



## Full wwPDB EM Validation Report ⓘ

Sep 2, 2025 – 01:28 AM JST

PDB ID : 9LVB / pdb\_00009lvb  
EMDB ID : EMD-63418  
Title : IAA-free AUX1  
Authors : Jing, D.; Kong, F.; Wang, C.C.; Shi, Y.G.; Huang, G.X.Y.  
Deposited on : 2025-02-12  
Resolution : 3.97 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](mailto: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>.

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

EMDB validation analysis : **FAILED**  
MolProbity : 4-5-2 with Phenix2.0rc1  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.45.1

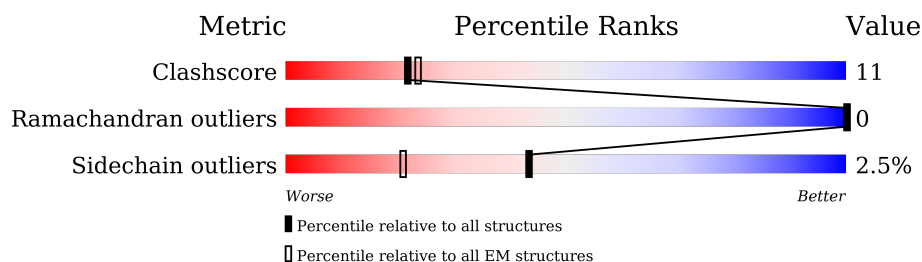
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.97 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  $\geq 3$ , 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	616	
2	H	257	
3	L	235	
4	N	173	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8192 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 Auxin transporter protein 1, Soluble cytochrome b562.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	505	Total	C	N	O	S	0	0
			3987	2634	641	694	18		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-24	MET	-	initiating methionine	UNP Q96247
A	-23	HIS	-	expression tag	UNP Q96247
A	-22	HIS	-	expression tag	UNP Q96247
A	-21	HIS	-	expression tag	UNP Q96247
A	-20	HIS	-	expression tag	UNP Q96247
A	-19	HIS	-	expression tag	UNP Q96247
A	-18	HIS	-	expression tag	UNP Q96247
A	-17	HIS	-	expression tag	UNP Q96247
A	-16	HIS	-	expression tag	UNP Q96247
A	-15	HIS	-	expression tag	UNP Q96247
A	-14	HIS	-	expression tag	UNP Q96247
A	-13	GLY	-	expression tag	UNP Q96247
A	-12	SER	-	expression tag	UNP Q96247
A	-11	VAL	-	expression tag	UNP Q96247
A	-10	GLU	-	expression tag	UNP Q96247
A	-9	ASP	-	expression tag	UNP Q96247
A	-8	TYR	-	expression tag	UNP Q96247
A	-7	LYS	-	expression tag	UNP Q96247
A	-6	ASP	-	expression tag	UNP Q96247
A	-5	ASP	-	expression tag	UNP Q96247
A	-4	ASP	-	expression tag	UNP Q96247
A	-3	ASP	-	expression tag	UNP Q96247
A	-2	LYS	-	expression tag	UNP Q96247
A	-1	GLY	-	expression tag	UNP Q96247
A	0	SER	-	expression tag	UNP Q96247
A	123	TRP	MET	conflict	UNP P0ABE7
A	218	ILE	HIS	conflict	UNP P0ABE7
A	222	LEU	-	linker	UNP P0ABE7

- Molecule 2 is a protein called heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	225	Total	C	N	O	S	0	0
			1686	1072	280	329	5		

- Molecule 3 is a protein called light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	212	Total	C	N	O	S	0	0
			1632	1025	272	330	5		

- Molecule 4 is a protein called Nanobody.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	118	Total	C	N	O	S	0	0
			887	551	152	180	4		





● Molecule 4: Nanobody



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	175799	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	0.19	0/4103	0.36	0/5590
2	H	0.14	0/1734	0.32	0/2369
3	L	0.11	0/1667	0.27	0/2264
4	N	0.17	0/905	0.44	0/1226
All	All	0.17	0/8409	0.35	0/11449

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	3987	0	3966	107	0
2	H	1686	0	1630	31	0
3	L	1632	0	1595	27	0
4	N	887	0	819	25	0
All	All	8192	0	8010	185	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 11.

