



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:27 PM UTC

PDB ID : 6XT5 / pdb_00006xt5
Title : Jack bean asparaginyl endopeptidase
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Deposited on : 2020-07-17
Resolution : 2.69 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

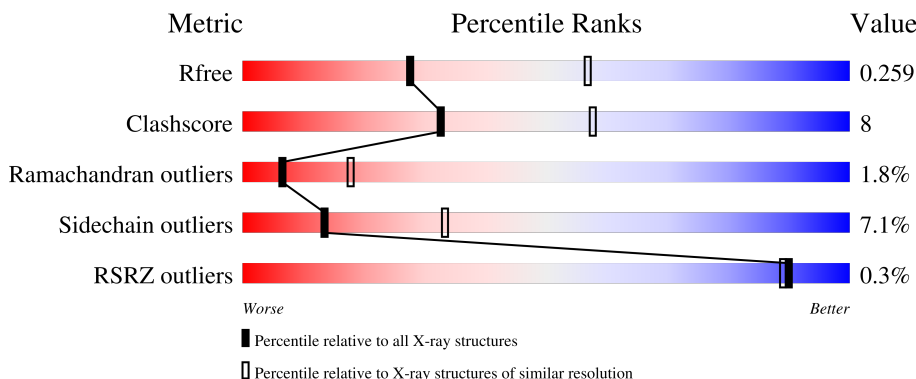
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.69 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	451	
1	B	451	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6794 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Legumain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	432	Total	C	N	O	S	0	1	0
			3369	2126	574	643	26			
1	B	435	Total	C	N	O	S	0	1	0
			3393	2142	578	647	26			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	25	ARG	-	expression tag	UNP P49046
A	26	GLY	-	expression tag	UNP P49046
A	27	SER	-	expression tag	UNP P49046
A	28	HIS	-	expression tag	UNP P49046
A	29	HIS	-	expression tag	UNP P49046
A	30	HIS	-	expression tag	UNP P49046
A	31	HIS	-	expression tag	UNP P49046
A	32	HIS	-	expression tag	UNP P49046
A	33	HIS	-	expression tag	UNP P49046
A	34	GLY	-	expression tag	UNP P49046
A	35	SER	-	expression tag	UNP P49046
A	157	SNN	ASP	conflict	UNP P49046
B	25	ARG	-	expression tag	UNP P49046
B	26	GLY	-	expression tag	UNP P49046
B	27	SER	-	expression tag	UNP P49046
B	28	HIS	-	expression tag	UNP P49046
B	29	HIS	-	expression tag	UNP P49046
B	30	HIS	-	expression tag	UNP P49046
B	31	HIS	-	expression tag	UNP P49046
B	32	HIS	-	expression tag	UNP P49046
B	33	HIS	-	expression tag	UNP P49046
B	34	GLY	-	expression tag	UNP P49046
B	35	SER	-	expression tag	UNP P49046
B	157	SNN	ASP	conflict	UNP P49046

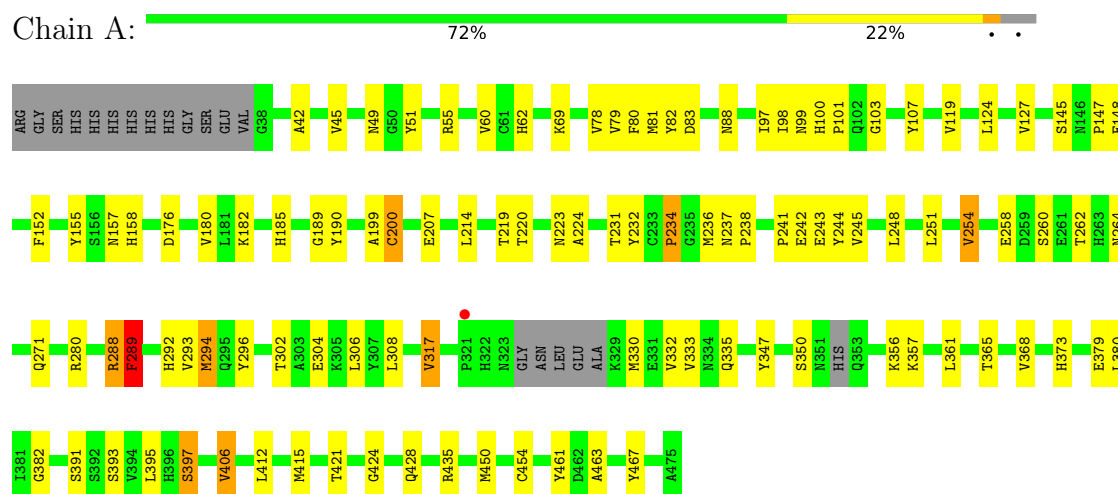
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	15	Total 15	O 15	0	0
2	B	17	Total 17	O 17	0	0

