



Full wwPDB EM Validation Report ⓘ

Nov 9, 2025 – 12:16 AM JST

PDB ID : 9IJS / pdb_00009ijs
EMDB ID : EMD-60643
Title : Cryo-EM structure of the orphan GPR52 bound to beta-arrestin 1 in ligand-free state
Authors : Lin, X.; Xu, F.
Deposited on : 2024-06-25
Resolution : 3.64 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : **FAILED**
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.46

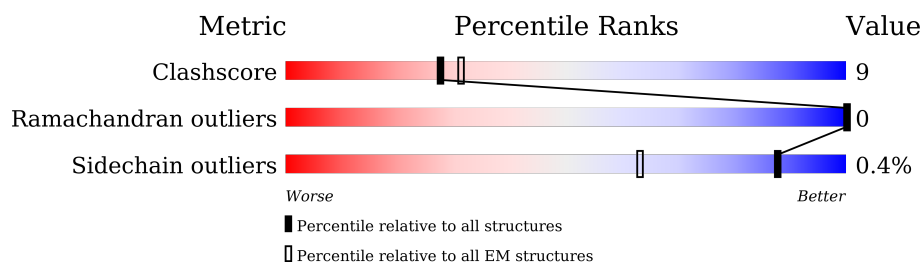
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.64 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	369	
2	C	402	
3	H	266	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6074 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 G-protein coupled receptor 52.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	280	Total	C	N	O	P	S	1	0
			2083	1357	324	383	6	13		

There are 31 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	130	TRP	ALA	conflict	UNP Q9Y2T5
A	314	PRO	CYS	conflict	UNP Q9Y2T5
A	474	ALA	-	expression tag	UNP Q9Y2T5
A	475	ARG	-	expression tag	UNP Q9Y2T5
A	476	GLY	-	expression tag	UNP Q9Y2T5
A	477	ARG	-	expression tag	UNP Q9Y2T5
A	478	PRO	-	expression tag	UNP Q9Y2T5
A	479	LEU	-	expression tag	UNP Q9Y2T5
A	480	PRO	-	expression tag	UNP Q9Y2T5
A	481	GLU	-	expression tag	UNP Q9Y2T5
A	482	THR	-	expression tag	UNP Q9Y2T5
A	483	GLY	-	expression tag	UNP Q9Y2T5
A	484	GLY	-	expression tag	UNP Q9Y2T5
A	485	GLY	-	expression tag	UNP Q9Y2T5
A	486	ASP	-	expression tag	UNP Q9Y2T5
A	487	GLU	-	expression tag	UNP Q9Y2T5
A	488	SEP	-	expression tag	UNP Q9Y2T5
A	489	ALA	-	expression tag	UNP Q9Y2T5
A	490	TPO	-	expression tag	UNP Q9Y2T5
A	491	TPO	-	expression tag	UNP Q9Y2T5
A	492	ALA	-	expression tag	UNP Q9Y2T5
A	493	SEP	-	expression tag	UNP Q9Y2T5
A	494	SEP	-	expression tag	UNP Q9Y2T5
A	495	SEP	-	expression tag	UNP Q9Y2T5
A	496	LEU	-	expression tag	UNP Q9Y2T5
A	497	ALA	-	expression tag	UNP Q9Y2T5
A	498	LYS	-	expression tag	UNP Q9Y2T5
A	499	ASP	-	expression tag	UNP Q9Y2T5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	500	THR	-	expression tag	UNP Q9Y2T5
A	501	SER	-	expression tag	UNP Q9Y2T5
A	502	SER	-	expression tag	UNP Q9Y2T5

- Molecule 2 is a protein called Beta-arrestin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	351	Total	C	N	O	S	0	0
			2446	1582	425	438	1		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-8	MET	-	initiating methionine	UNP P49407
C	-7	GLY	-	expression tag	UNP P49407
C	-6	SER	-	expression tag	UNP P49407
C	-5	PRO	-	expression tag	UNP P49407
C	-4	GLU	-	expression tag	UNP P49407
C	-3	PHE	-	expression tag	UNP P49407
C	-2	PRO	-	expression tag	UNP P49407
C	-1	GLY	-	expression tag	UNP P49407
C	0	ARG	-	expression tag	UNP P49407
C	1	LEU	-	expression tag	UNP P49407
C	59	VAL	CYS	conflict	UNP P49407
C	125	SER	CYS	conflict	UNP P49407
C	140	LEU	CYS	conflict	UNP P49407
C	150	VAL	CYS	conflict	UNP P49407
C	242	VAL	CYS	conflict	UNP P49407
C	251	VAL	CYS	conflict	UNP P49407
C	269	SER	CYS	conflict	UNP P49407
C	368	SER	ASN	conflict	UNP P49407

