



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 02:42 AM UTC

PDB ID : 4NOL / pdb_00004nol
Title : Crystal structure of proenzyme asparaginyl endopeptidase (AEP)/Legumain mutant D233A at pH 7.5
Authors : Zhao, L.; Hua, T.; Ru, H.; Ni, X.; Shaw, N.; Jiao, L.; Ding, W.; Qu, L.; Ouyang, S.; Liu, Z.J.
Deposited on : 2013-11-19
Resolution : 2.70 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
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

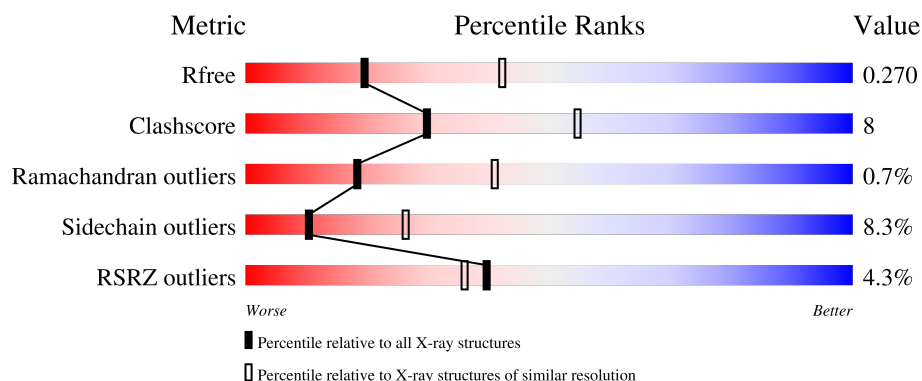
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	441	3% 65% 20% • 13%
1	B	441	5% 65% 20% • 13%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6273 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	385	Total	C	N	O	S	0	0	0
			3095	1962	531	581	21			
1	B	385	Total	C	N	O	S	0	0	0
			3095	1962	531	581	21			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	233	ALA	ASP	engineered mutation	UNP O89017
A	436	HIS	-	expression tag	UNP O89017
A	437	HIS	-	expression tag	UNP O89017
A	438	HIS	-	expression tag	UNP O89017
A	439	HIS	-	expression tag	UNP O89017
A	440	HIS	-	expression tag	UNP O89017
A	441	HIS	-	expression tag	UNP O89017
B	233	ALA	ASP	engineered mutation	UNP O89017
B	436	HIS	-	expression tag	UNP O89017
B	437	HIS	-	expression tag	UNP O89017
B	438	HIS	-	expression tag	UNP O89017
B	439	HIS	-	expression tag	UNP O89017
B	440	HIS	-	expression tag	UNP O89017
B	441	HIS	-	expression tag	UNP O89017

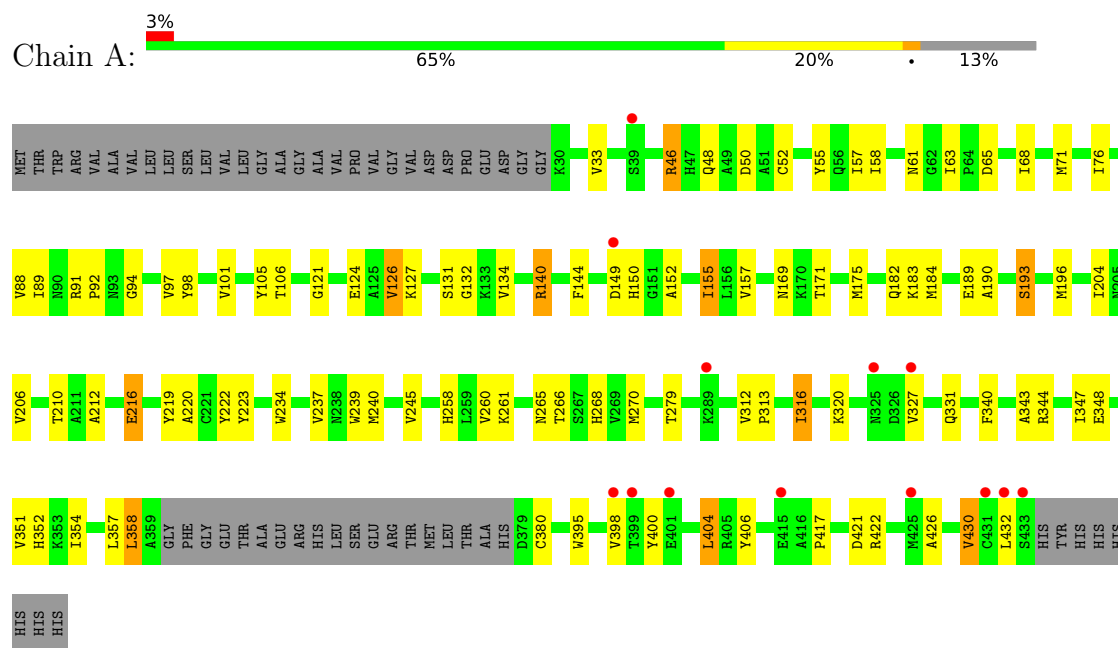
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	45	Total	O	0	0
			45	45		
2	B	38	Total	O	0	0
			38	38		