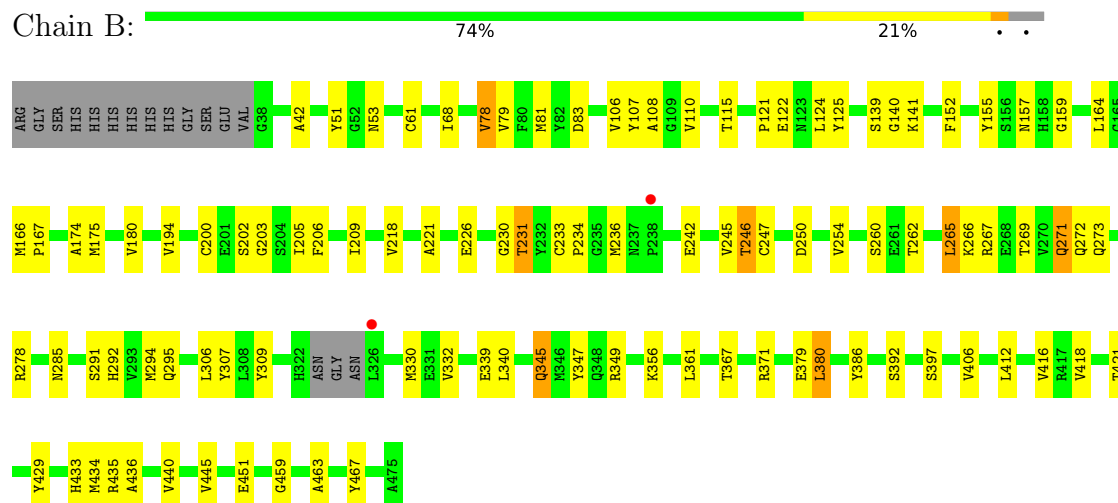
3 Residue-property plots

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: Legumain



• Molecule 1: Legumain



4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	106.99Å 88.88Å 109.85Å 90.00° 111.72° 90.00°	Depositor
Resolution (Å)	45.61 – 2.69 45.61 – 2.69	Depositor EDS
% Data completeness (in resolution range)	98.7 (45.61-2.69) 98.7 (45.61-2.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0258, PHENIX 1.16-3549-000	Depositor
R, R_{free}	0.196 , 0.268 (Not available) , 0.259	Depositor DCC
R_{free} test set	1323 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	71.8	Xtriage
Anisotropy	0.288	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 39.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.017 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6794	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.06% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	1.00	0/3444	1.45	1/4665 (0.0%)
1	B	1.02	0/3470	1.46	4/4702 (0.1%)
All	All	1.01	0/6914	1.45	5/9367 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	236	MET	CA-C-N	5.56	127.91	120.58
1	B	236	MET	C-N-CA	5.56	127.91	120.58
1	B	53	ASN	CA-C-N	5.51	127.98	120.54
1	B	53	ASN	C-N-CA	5.51	127.98	120.54
1	A	424	GLY	CA-C-O	-5.34	118.60	122.45