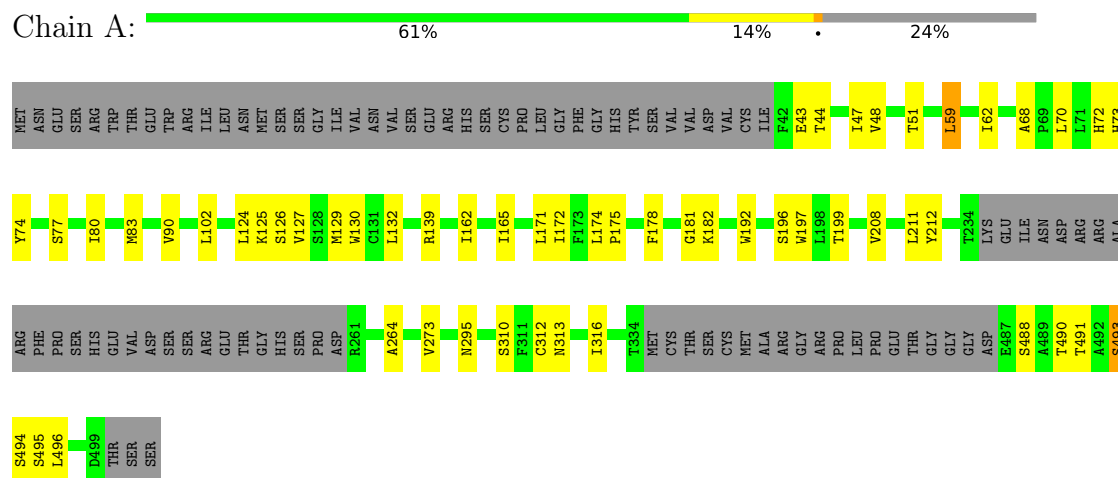
- Molecule 3 is a protein called scFv30 antibody.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	225	Total	C	N	O	S	0	0
			1545	981	260	300	4		

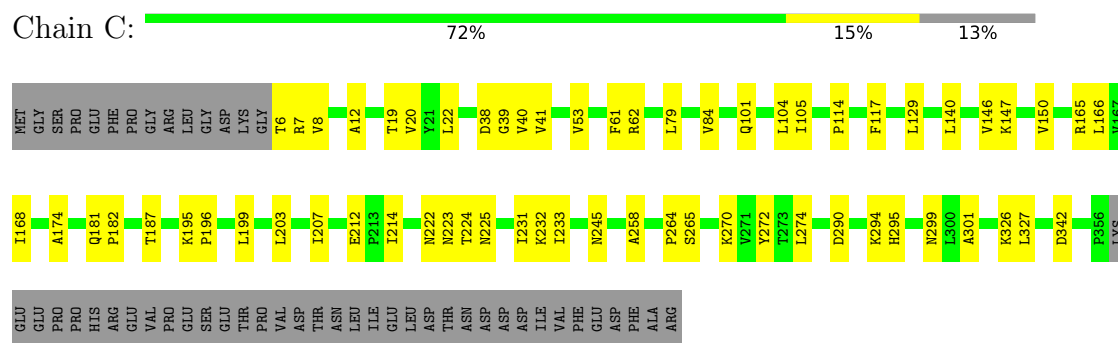
3 Residue-property plots

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

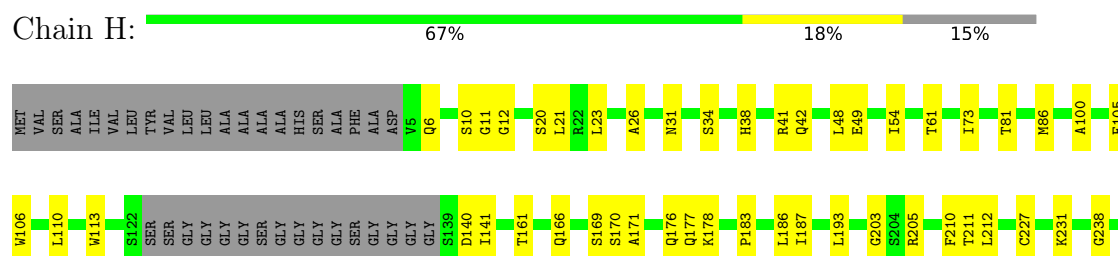
• Molecule 1: G-protein coupled receptor 52



• Molecule 2: Beta-arrestin-1



• Molecule 3: scFv30 antibody



I245
LYS
ALA
ALA
ALA

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	136991	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k 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: SEP, TPO

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.17	0/2076	0.42	0/2849
2	C	0.15	0/2496	0.35	0/3427
3	H	0.13	0/1580	0.33	0/2164
All	All	0.15	0/6152	0.37	0/8440

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	2083	0	1871	40	0
2	C	2446	0	2270	43	0
3	H	1545	0	1322	32	0
All	All	6074	0	5463	109	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 9.