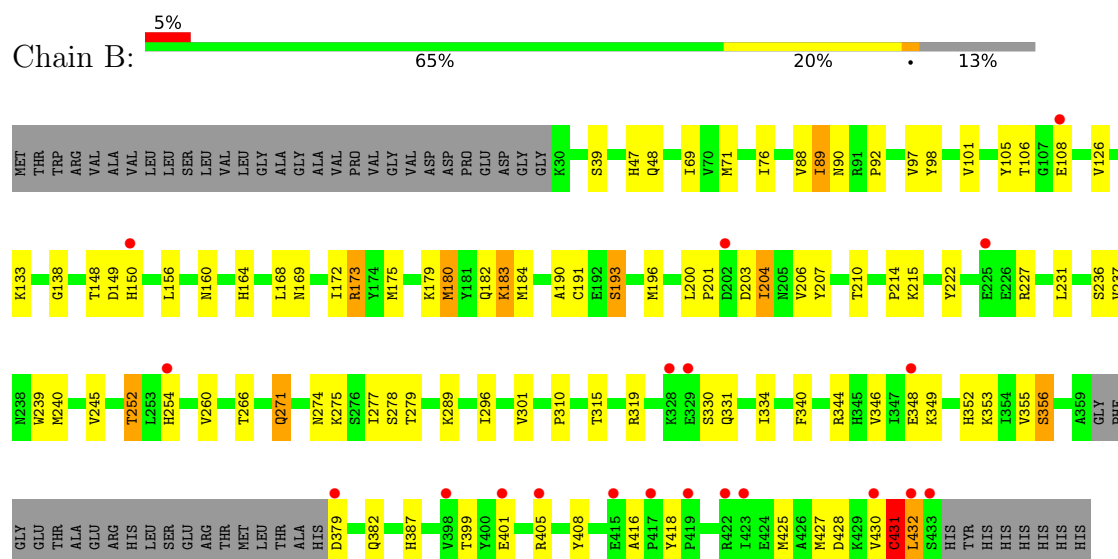
3 Residue-property plots [i](#)

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	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	51.96Å 163.36Å 59.28Å 90.00° 104.32° 90.00°	Depositor
Resolution (Å)	43.58 – 2.70 43.58 – 2.70	Depositor EDS
% Data completeness (in resolution range)	91.0 (43.58-2.70) 87.2 (43.58-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.29 (at 2.69Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.217 , 0.275 0.212 , 0.270	Depositor DCC
R_{free} test set	1225 reflections (4.66%)	wwPDB-VP
Wilson B-factor (Å ²)	20.7	Xtriage
Anisotropy	0.049	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 30.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	6273	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.27% 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

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	0.31	0/3174	0.75	0/4309
1	B	0.32	0/3174	0.76	2/4309 (0.0%)
All	All	0.31	0/6348	0.76	2/8618 (0.0%)

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	B	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	138	GLY	CA-C-N	5.11	124.82	119.82
1	B	138	GLY	C-N-CA	5.11	124.82	119.82

