:290:LEU:O	2.45	0.48
3:D:9:ALA:HB3	3:D:12:LEU:HD12	1.95	0.48
2:B:55:GLU:HB3	2:B:114:HIS:HB2	1.95	0.48
3:F:259:LYS:NZ	5:M:22:U:OP1	2.47	0.48
3:F:147:PHE:HB2	3:F:260:ILE:HG13	1.95	0.48
3:D:250:ARG:NH1	3:D:251:ASP:OD2	2.47	0.48
3:D:136:ARG:O	3:D:140:HIS:ND1	2.38	0.48
3:H:23:ALA:HB2	3:H:95:PHE:HB3	1.95	0.48
3:E:164:HIS:H	3:E:170:VAL:HG23	1.79	0.48
3:E:50:ARG:O	5:M:31:C:O2'	2.32	0.48
2:B:17:ILE:HD13	2:B:139:LEU:HD21	1.95	0.47
3:D:23:ALA:HB1	3:D:93:VAL:HG13	1.96	0.47
1:A:219:ARG:O	1:A:223:SER:HB3	2.13	0.47
2:B:192:LEU:O	2:B:196:HIS:HB3	2.12	0.47
3:G:266:THR:HA	3:G:281:ALA:HA	1.96	0.47
3:G:68:ASP:N	3:G:68:ASP:OD1	2.39	0.47
3:G:162:ILE:HG12	3:G:213:VAL:HG22	1.96	0.47
3:G:271:TYR:OH	3:G:278:GLY:O	2.26	0.47
3:C:14:PHE:O	5:M:35:U:O2'	2.32	0.47
3:C:259:LYS:NZ	5:M:40:G:OP1	2.38	0.47
2:B:62:VAL:HG11	2:B:180:LEU:HD11	1.96	0.47
3:F:225:VAL:HG23	3:F:227:PRO:HD3	1.97	0.47
3:C:17:LYS:HG3	3:C:100:LEU:HB3	1.97	0.47
3:C:219:ILE:HD13	3:C:225:VAL:HG11	1.97	0.47
3:H:120:GLN:HA	3:H:123:ALA:HB3	1.96	0.47
3:G:174:TRP:HD1	3:G:191:GLU:HG3	1.80	0.47
3:C:146:ARG:NH1	3:C:183:LEU:O	2.48	0.47
3:F:265:ARG:NH2	5:M:20:C:OP2	2.48	0.47
3:D:104:GLY:HA3	3:D:122:VAL:HG11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:113:VAL:HG12	2:B:115:GLY:H	1.80	0.47
3:H:265:ARG:NH2	5:M:8:A:OP2	2.48	0.47
3:D:158:VAL:HG12	3:D:217:ALA:HA	1.95	0.46
3:D:93:VAL:HG21	3:D:148:LEU:HD21	1.97	0.46
3:F:166:ARG:HG3	3:F:167:GLN:HG2	1.98	0.46
3:D:133:GLU:HA	3:D:136:ARG:HG2	1.98	0.46
2:B:87:PRO:HD3	5:M:7:A:H1'	1.98	0.46
2:B:47:ARG:NH1	2:B:137:MET:SD	2.89	0.46
3:G:310:ASN:HA	3:G:314:ARG:HB2	1.98	0.46
3:H:102:GLY:H	3:H:205:GLY:HA2	1.81	0.46
2:B:85:ARG:O	5:M:7:A:O2'	2.33	0.45
3:F:50:ARG:N	5:M:27:U:OP2	2.45	0.45
3:D:8:THR:HG21	3:E:56:ARG:HH12	1.81	0.45
3:G:96:THR:HG21	3:H:221:ASP:HB3	1.97	0.45
3:H:149:TRP:CD1	3:H:259:LYS:HE2	2.52	0.45
1:A:178:LEU:HD22	5:M:2:U:H5''	1.99	0.45
3:D:91:LEU:HG	3:D:93:VAL:HG23	1.98	0.45
3:D:145:ALA:HB1	3:D:148:LEU:HD12	1.98	0.45
3:G:249:VAL:HG12	3:G:250:ARG:H	1.82	0.45
3:H:16:ARG:HB3	3:H:19:ASP:HB3	1.99	0.45
3:C:156:GLU:HB3	3:C:218:ARG:HB2	1.98	0.45
3:C:229:GLN:HB3	3:C:246:LEU:HG	1.99	0.45
3:G:177:ASP:N	3:G:177:ASP:OD1	2.47	0.45
3:D:142:LEU:HD22	3:D:213:VAL:HG11	2.00	0.45
1:A:107:ASP:O	1:A:252:SER:OG	2.32	0.44
3:G:62:ARG:HA	3:G:66:LYS:HE2	1.99	0.44
1:A:182:LEU:HD21	1:A:188:HIS:HD2	1.81	0.44
3:E:174:TRP:CD2	3:E:195:LEU:HD12	2.53	0.44
1:A:243:PHE:O	1:A:250:ASN:ND2	2.41	0.44
3:F:302:LEU:HD21	3:F:322:GLN:HE22	1.82	0.44
3:H:50:ARG:HB3	5:M:14:G:H3'	1.99	0.44
2:B:196:HIS:HE1	2:B:214:LEU:HD21	1.83	0.44
3:E:302:LEU:HD22	3:E:322:GLN:HE22	1.83	0.44
3:G:91:LEU:HD13	3:G:225:VAL:HG11	1.98	0.44
1:A:217:ALA:O	1:A:221:ALA:CB	2.66	0.44
3:H:329:ASN:HA	3:H:332:ARG:HB3	1.99	0.44
3:G:16:ARG:NH2	5:M:13:C:OP2	2.50	0.44
3:E:26:SER:HA	3:E:41:ALA:HA	2.00	0.44
3:F:304:PHE:HE1	3:F:326:VAL:HG13	1.83	0.44
3:D:64:PRO:O	3:D:68:ASP:HB3	2.17	0.43
3:D:278:GLY:HA3	3:D:279:PRO:HD3	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:213:LEU:HA	2:B:216:LEU:HD21	2.00	0.43
2:B:4:THR:HB	2:B:114:HIS:HE1	1.82	0.43
3:D:26:SER:HA	3:D:41:ALA:HA	2.01	0.43
3:E:17:LYS:HB2	3:E:331:ILE:HG23	2.00	0.43
3:F:161:ARG:HB2	3:F:214:VAL:HB	1.99	0.43
3:F:21:SER:OG	3:F:22:ASP:N	2.52	0.43
2:B:85:ARG:HB3	5:M:8:A:H3'	2.00	0.43
3:C:268:ASP:HB2	3:C:282:VAL:HG12	2.00	0.43