All (109) 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:182:LYS:HB2	1:A:199:THR:HG22	1.77	0.67
1:A:44:THR:HG21	1:A:102:LEU:HD13	1.77	0.65
3:H:26:ALA:HB2	3:H:81:THR:HG23	1.80	0.64
3:H:177:GLN:HB2	3:H:183:PRO:HB3	1.79	0.64
3:H:11:GLY:HA3	3:H:23:LEU:HA	1.80	0.63
1:A:125:LYS:NZ	1:A:310:SER:OG	2.32	0.62
3:H:42:GLN:HB2	3:H:48:LEU:HD13	1.82	0.62
2:C:40:VAL:HG11	2:C:105:ILE:HG23	1.83	0.60
2:C:53:VAL:HA	2:C:150:VAL:HA	1.84	0.60
2:C:270:LYS:HG3	2:C:272:TYR:HE1	1.67	0.59
1:A:172:ILE:HG12	1:A:211:LEU:HD23	1.87	0.57
2:C:195:LYS:O	2:C:224:THR:OG1	2.21	0.57
1:A:175:PRO:HA	1:A:178:PHE:HB3	1.86	0.57
1:A:73:HIS:O	1:A:73:HIS:ND1	2.38	0.56
3:H:176:GLN:HB2	3:H:186:LEU:HD11	1.87	0.56
2:C:222:ASN:O	2:C:265:SER:N	2.40	0.55
2:C:233:ILE:HG13	2:C:272:TYR:HD2	1.72	0.55
3:H:6:GLN:N	3:H:6:GLN:OE1	2.40	0.55
2:C:233:ILE:HG13	2:C:272:TYR:CD2	2.42	0.55
1:A:496:LEU:O	2:C:6:THR:N	2.41	0.54
2:C:225:ASN:HA	2:C:264:PRO:HB3	1.88	0.54
1:A:139:ARG:HH12	1:A:264:ALA:HA	1.71	0.54
1:A:171:LEU:HA	1:A:174:LEU:HD23	1.90	0.54
2:C:40:VAL:HA	2:C:114:PRO:HA	1.90	0.54
1:A:493:SEP:O2P	3:H:205:ARG:NH2	2.40	0.54
1:A:192:TRP:HZ3	1:A:197:TRP:HE3	1.56	0.54
1:A:73:HIS:HB2	2:C:245:ASN:HB2	1.89	0.53
2:C:40:VAL:HG22	2:C:104:LEU:HD23	1.90	0.53
3:H:12:GLY:HA2	3:H:21:LEU:HD11	1.89	0.53
3:H:170:SER:HB3	3:H:205:ARG:HD2	1.90	0.53
2:C:212:GLU:HA	3:H:31:ASN:HD22	1.73	0.53
2:C:231:ILE:HB	2:C:258:ALA:HB3	1.91	0.53
2:C:146:VAL:HG13	2:C:166:LEU:HB3	1.91	0.52
3:H:169:SER:HB2	3:H:231:LYS:HE2	1.92	0.52
1:A:44:THR:O	1:A:48:VAL:HG22	2.10	0.51
1:A:74:TYR:HA	1:A:77:SER:HB3	1.91	0.51
3:H:31:ASN:N	3:H:31:ASN:OD1	2.44	0.51
2:C:22:LEU:HD21	2:C:168:ILE:HD11	1.91	0.51
2:C:182:PRO:HG2	2:C:203:LEU:HD12	1.92	0.51
2:C:20:VAL:HA	2:C:41:VAL:HG12	1.93	0.50
1:A:127:VAL:HG23	1:A:165:ILE:HG12	1.94	0.50
3:H:203:GLY:HA2	3:H:212:LEU:HA	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:10:SER:OG	3:H:11:GLY:N	2.44	0.49
3:H:110:LEU:O	3:H:113:TRP:NE1	2.43	0.49
1:A:182:LYS:HD2	1:A:197:TRP:CE2	2.48	0.49
3:H:20:SER:OG	3:H:86:MET:O	2.29	0.49
2:C:299:ASN:HB3	3:H:105:PHE:CE1	2.48	0.48
1:A:59:LEU:HA	1:A:62:ILE:HG22	1.96	0.48
1:A:174:LEU:HG	1:A:175:PRO:HD3	1.95	0.48
2:C:129:LEU:HB2	2:C:140:LEU:HB2	1.94	0.48
1:A:295:ASN:OD1	1:A:295:ASN:N	2.44	0.48
3:H:141:ILE:HD12	3:H:166:GLN:HB3	1.96	0.48
1:A:192:TRP:O	1:A:196:SER:OG	2.24	0.47
1:A:139:ARG:HH22	1:A:264:ALA:N	2.12	0.47
3:H:105:PHE:HB3	3:H:106:TRP:HD1	1.80	0.47
3:H:140:ASP:N	3:H:140:ASP:OD1	2.37	0.47
1:A:70:LEU:HB3	1:A:72:HIS:CE1	2.50	0.47
2:C:84:VAL:HG22	2:C:117:PHE:HE1	1.81	0.46
3:H:187:ILE:HA	3:H:193:LEU:HA	1.98	0.46