All (185) 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)
2:H:105:TRP:CE2	2:H:106:PRO:HB3	2.10	0.85
1:A:63:VAL:HG11	1:A:351:THR:OG1	1.79	0.82
1:A:53:PHE:CZ	1:A:307:LEU:HD12	2.18	0.79
1:A:53:PHE:HZ	1:A:307:LEU:CD1	1.98	0.77
2:H:102:TRP:HZ3	3:L:95:TYR:HA	1.47	0.76
3:L:78:SER:OG	3:L:80:GLN:OE1	2.06	0.74
1:A:253:LEU:HD12	1:A:254:PHE:N	2.03	0.72
1:A:62:GLN:NE2	1:A:259:GLN:OE1	2.21	0.72
1:A:53:PHE:HZ	1:A:307:LEU:HD12	1.51	0.72
1:A:126:LEU:HD22	1:A:149:MET:HB2	1.71	0.71
1:A:157:GLN:NE2	1:A:182:ASP:OD1	2.24	0.70
4:N:86:LEU:HD11	4:N:117:VAL:HG13	1.75	0.68
1:A:55:CYS:HB2	1:A:358:THR:HG22	1.76	0.68
1:A:406:ASN:HD21	1:A:409:SER:HB3	1.60	0.66
1:A:276:LYS:O	1:A:280:THR:OG1	2.13	0.65
4:N:38:ARG:O	4:N:46:GLU:N	2.28	0.65
1:A:570:CYS:SG	1:A:571:TYR:N	2.70	0.65
1:A:339:VAL:HG22	1:A:552:ALA:HB2	1.78	0.64
4:N:13:GLN:HB3	4:N:14:PRO:HD2	1.80	0.63
3:L:145:GLU:OE1	3:L:145:GLU:N	2.26	0.62
1:A:219:GLN:OE1	1:A:219:GLN:N	2.32	0.62
1:A:408:PHE:HA	1:A:411:MET:HG2	1.80	0.62
3:L:7:GLN:OE1	3:L:103:GLY:N	2.33	0.61
1:A:130:LEU:HD23	1:A:149:MET:HE1	1.82	0.61
1:A:508:ARG:O	1:A:513:ARG:NH2	2.34	0.61
1:A:154:LEU:O	1:A:158:LYS:NZ	2.31	0.60
1:A:53:PHE:CZ	1:A:307:LEU:CD1	2.80	0.60
1:A:403:ASP:OD1	1:A:404:HIS:ND1	2.35	0.59
1:A:503:HIS:NE2	1:A:530:MET:SD	2.75	0.59
3:L:30:VAL:HG23	3:L:93:LEU:HD13	1.85	0.59
1:A:74:LEU:HD23	1:A:79:GLY:HA2	1.84	0.59
1:A:132:VAL:O	1:A:136:ALA:N	2.35	0.59
4:N:91:THR:HA	4:N:117:VAL:O	2.03	0.59
2:H:184:LEU:O	3:L:162:GLN:NE2	2.36	0.58
4:N:71:SER:O	4:N:80:TYR:N	2.34	0.58
4:N:91:THR:HG23	4:N:118:THR:HB	1.85	0.57
1:A:125:THR:O	1:A:129:ASN:ND2	2.36	0.57
3:L:152:VAL:HG13	3:L:194:TYR:HE1	1.70	0.57
1:A:218:ILE:HG22	1:A:222:LEU:HD22	1.87	0.56
1:A:185:VAL:HG11	2:H:105:TRP:CZ2	2.39	0.56
4:N:81:LEU:HD23	4:N:82:GLN:N	2.21	0.56
1:A:83:GLN:HB2	1:A:348:ILE:HD11	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:PHE:CD2	1:A:486:VAL:HG22	2.40	0.56
2:H:76:ASP:OD2	2:H:83:TYR:OH	2.22	0.56
2:H:210:CYS:N	2:H:223:LYS:O	2.36	0.56
3:L:187:ASP:OD1	3:L:188:TYR:N	2.40	0.55
2:H:108:GLU:O	2:H:109:PRO:C	2.49	0.55
1:A:488:ALA:O	1:A:492:SER:OG	2.22	0.55
3:L:25:ARG:NE	3:L:71:ASP:OD1	2.40	0.55
4:N:101:ASP:OD1	4:N:101:ASP:C	2.50	0.55
1:A:63:VAL:HG21	1:A:351:THR:OG1	2.07	0.54
4:N:19:ARG:NH1	4:N:81:LEU:O	2.41	0.54