3:D:227:PRO:HG2	3:D:246:LEU:HD22	2.01	0.43
3:G:283:GLU:O	3:G:325:TYR:OH	2.34	0.43
2:B:147:TRP:HB3	2:B:151:ARG:HD2	2.00	0.43
3:C:86:SER:OG	3:C:221:ASP:OD2	2.26	0.43
3:D:147:PHE:HB2	3:D:260:ILE:HG13	2.01	0.43
3:E:100:LEU:HD22	3:F:154:GLY:HA3	2.01	0.43
2:B:48:VAL:HG11	2:B:130:VAL:HG22	2.00	0.42
2:B:18:GLN:NE2	3:H:22:ASP:OD1	2.52	0.42
3:C:101:GLY:HA3	3:C:208:HIS:HE1	1.84	0.42
2:B:18:GLN:NE2	3:H:22:ASP:H	2.16	0.42
3:H:22:ASP:N	3:H:22:ASP:OD1	2.50	0.42
1:A:190:LEU:HD11	2:B:314:TYR:HD2	1.83	0.42
3:C:96:THR:HA	3:C:212:GLU:HA	2.01	0.42
3:E:229:GLN:HA	3:E:246:LEU:HA	2.01	0.42
3:F:8:THR:HB	3:F:313:LEU:HD11	2.01	0.42
3:H:140:HIS:NE2	3:H:187:LYS:O	2.53	0.42
3:C:228:SER:HB2	3:C:259:LYS:HD3	2.01	0.42
3:D:268:ASP:OD2	3:D:296:ARG:NH1	2.52	0.42
3:D:233:LEU:HD21	3:E:239:LYS:HD2	2.02	0.42
3:F:249:VAL:HG12	3:F:250:ARG:H	1.83	0.42
3:E:164:HIS:HE1	3:E:209:VAL:HG12	1.84	0.42
3:F:262:ASN:HB2	5:M:20:C:H5'	2.00	0.42
2:B:54:ILE:HA	2:B:115:GLY:HA3	2.01	0.42
3:E:266:THR:HA	3:E:281:ALA:HA	2.01	0.42
3:G:136:ARG:O	3:G:140:HIS:ND1	2.52	0.42
3:G:318:PRO:HD2	3:G:323:GLN:HE21	1.84	0.42
4:L:-1:MET:CB	4:L:184:VAL:N	2.82	0.42
2:B:211:ASP:HB3	2:B:250:PRO:HG3	2.01	0.42
3:C:101:GLY:HA3	3:C:208:HIS:CE1	2.54	0.42
3:F:231:LEU:HD11	3:F:233:LEU:HD23	2.01	0.42
3:F:120:GLN:HA	3:F:123:ALA:HB3	2.02	0.42
3:G:288:VAL:HB	3:G:291:GLN:HB2	2.01	0.42
2:B:255:TYR:HB3	2:B:280:VAL:HG21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:270:TRP:HB3	3:H:322:GLN:HG3	2.02	0.42
1:A:217:ALA:O	1:A:221:ALA:HB2	2.20	0.42
3:D:19:ASP:OD1	3:D:19:ASP:N	2.53	0.41
3:H:282:VAL:HG12	3:H:329:ASN:HB3	2.02	0.41
3:H:77:GLN:OE1	5:M:13:C:N4	2.53	0.41
1:A:190:LEU:HD13	2:B:280:VAL:HG21	2.02	0.41
2:B:132:GLU:OE2	3:H:208:HIS:NE2	2.50	0.41
3:E:265:ARG:NH2	5:M:26:G:OP2	2.53	0.41
3:C:149:TRP:CD1	3:C:259:LYS:HE2	2.55	0.41
3:H:161:ARG:HD2	3:H:175:ARG:HE	1.84	0.41
3:C:30:TRP:CD2	3:C:218:ARG:HD2	2.55	0.41
3:F:259:LYS:HE3	3:F:259:LYS:HB2	1.89	0.41
3:C:262:ASN:ND2	5:M:38:C:OP2	2.54	0.41
3:F:141:ASN:ND2	3:F:266:THR:O	2.41	0.41
3:G:134:LEU:HD11	3:G:328:ALA:HB2	2.03	0.41
2:B:19:ASN:H	2:B:104:HIS:CD2	2.39	0.41
1:A:190:LEU:HD22	2:B:280:VAL:HB	2.03	0.41
3:C:159:GLU:HB3	3:C:216:PHE:HD2	1.86	0.41
3:C:145:ALA:HB1	3:C:148:LEU:HD21	2.02	0.41
3:D:318:PRO:HG2	3:D:323:GLN:HG2	2.01	0.41
3:F:44:VAL:HG13	3:F:246:LEU:HD12	2.02	0.41
3:H:170:VAL:HG11	3:H:173:ALA:HB2	2.03	0.41
2:B:213:LEU:HD22	2:B:216:LEU:HD11	2.02	0.41
3:D:92:LYS:HG3	3:D:216:PHE:HE1	1.85	0.41
3:F:26:SER:HA	3:F:41:ALA:HA	2.03	0.41
2:B:23:ILE:HG13	2:B:24:SER:H	1.86	0.41
3:G:305:TYR:OH	3:H:54:SER:O	2.30	0.41
3:C:296:ARG:NH1	3:C:302:LEU:O	2.54	0.40
3:E:33:ARG:HA	3:E:36:SER:HB3	2.02	0.40
3:D:318:PRO:O	3:D:323:GLN:NE2	2.54	0.40
3:G:134:LEU:HD12	3:G:134:LEU:HA	1.94	0.40
1:A:264:LEU:HD21	2:B:23:ILE:HG22	2.03	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	422/436 (97%)	355 (84%)	66 (16%)	1 (0%)	51	85
2	B	301/329 (92%)	266 (88%)	35 (12%)	0	100	100
3	C	287/344 (83%)	255 (89%)	32 (11%)	0	100	100
3	D	331/344 (96%)	297 (90%)	34 (10%)	0	100	100
3	E	332/344 (96%)	292 (88%)	40 (12%)	0	100	100
3	F	333/344 (97%)	302 (91%)	31 (9%)	0	100	100
3	G	331/344 (96%)	295 (89%)	34 (10%)	2 (1%)	28	70
3	H	331/344 (96%)	297 (90%)	34 (10%)	0	100	100
4	L	187/189 (99%)	143 (76%)	44 (24%)	0	100	100
All	All	2855/3018 (95%)	2502 (88%)	350 (12%)	3 (0%)	58	88