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	431	CYS	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	3095	0	2998	55	0
1	B	3095	0	2998	49	0
2	A	45	0	0	3	0
2	B	38	0	0	5	0
All	All	6273	0	5996	103	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 (103) 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:B:193:SER:HB2	1:B:210:THR:HG23	1.61	0.80
1:B:254:HIS:HB2	1:B:278:SER:HB2	1.69	0.71
1:B:149:ASP:CG	1:B:150:HIS:H	2.00	0.69
1:B:349:LYS:HG2	1:B:353:LYS:HE2	1.76	0.68
1:B:39:SER:OG	1:B:149:ASP:OD2	2.06	0.67
1:A:223:TYR:HE1	1:A:316:ILE:HG23	1.60	0.66
1:B:191:CYS:SG	2:B:506:HOH:O	2.53	0.66
1:B:108:GLU:OE2	1:B:160:ASN:ND2	2.29	0.66
1:A:426:ALA:O	1:A:430:VAL:HG12	1.98	0.64
1:A:190:ALA:O	1:A:193:SER:OG	2.15	0.63
1:A:212:ALA:HB1	1:A:216:GLU:HB3	1.80	0.62
1:B:387:HIS:NE2	1:B:428:ASP:OD1	2.22	0.62
1:A:312:VAL:O	1:A:316:ILE:HG13	2.01	0.61
1:A:155:ILE:N	1:A:196:MET:HE1	2.16	0.60
1:A:261:LYS:NZ	2:A:524:HOH:O	2.29	0.60
1:B:427:MET:O	1:B:431:CYS:N	2.29	0.58
1:B:430:VAL:O	1:B:432:LEU:N	2.36	0.58
1:B:190:ALA:O	1:B:193:SER:OG	2.22	0.57
1:A:351:VAL:HA	1:A:354:ILE:HD12	1.87	0.56
1:A:58:ILE:HG23	1:A:63:ILE:HB	1.86	0.56
1:A:268:HIS:HB3	1:A:270:MET:HE3	1.88	0.56
1:B:416:ALA:O	1:B:418:TYR:N	2.40	0.55
1:B:90:ASN:ND2	1:B:231:LEU:O	2.40	0.54
1:B:69:ILE:HG13	1:B:133:LYS:HD2	1.91	0.54
1:A:157:VAL:HG21	1:A:404:LEU:HD11	1.90	0.53
1:A:184:MET:HB3	1:A:206:VAL:HG22	1.91	0.53
1:B:184:MET:HB3	1:B:206:VAL:HG22	1.90	0.52
1:A:312:VAL:HG12	1:A:316:ILE:HD11	1.90	0.52
1:A:343:ALA:O	1:A:347:ILE:HG12	2.10	0.52
1:A:121:GLY:HA2	1:A:134:VAL:HB	1.91	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:265:ASN:ND2	2:A:516:HOH:O	2.44	0.52
1:B:379:ASP:N	1:B:379:ASP:OD1	2.43	0.51
1:A:91:ARG:HG3	1:A:94:GLY:HA3	1.92	0.50
1:B:315:THR:O	1:B:319:ARG:HG2	2.11	0.50
1:A:312:VAL:HB	1:A:313:PRO:HD3	1.93	0.50
1:B:330:SER:O	1:B:334:ILE:HG12	2.11	0.50
1:B:182:GLN:HG2	1:B:183:LYS:HD2	1.94	0.50
1:A:354:ILE:CG1	1:A:430:VAL:HG11	2.42	0.50
1:A:149:ASP:CG	1:A:150:HIS:N	2.70	0.49
1:A:358:LEU:HD23	1:A:422:ARG:HD3	1.93	0.49
1:A:348:GLU:O	1:A:352:HIS:ND1	2.46	0.49
1:B:92:PRO:HD3	1:B:222:TYR:CG	2.48	0.49
1:B:47:HIS:HD2	1:B:148:THR:OG1	1.96	0.48
1:B:274:ASN:ND2	2:B:505:HOH:O	2.47	0.48
1:B:89:ILE:HG22	1:B:231:LEU:HD13	1.96	0.48
1:A:140:ARG:CG	1:A:140:ARG:HH11	2.27	0.48