1:A:406:ASN:ND2	1:A:409:SER:HB3	2.23	0.53
1:A:254:PHE:HD2	1:A:486:VAL:HG22	1.74	0.53
4:N:94:TYR:CE1	4:N:117:VAL:HB	2.44	0.53
2:H:192:LEU:HD23	2:H:193:SER:N	2.23	0.52
2:H:121:THR:OG1	2:H:122:LEU:N	2.42	0.52
1:A:233:ASP:OD1	1:A:233:ASP:C	2.53	0.52
2:H:41:ARG:NH1	2:H:93:ASP:OD1	2.40	0.52
3:L:55:LEU:HD11	3:L:59:VAL:HG23	1.92	0.52
1:A:339:VAL:CG2	1:A:552:ALA:HB2	2.40	0.52
2:H:54:ILE:HD11	2:H:75:ALA:HB2	1.91	0.51
2:H:65:ASP:OD1	2:H:65:ASP:C	2.53	0.51
1:A:279:TRP:HA	1:A:282:ILE:HG22	1.91	0.51
3:L:171:LYS:HA	3:L:171:LYS:HE2	1.92	0.51
1:A:51:ALA:HB1	1:A:358:THR:HB	1.91	0.51
4:N:109:ASP:N	4:N:109:ASP:OD1	2.43	0.51
1:A:104:TYR:CG	1:A:231:VAL:HG13	2.45	0.51
4:N:100:SER:OG	4:N:109:ASP:OD1	2.23	0.51
1:A:487:GLY:HA2	1:A:491:VAL:HG12	1.92	0.51
4:N:6:GLU:OE1	4:N:6:GLU:N	2.44	0.51
1:A:358:THR:OG1	1:A:359:VAL:N	2.44	0.50
4:N:23:ALA:CA	4:N:78:THR:HG23	2.42	0.50
1:A:342:PHE:CE2	1:A:548:PHE:HB3	2.47	0.49
1:A:118:ASP:OD1	1:A:119:LEU:HD12	2.13	0.49
4:N:47:PHE:HZ	4:N:50:VAL:HG13	1.77	0.49
1:A:202:GLU:N	1:A:202:GLU:OE1	2.45	0.49
1:A:210:LEU:HD12	1:A:210:LEU:C	2.38	0.49
1:A:209:GLN:OE1	1:A:213:THR:OG1	2.31	0.49
3:L:117:VAL:HG21	3:L:198:VAL:HG11	1.95	0.49
1:A:52:TRP:HA	1:A:358:THR:HG21	1.94	0.48
2:H:104:TYR:C	2:H:110:TRP:HB2	2.39	0.48
4:N:83:MET:CE	4:N:86:LEU:HD12	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:23:ALA:HA	4:N:78:THR:HG23	1.95	0.48
1:A:119:LEU:HD12	1:A:119:LEU:H	1.76	0.48
2:H:96:VAL:HG13	2:H:121:THR:O	2.13	0.48
4:N:101:ASP:OD1	4:N:104:TYR:N	2.41	0.48
1:A:53:PHE:HZ	1:A:307:LEU:HD13	1.78	0.48
1:A:104:TYR:CD2	1:A:231:VAL:HG22	2.49	0.48
2:H:108:GLU:HA	2:H:111:TRP:HB2	1.95	0.48
1:A:342:PHE:CD2	1:A:548:PHE:HB3	2.48	0.47
1:A:59:GLN:NE2	1:A:350:TYR:O	2.47	0.47
2:H:108:GLU:N	2:H:109:PRO:HD2	2.28	0.47
1:A:258:ILE:HD11	1:A:482:ILE:HG13	1.95	0.47
1:A:50:ASP:OD1	1:A:51:ALA:N	2.45	0.47
1:A:155:ASP:OD1	3:L:31:SER:HB2	2.14	0.47
2:H:105:TRP:HE3	2:H:110:TRP:CD2	2.33	0.47
4:N:83:MET:HE1	4:N:86:LEU:HD12	1.97	0.47
1:A:291:VAL:HG11	1:A:463:LEU:HD23	1.96	0.47
2:H:9:GLU:OE1	2:H:120:GLY:N	2.40	0.47
1:A:104:TYR:CB	1:A:231:VAL:HG13	2.45	0.46
1:A:127:ASN:OD1	1:A:214:ARG:NH2	2.48	0.46
3:L:34:VAL:HG22	3:L:52:ALA:HB2	1.98	0.46
4:N:47:PHE:CZ	4:N:50:VAL:HG13	2.50	0.46
2:H:14:LEU:C	2:H:14:LEU:HD12	2.40	0.46
3:L:91:GLN:OE1	3:L:92:TYR:N	2.49	0.46