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	3369	0	3228	58	0
1	B	3393	0	3252	48	0
2	A	15	0	0	0	0
2	B	17	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6794	0	6480	105	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (105) 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:231:THR:HG22	1:A:332:VAL:HG12	1.48	0.94
1:B:271:GLN:HE21	1:B:271:GLN:HA	1.35	0.92
1:A:62:HIS:CD2	1:A:99:ASN:HD22	1.91	0.87
1:B:416:VAL:HG21	1:B:434:MET:HE1	1.65	0.79
1:A:62:HIS:HD2	1:A:99:ASN:HD22	1.29	0.77
1:B:51:TYR:O	1:B:246:THR:HG21	1.90	0.71
1:A:231:THR:HG21	1:A:251:LEU:HD13	1.74	0.69
1:A:98:ILE:HD11	1:A:244:TYR:CE2	2.28	0.68
1:B:271:GLN:HA	1:B:271:GLN:NE2	2.10	0.67
1:B:463:ALA:HB3	1:B:467:TYR:CE2	2.31	0.65
1:A:382:GLY:HA3	1:A:395:LEU:HD11	1.76	0.65
1:A:55:ARG:NH2	1:A:335:GLN:OE1	2.30	0.64
1:B:271:GLN:HE22	1:B:295:GLN:HE22	1.46	0.63
1:A:62:HIS:HD2	1:A:99:ASN:ND2	1.99	0.60
1:A:393:SER:O	1:A:397:SER:HB2	2.02	0.60
1:B:61:CYS:HB3	1:B:106:VAL:HG23	1.83	0.59
1:A:294:MET:HA	1:A:294:MET:HE2	1.85	0.59
1:B:226:GLU:OE2	1:B:292:HIS:HD2	1.86	0.59
1:A:207:GLU:HG2	1:A:296:TYR:CE1	2.39	0.58
1:A:361:LEU:O	1:A:365:THR:HG23	2.04	0.57
1:B:269:THR:H	1:B:272:GLN:HE21	1.53	0.57
1:B:231:THR:HG23	1:B:332:VAL:HG12	1.88	0.56
1:A:145:SER:OG	1:A:189:GLY:O	2.20	0.55
1:A:158:HIS:HD2	1:A:428:GLN:HE21	1.55	0.55
1:B:412:LEU:HD11	1:B:434:MET:SD	2.46	0.55
1:B:107:TYR:O	1:B:110:VAL:HG23	2.08	0.54
1:B:245:VAL:HG12	1:B:245:VAL:O	2.07	0.54
1:B:155:TYR:CE2	1:B:164:LEU:HD22	2.43	0.53
1:A:81:MET:HE1	1:A:107:TYR:HE1	1.74	0.53
1:B:205:ILE:O	1:B:209:ILE:HD11	2.09	0.53
1:B:379:GLU:HA	1:B:379:GLU:OE1	2.09	0.53
1:A:304:GLU:HB3	1:A:308:LEU:HD12	1.91	0.53
1:B:260:SER:HA	1:B:265:LEU:HD11	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:262:THR:HG22	1:B:262:THR:O	2.08	0.52
1:A:463:ALA:HB3	1:A:467:TYR:CE2	2.45	0.52
1:A:158:HIS:HD2	1:A:428:GLN:NE2	2.10	0.50
1:A:271:GLN:HB2	1:A:302:THR:HB	1.93	0.50
1:B:347:TYR:CE1	1:B:361:LEU:HD13	2.48	0.49
1:B:345:GLN:O	1:B:349:ARG:HG2	2.13	0.49
1:B:371:ARG:HD3	1:B:429:TYR:CG	2.47	0.49
1:A:347:TYR:CE1	1:A:361:LEU:HB2	2.48	0.49
1:A:224:ALA:O	1:A:435:ARG:NH2	2.45	0.48
1:A:237:ASN:HB3	1:A:238:PRO:HD3	1.95	0.48
1:B:433:HIS:O	1:B:436:ALA:HB3	2.13	0.48
1:B:206:PHE:CZ	1:B:218:VAL:HG11	2.48	0.48
1:B:245:VAL:O	1:B:245:VAL:CG1	2.61	0.48
1:A:49:ASN:OD1	1:A:82:TYR:CG	2.67	0.48
1:A:98:ILE:HG13	1:A:248:LEU:HD22	1.96	0.47
1:A:288:ARG:O	1:A:289:PHE:HB2	2.14	0.47
1:B:294:MET:HA	1:B:294:MET:HE2	1.97	0.47