2:C:294:LYS:HG3	2:C:295:HIS:H	1.81	0.46
2:C:232:LYS:N	2:C:326:LYS:O	2.47	0.45
1:A:496:LEU:HD13	2:C:104:LEU:HD12	1.99	0.45
2:C:214:ILE:N	2:C:274:LEU:O	2.49	0.45
1:A:181:GLY:C	1:A:197:TRP:HE1	2.25	0.45
3:H:177:GLN:NE2	3:H:178:LYS:O	2.50	0.45
2:C:182:PRO:HD2	2:C:203:LEU:HB2	2.00	0.44
2:C:6:THR:OG1	2:C:7:ARG:N	2.47	0.44
3:H:38:HIS:O	3:H:100:ALA:N	2.47	0.44
2:C:174:ALA:HB1	2:C:207:ILE:HD13	2.00	0.44
2:C:199:LEU:HD22	2:C:327:LEU:HD22	1.99	0.44
1:A:208:VAL:HG22	1:A:212:TYR:HD2	1.83	0.44
1:A:132:LEU:HD12	1:A:132:LEU:HA	1.87	0.44
3:H:170:SER:HA	3:H:210:PHE:CZ	2.53	0.44
2:C:38:ASP:OD1	2:C:39:GLY:N	2.51	0.43
1:A:312:CYS:SG	1:A:313:ASN:N	2.91	0.43
1:A:130:TRP:HB3	1:A:165:ILE:HD11	2.00	0.43
2:C:101:GLN:O	2:C:105:ILE:HG13	2.17	0.43
2:C:223:ASN:OD1	2:C:224:THR:N	2.52	0.43
1:A:47:ILE:O	1:A:51:THR:HG23	2.18	0.43
1:A:83:MET:HE3	1:A:83:MET:HB2	1.80	0.43
3:H:54:ILE:HG13	3:H:73:ILE:HG21	1.99	0.43
1:A:162:ILE:HA	1:A:165:ILE:HG22	2.00	0.43
3:H:227:CYS:O	3:H:238:GLY:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:8:VAL:HG21	2:C:104:LEU:HD11	2.01	0.42
3:H:34:SER:O	3:H:34:SER:OG	2.33	0.42
1:A:43:GLU:O	1:A:47:ILE:HG23	2.19	0.42
2:C:12:ALA:HA	2:C:19:THR:HG22	2.01	0.42
2:C:62:ARG:HB3	2:C:140:LEU:HA	2.01	0.42
2:C:290:ASP:HB2	2:C:301:ALA:HA	2.02	0.42
1:A:68:ALA:O	1:A:70:LEU:N	2.50	0.42
2:C:181:GLN:HA	2:C:182:PRO:HD3	1.93	0.42
2:C:342:ASP:OD1	2:C:342:ASP:N	2.53	0.42
1:A:124:LEU:HA	1:A:127:VAL:HG12	2.01	0.42
1:A:162:ILE:HA	1:A:162:ILE:HD13	1.85	0.42
1:A:208:VAL:HA	1:A:212:TYR:HB2	2.01	0.41
3:H:41:ARG:N	3:H:49:GLU:O	2.36	0.41
1:A:44:THR:HA	1:A:47:ILE:HG12	2.02	0.41
1:A:273:VAL:HG21	1:A:316:ILE:HG21	2.02	0.41
2:C:146:VAL:O	2:C:166:LEU:N	2.51	0.41
3:H:161:THR:HG22	3:H:211:THR:HB	2.03	0.41
3:H:110:LEU:H	3:H:110:LEU:HD12	1.85	0.41
2:C:61:PHE:HD2	2:C:79:LEU:HD11	1.86	0.41
2:C:147:LYS:HA	2:C:165:ARG:HA	2.03	0.41
1:A:80:ILE:HD13	1:A:80:ILE:HA	1.93	0.41
2:C:187:THR:OG1	2:C:196:PRO:HB2	2.21	0.41
2:C:270:LYS:HG3	2:C:272:TYR:CE1	2.52	0.40
1:A:126:SER:HA	1:A:129:MET:HE2	2.02	0.40
3:H:61:THR:O	3:H:61:THR:OG1	2.37	0.40
3:H:171:ALA:HB3	3:H:231:LYS:HB2	2.03	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	268/369 (73%)	258 (96%)	10 (4%)	0	100	100
2	C	349/402 (87%)	325 (93%)	24 (7%)	0	100	100
3	H	221/266 (83%)	208 (94%)	13 (6%)	0	100	100
All	All	838/1037 (81%)	791 (94%)	47 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	195/327 (60%)	193 (99%)	2 (1%)	73	83
2	C	219/357 (61%)	219 (100%)	0	100	100
3	H	135/207 (65%)	135 (100%)	0	100	100
All	All	549/891 (62%)	547 (100%)	2 (0%)	88	94