1:A:55:CYS:CB	1:A:358:THR:HG22	2.43	0.46
3:L:177:LEU:C	3:L:177:LEU:HD23	2.40	0.46
1:A:317:LEU:HD12	1:A:393:VAL:HG21	1.97	0.46
1:A:84:ILE:HA	1:A:383:PHE:CE1	2.51	0.46
1:A:307:LEU:HD23	1:A:308:GLY:N	2.31	0.46
1:A:310:THR:HA	1:A:313:THR:HG22	1.97	0.46
1:A:353:GLY:O	1:A:495:VAL:HG21	2.15	0.46
2:H:76:ASP:OD1	2:H:77:THR:N	2.49	0.46
1:A:53:PHE:CE1	1:A:307:LEU:HD12	2.50	0.46
1:A:145:ALA:O	1:A:148:LYS:N	2.49	0.45
1:A:354:GLY:O	1:A:358:THR:HG23	2.17	0.45
1:A:71:PHE:CE2	1:A:76:MET:HE1	2.51	0.45
1:A:338:LEU:HD13	1:A:338:LEU:HA	1.86	0.45
4:N:39:GLN:O	4:N:93:VAL:HG12	2.16	0.45
1:A:293:ILE:HD11	1:A:437:THR:HG22	1.98	0.45
1:A:73:GLN:NE2	1:A:340:LEU:HD13	2.32	0.45
1:A:309:MET:HE1	1:A:426:ILE:CG1	2.47	0.45
2:H:37:LEU:HD12	2:H:82:ALA:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:169:ASN:O	2:H:170:SER:OG	2.33	0.45
1:A:351:THR:HG22	1:A:352:PHE:CD2	2.52	0.44
1:A:467:ILE:N	1:A:468:PRO:HD2	2.32	0.44
1:A:115:PHE:O	1:A:116:LYS:HB2	2.16	0.44
2:H:102:TRP:CZ2	2:H:110:TRP:NE1	2.86	0.44
3:L:118:PHE:O	3:L:137:LEU:N	2.42	0.44
4:N:87:LYS:HB2	4:N:88:PRO:HD2	1.99	0.44
3:L:3:ILE:HD11	3:L:91:GLN:NE2	2.33	0.44
1:A:235:LEU:HD12	1:A:506:THR:HG21	2.00	0.44
1:A:314:ALA:HB3	1:A:385:LEU:CD1	2.47	0.44
1:A:442:VAL:O	1:A:446:VAL:N	2.50	0.44
2:H:5:VAL:HG11	2:H:30:PHE:HB3	2.00	0.44
1:A:122:ASN:O	1:A:126:LEU:HG	2.17	0.44
1:A:558:VAL:HA	1:A:561:VAL:HG12	1.99	0.43
2:H:4:GLU:OE1	2:H:4:GLU:N	2.51	0.43
3:L:172:ASP:OD1	3:L:174:THR:HG22	2.17	0.43
1:A:120:GLU:N	1:A:120:GLU:OE1	2.51	0.43
1:A:121:ASP:O	1:A:125:THR:OG1	2.32	0.43
2:H:105:TRP:CD2	2:H:106:PRO:HB3	2.51	0.43
2:H:54:ILE:CG2	2:H:73:ILE:HD11	2.49	0.43
1:A:522:PHE:CG	1:A:522:PHE:O	2.72	0.43
1:A:274:LEU:HD23	1:A:274:LEU:HA	1.94	0.42
1:A:343:THR:HG21	1:A:556:ASN:HD22	1.84	0.42
1:A:309:MET:HE2	1:A:423:LEU:HB3	2.00	0.42
3:L:90:GLN:NE2	3:L:91:GLN:O	2.47	0.42
3:L:204:SER:OG	3:L:205:SER:N	2.51	0.42
3:L:182:THR:O	3:L:183:LEU:HD22	2.19	0.42
2:H:25:CYS:C	2:H:81:THR:HG23	2.45	0.42
1:A:475:ILE:HG22	1:A:476:PHE:CE1	2.54	0.42
2:H:104:TYR:O	2:H:110:TRP:HB2	2.18	0.42
1:A:104:TYR:CE2	1:A:231:VAL:HG22	2.54	0.42
1:A:427:HIS:ND1	1:A:427:HIS:C	2.77	0.42
1:A:117:ALA:O	1:A:121:ASP:OD1	2.38	0.42
1:A:332:HIS:O	1:A:332:HIS:CG	2.73	0.42
1:A:211:LYS:O	1:A:214:ARG:HG3	2.19	0.42