1:A:245:VAL:HG12	1:A:245:VAL:O	2.14	0.47
1:A:280:ARG:NH1	1:A:330:MET:SD	2.88	0.47
1:B:174:ALA:HB1	1:B:209:ILE:HD11	1.97	0.47
1:A:258:GLU:OE2	1:A:280:ARG:NH2	2.43	0.47
1:A:200[B]:CYS:SG	1:A:335:GLN:HB2	2.55	0.47
1:B:418:VAL:O	1:B:421:THR:HG22	2.16	0.46
1:A:373:HIS:CE1	1:A:461:TYR:CD2	3.04	0.46
1:A:368:VAL:HG11	1:B:380:LEU:HG	1.98	0.46
1:A:450:MET:HE3	1:A:454:CYS:SG	2.56	0.46
1:B:139:SER:O	1:B:141:LYS:N	2.49	0.46
1:A:463:ALA:HB3	1:A:467:TYR:CZ	2.51	0.46
1:A:155:TYR:C	1:A:155:TYR:CD1	2.94	0.45
1:B:406:VAL:HG21	1:B:412:LEU:HD22	1.98	0.45
1:B:221:ALA:O	1:B:291:SER:OG	2.30	0.45
1:A:51:TYR:HB2	1:A:88:ASN:OD1	2.16	0.45
1:A:97:ILE:HD12	1:A:107:TYR:CD1	2.51	0.45
1:B:230:GLY:HA2	1:B:250:ASP:HA	1.99	0.45
1:A:81:MET:HE1	1:A:107:TYR:CE1	2.51	0.45
1:A:264:ASN:HD22	1:A:317:VAL:HA	1.82	0.45
1:B:278:ARG:NH1	1:B:285:ASN:HD21	2.15	0.44
1:B:42:ALA:HA	1:B:152:PHE:O	2.18	0.44
1:B:262:THR:O	1:B:262:THR:CG2	2.65	0.43
1:B:245:VAL:HG22	1:B:349:ARG:NH1	2.33	0.43
1:B:416:VAL:CG2	1:B:434:MET:HE1	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:292:HIS:O	1:A:294:MET:HG2	2.19	0.43
1:A:78:VAL:HG11	1:A:127:VAL:HG11	2.01	0.43
1:A:271:GLN:HE21	1:A:302:THR:HB	1.84	0.43
1:B:78:VAL:O	1:B:78:VAL:HG22	2.18	0.42
1:A:42:ALA:HA	1:A:152:PHE:O	2.19	0.42
1:A:101:PRO:HD3	1:A:232:TYR:CG	2.54	0.42
1:B:166:MET:O	1:B:167:PRO:C	2.63	0.42
1:A:406:VAL:HG21	1:A:412:LEU:HD22	2.01	0.42
1:A:79:VAL:HG12	1:A:81:MET:HG2	2.01	0.42
1:B:245:VAL:HG13	1:B:345:GLN:HB3	2.01	0.42
1:A:101:PRO:HA	1:A:241:PRO:HD3	2.00	0.42
1:A:182:LYS:HG2	1:A:214:LEU:HD11	2.00	0.42
1:A:176:ASP:O	1:A:180:VAL:HG23	2.20	0.41
1:A:45:VAL:HA	1:A:80:PHE:HB2	2.02	0.41
1:B:79:VAL:HG11	1:B:110:VAL:CG1	2.50	0.41
1:B:125:TYR:CG	1:B:180:VAL:HG21	2.55	0.41
1:A:100:HIS:ND1	1:A:101:PRO:HD2	2.36	0.41
1:B:386:TYR:OH	1:B:440:VAL:HA	2.21	0.41
1:B:194:VAL:HG23	1:B:309:TYR:CE1	2.56	0.41
1:A:350:SER:HB3	1:A:357:LYS:HB2	2.02	0.41
1:B:81:MET:O	1:B:115:THR:HA	2.21	0.41
1:B:121:PRO:HG2	1:B:122:GLU:OE1	2.21	0.41
1:B:266:LYS:HA	1:B:307:TYR:CD1	2.55	0.40
1:A:185:HIS:HB2	1:A:190:TYR:OH	2.21	0.40
1:B:159:GLY:O	1:B:200[A]:CYS:HB2	2.21	0.40
1:A:79:VAL:CG1	1:A:81:MET:HG2	2.51	0.40
1:A:148:GLU:OE2	1:A:148:GLU:N	2.54	0.40
1:A:220:THR:O	1:A:293:VAL:HG13	2.22	0.40
1:A:254:VAL:O	1:A:258:GLU:HB2	2.21	0.40
1:A:264:ASN:ND2	1:A:317:VAL:HA	2.37	0.40
1:A:415:MET:SD	1:A:450:MET:HG2	2.61	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 X-ray entries followed by that with respect to entries of similar resolution.