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	LEU
1	A	90	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 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	SEP	A	494	1	8,9,10	1.55	1 (12%)	8,12,14	1.59	2 (25%)
1	TPO	A	491	1	8,10,11	1.06	0	10,14,16	1.95	2 (20%)
1	SEP	A	488	1	8,9,10	1.54	1 (12%)	8,12,14	1.78	2 (25%)
1	SEP	A	493	1	8,9,10	1.52	1 (12%)	8,12,14	1.49	2 (25%)
1	TPO	A	490	1	8,10,11	1.18	0	10,14,16	1.10	1 (10%)
1	SEP	A	495	1	8,9,10	1.54	1 (12%)	8,12,14	1.56	2 (25%)

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	SEP	A	494	1	-	2/5/8/10	-
1	TPO	A	491	1	-	1/9/11/13	-
1	SEP	A	488	1	-	3/5/8/10	-
1	SEP	A	493	1	-	3/5/8/10	-
1	TPO	A	490	1	-	6/9/11/13	-
1	SEP	A	495	1	-	3/5/8/10	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	488	SEP	P-O1P	3.36	1.61	1.50
1	A	495	SEP	P-O1P	3.36	1.61	1.50
1	A	494	SEP	P-O1P	3.36	1.61	1.50
1	A	493	SEP	P-O1P	3.30	1.61	1.50

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	491	TPO	P-OG1-CB	-5.33	107.10	123.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	488	SEP	OG-CB-CA	3.32	111.38	108.14
1	A	488	SEP	P-OG-CB	-3.30	109.21	118.30
1	A	494	SEP	P-OG-CB	-3.03	109.96	118.30
1	A	495	SEP	P-OG-CB	-3.02	109.98	118.30
1	A	493	SEP	P-OG-CB	-2.87	110.38	118.30
1	A	494	SEP	OG-CB-CA	2.68	110.75	108.14
1	A	495	SEP	OG-CB-CA	2.60	110.68	108.14
1	A	493	SEP	OG-CB-CA	2.41	110.49	108.14
1	A	491	TPO	CG2-CB-CA	-2.31	108.60	113.16
1	A	490	TPO	P-OG1-CB	-2.11	116.83	123.21

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	488	SEP	CB-OG-P-O1P
1	A	488	SEP	CB-OG-P-O2P
1	A	488	SEP	CB-OG-P-O3P
1	A	490	TPO	N-CA-CB-OG1
1	A	490	TPO	C-CA-CB-CG2
1	A	490	TPO	O-C-CA-CB
1	A	490	TPO	CG2-CB-OG1-P
1	A	491	TPO	CB-OG1-P-O3P
1	A	493	SEP	CB-OG-P-O1P
1	A	493	SEP	CB-OG-P-O2P
1	A	493	SEP	CB-OG-P-O3P
1	A	494	SEP	N-CA-CB-OG
1	A	495	SEP	CB-OG-P-O2P
1	A	495	SEP	CB-OG-P-O3P
1	A	495	SEP	CB-OG-P-O1P
1	A	490	TPO	N-CA-CB-CG2
1	A	490	TPO	CB-OG1-P-O3P
1	A	494	SEP	CA-CB-OG-P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	493	SEP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.