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	G	320	VAL
3	G	250	ARG
1	A	34	PRO

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	78/366 (21%)	78 (100%)	0	100	100
2	B	245/271 (90%)	242 (99%)	3 (1%)	75	90
3	C	230/274 (84%)	230 (100%)	0	100	100
3	D	258/274 (94%)	256 (99%)	2 (1%)	85	94
3	E	259/274 (94%)	259 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F	259/274 (94%)	258 (100%)	1 (0%)	93	97
3	G	259/274 (94%)	257 (99%)	2 (1%)	85	94
3	H	258/274 (94%)	257 (100%)	1 (0%)	93	97
All	All	1846/2281 (81%)	1837 (100%)	9 (0%)	91	96

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	213	LEU
2	B	216	LEU
2	B	286	LEU
3	D	94	ARG
3	D	265	ARG
3	F	213	VAL
3	G	94	ARG
3	G	98	ARG
3	H	314	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	188	HIS
2	B	18	GLN
2	B	114	HIS
3	C	140	HIS
3	C	208	HIS
3	C	322	GLN
3	E	164	HIS
3	E	300	GLN
3	E	310	ASN
3	E	322	GLN
3	F	223	GLN
3	F	322	GLN
3	G	310	ASN
3	G	322	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	M	59/60 (98%)	38 (64%)	0

All (38) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	M	6	A
5	M	7	A
5	M	9	U
5	M	12	A
5	M	15	G
5	M	16	C
5	M	17	G
5	M	19	G
5	M	20	C
5	M	21	U
5	M	23	G
5	M	27	U
5	M	32	G
5	M	33	U
5	M	36	A
5	M	37	C
5	M	38	C
5	M	39	U
5	M	40	G
5	M	41	G
5	M	42	U
5	M	43	U
5	M	44	C
5	M	45	A
5	M	46	C
5	M	48	G
5	M	49	C
5	M	50	C
5	M	51	G
5	M	52	U
5	M	53	G
5	M	54	U
5	M	55	A
5	M	56	G
5	M	57	G
5	M	58	C
5	M	59	A
5	M	60	G

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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.