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	425/451 (94%)	387 (91%)	28 (7%)	10 (2%)	4	12
1	B	430/451 (95%)	391 (91%)	34 (8%)	5 (1%)	10	27
All	All	855/902 (95%)	778 (91%)	62 (7%)	15 (2%)	6	18

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	391	SER
1	A	103	GLY
1	A	289	PHE
1	B	108	ALA
1	B	459	GLY
1	B	140	GLY
1	A	83	ASP
1	A	223	ASN
1	A	242	GLU
1	B	83	ASP
1	A	119	VAL
1	A	199	ALA
1	A	147	PRO
1	A	234	PRO
1	B	203	GLY

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 X-ray entries followed by that with respect to entries of similar resolution.

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	365/380 (96%)	341 (93%)	24 (7%)	15	36
1	B	367/380 (97%)	338 (92%)	29 (8%)	11	28
All	All	732/760 (96%)	679 (93%)	53 (7%)	13	32

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	VAL
1	A	69	LYS
1	A	124	LEU
1	A	200[A]	CYS
1	A	200[B]	CYS
1	A	219	THR
1	A	234	PRO
1	A	236	MET
1	A	243	GLU
1	A	254	VAL
1	A	260	SER
1	A	262	THR
1	A	288	ARG
1	A	289	PHE
1	A	294	MET
1	A	306	LEU
1	A	317	VAL
1	A	333	VAL
1	A	356	LYS
1	A	379	GLU
1	A	380	LEU
1	A	397	SER
1	A	406	VAL
1	A	421	THR
1	B	68	ILE
1	B	78	VAL
1	B	124	LEU
1	B	175	MET
1	B	202	SER
1	B	231	THR
1	B	233	CYS
1	B	234	PRO
1	B	242	GLU
1	B	246	THR
1	B	247	CYS
1	B	254	VAL
1	B	265	LEU
1	B	267	ARG
1	B	271	GLN
1	B	273	GLN
1	B	306	LEU
1	B	330	MET
1	B	339	GLU

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Mol	Chain	Res	Type
1	B	340	LEU
1	B	345	GLN
1	B	356	LYS
1	B	367	THR
1	B	380	LEU
1	B	392	SER
1	B	397	SER
1	B	435	ARG
1	B	445	VAL
1	B	451	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	HIS
1	A	227	ASN
1	A	271	GLN
1	A	359	HIS
1	A	428	GLN
1	B	99	ASN
1	B	102	GLN
1	B	144	ASN
1	B	185	HIS
1	B	271	GLN
1	B	272	GLN
1	B	273	GLN
1	B	285	ASN
1	B	292	HIS
1	B	370	HIS
1	B	428	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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	SNN	B	157	1	7,8,8	4.95	5 (71%)	10,11,11	2.51	6 (60%)
1	SNN	A	157	1	7,8,8	5.10	5 (71%)	10,11,11	2.47	6 (60%)

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	SNN	B	157	1	-	-	0/1/1/1
1	SNN	A	157	1	-	-	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	157	SNN	C-N1	9.20	1.49	1.37
1	B	157	SNN	C-N1	8.80	1.49	1.37
1	B	157	SNN	C4-C5	7.95	1.62	1.51
1	A	157	SNN	C4-C5	7.79	1.62	1.51
1	A	157	SNN	C5-N1	5.01	1.45	1.37
1	B	157	SNN	C5-N1	4.00	1.43	1.37
1	B	157	SNN	O5-C5	-3.12	1.17	1.23
1	A	157	SNN	O5-C5	-2.56	1.18	1.23
1	A	157	SNN	O-C	-2.24	1.19	1.23
1	B	157	SNN	O-C	-2.14	1.19	1.23

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	157	SNN	C5-N1-C	-4.15	109.79	113.96
1	B	157	SNN	C5-N1-C	-4.12	109.82	113.96
1	B	157	SNN	C4-C5-N1	-3.83	103.46	108.02
1	A	157	SNN	C4-C5-N1	-3.33	104.05	108.02
1	B	157	SNN	C4-CA-N	-3.02	98.47	114.18
1	B	157	SNN	O5-C5-C4	3.00	130.31	126.48
1	A	157	SNN	O5-C5-N1	2.85	128.86	125.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	157	SNN	CA-C4-C5	-2.73	100.35	103.55
1	A	157	SNN	CA-C4-C5	-2.62	100.48	103.55
1	A	157	SNN	C4-CA-N	-2.51	101.11	114.18
1	A	157	SNN	O-C-N1	2.41	127.77	124.93
1	B	157	SNN	O-C-CA	2.16	127.73	126.19

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 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.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	431/451 (95%)	-0.22	1 (0%) 91 90	29, 70, 110, 151	1 (0%)
1	B	434/451 (96%)	-0.19	2 (0%) 87 86	29, 75, 102, 127	1 (0%)
All	All	865/902 (95%)	-0.21	3 (0%) 90 89	29, 73, 106, 151	2 (0%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	326	LEU	2.3
1	A	321	PRO	2.2
1	B	238	PRO	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	SNN	A	157	8/8	0.94	0.09	40,41,43,44	0
1	SNN	B	157	8/8	0.94	0.07	55,56,58,59	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.