1:A:555:THR:O	1:A:558:VAL:HG12	2.20	0.42
3:L:4:GLN:OE1	3:L:4:GLN:N	2.52	0.42
2:H:103:GLY:O	2:H:110:TRP:HA	2.19	0.42
1:A:52:TRP:C	1:A:52:TRP:CD1	2.98	0.41
1:A:98:SER:O	1:A:102:VAL:HG23	2.21	0.41
4:N:39:GLN:HB3	4:N:93:VAL:HG13	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:351:THR:HG22	1:A:352:PHE:N	2.34	0.41
1:A:421:VAL:O	1:A:425:LEU:HD13	2.20	0.41
4:N:99:ASP:OD1	4:N:100:SER:N	2.53	0.41
2:H:162:GLU:N	2:H:163:PRO:HD2	2.36	0.41
1:A:117:ALA:O	1:A:120:GLU:N	2.53	0.41
3:L:119:ILE:HG22	3:L:136:CYS:HB2	2.03	0.41
1:A:288:ALA:HB2	1:A:466:VAL:HG11	2.02	0.41
1:A:493:PHE:HA	1:A:497:ILE:HG22	2.02	0.41
1:A:103:GLU:OE2	1:A:107:ARG:HD3	2.21	0.40
1:A:104:TYR:CE1	1:A:231:VAL:HA	2.57	0.40
1:A:218:ILE:HA	1:A:221:TYR:HB3	2.02	0.40
3:L:29:SER:O	3:L:29:SER:OG	2.33	0.40
1:A:309:MET:SD	1:A:427:HIS:HB2	2.60	0.40
1:A:123:TRP:CE3	1:A:126:LEU:HD12	2.56	0.40
1:A:154:LEU:HB3	3:L:31:SER:HB3	2.04	0.40
1:A:357:VAL:O	1:A:357:VAL:HG22	2.20	0.40
1:A:471:PHE:CZ	1:A:475:ILE:HD11	2.55	0.40
3:L:25:ARG:HG2	3:L:71:ASP:OD1	2.20	0.40
1:A:72:SER:HG	1:A:394:TYR:HD1	1.68	0.40
4:N:81:LEU:HD23	4:N:81:LEU:C	2.46	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	499/616 (81%)	478 (96%)	21 (4%)	0	100	100
2	H	223/257 (87%)	204 (92%)	19 (8%)	0	100	100
3	L	210/235 (89%)	199 (95%)	11 (5%)	0	100	100
4	N	116/173 (67%)	106 (91%)	10 (9%)	0	100	100
All	All	1048/1281 (82%)	987 (94%)	61 (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	413/506 (82%)	400 (97%)	13 (3%)	35	56
2	H	186/215 (86%)	184 (99%)	2 (1%)	70	80
3	L	188/206 (91%)	185 (98%)	3 (2%)	58	74
4	N	90/142 (63%)	86 (96%)	4 (4%)	24	47
All	All	877/1069 (82%)	855 (98%)	22 (2%)	43	62

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	99	VAL
1	A	170	ASP
1	A	222	LEU
1	A	243	LEU
1	A	245	LEU
1	A	273	HIS
1	A	277	ARG
1	A	293	ILE
1	A	307	LEU
1	A	339	VAL
1	A	411	MET
1	A	551	TRP
1	A	573	CYS
2	H	58	SER
2	H	121	THR
3	L	73	THR
3	L	129	SER
3	L	156	LEU
4	N	29	ILE
4	N	35	SER
4	N	69	THR
4	N	93	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	GLN
1	A	196	ASN
1	A	266	ASN
1	A	271	ASN
1	A	326	GLN
1	A	406	ASN
1	A	556	ASN
2	H	42	GLN
2	H	87	ASN
3	L	39	GLN
3	L	201	GLN
4	N	116	GLN

### 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 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.