1:B:239:TRP:HB3	1:B:260:VAL:HG21	1.96	0.47
1:B:352:HIS:O	1:B:356:SER:N	2.46	0.47
1:B:71:MET:HG2	1:B:105:TYR:HB2	1.97	0.47
1:B:169:ASN:ND2	2:B:511:HOH:O	2.31	0.47
1:A:169:ASN:OD1	2:A:508:HOH:O	2.20	0.47
1:A:354:ILE:HG12	1:A:430:VAL:HG11	1.97	0.47
1:A:149:ASP:CG	1:A:150:HIS:H	2.24	0.46
1:B:203:ASP:OD1	1:B:203:ASP:N	2.44	0.46
1:A:88:VAL:HB	1:A:98:TYR:HB2	1.97	0.46
1:A:33:VAL:HG22	1:A:144:PHE:HB3	1.98	0.46
1:A:71:MET:HG2	1:A:105:TYR:HB2	1.98	0.46
1:B:48:GLN:NE2	2:B:504:HOH:O	2.44	0.46
1:B:430:VAL:C	1:B:432:LEU:H	2.24	0.45
1:A:140:ARG:HH11	1:A:140:ARG:HB2	1.81	0.45
1:B:184:MET:HE3	1:B:184:MET:HB2	1.81	0.45
1:B:252:THR:HG23	1:B:254:HIS:H	1.82	0.45
1:A:55:TYR:CE2	1:A:101:VAL:HA	2.52	0.45
1:A:65:ASP:HA	1:A:68:ILE:HD12	1.99	0.45
1:A:140:ARG:HH11	1:A:140:ARG:CB	2.30	0.44
1:B:164:HIS:CE1	1:B:382:GLN:HA	2.53	0.44
1:A:52:CYS:HB3	1:A:97:VAL:O	2.18	0.44
1:B:168:LEU:O	1:B:172:ILE:HG12	2.16	0.44
1:B:201:PRO:HB2	1:B:203:ASP:OD1	2.18	0.44
1:A:92:PRO:HD3	1:A:222:TYR:CG	2.53	0.44
1:B:207:TYR:HB2	1:B:277:ILE:HB	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:175:MET:HA	1:B:180:MET:HG3	2.00	0.43
1:A:126:VAL:HG13	1:A:132:GLY:HA2	2.00	0.43
1:A:265:ASN:OD1	1:A:265:ASN:N	2.51	0.43
1:B:173:ARG:HD3	1:B:173:ARG:HA	1.67	0.43
1:A:50:ASP:HA	1:A:240:MET:HE1	2.00	0.43
1:A:131:SER:HB3	1:B:179:LYS:NZ	2.33	0.43
1:A:316:ILE:HG13	1:A:316:ILE:H	1.58	0.42
1:A:57:ILE:O	1:A:61:ASN:ND2	2.41	0.42
1:A:149:ASP:OD1	1:A:157:VAL:HB	2.18	0.42
1:A:340:PHE:O	1:A:344:ARG:HB2	2.19	0.42
1:B:89:ILE:HD13	1:B:89:ILE:HA	1.76	0.42
1:A:171:THR:O	1:A:175:MET:HG3	2.19	0.42
1:B:236:SER:HB3	1:B:240:MET:HE2	2.01	0.42
1:B:156:LEU:HG	1:B:196:MET:HE2	2.02	0.42
1:A:48:GLN:HG3	1:A:76:ILE:HG13	2.02	0.42
1:A:210:THR:OG1	1:A:270:MET:HB2	2.20	0.42
1:A:239:TRP:HB3	1:A:260:VAL:HG21	2.02	0.42
1:B:204:ILE:HD12	1:B:204:ILE:HA	1.86	0.41
1:B:88:VAL:HB	1:B:98:TYR:HB2	2.01	0.41
1:A:152:ALA:HB2	1:A:404:LEU:HD22	2.02	0.41
1:A:46:ARG:HD3	1:A:220:ALA:CB	2.51	0.41
1:A:348:GLU:HB3	1:A:406:TYR:OH	2.21	0.41
1:A:395:TRP:HA	1:A:400:TYR:O	2.20	0.41
1:B:200:LEU:HD21	1:B:206:VAL:HG12	2.03	0.41
1:B:340:PHE:O	1:B:344:ARG:HB2	2.21	0.41
1:B:310:PRO:HD3	2:B:506:HOH:O	2.21	0.40
1:B:271:GLN:HG2	1:B:275:LYS:HE3	2.03	0.40
1:A:219:TYR:HB2	1:A:266:THR:HG21	2.03	0.40
1:B:405:ARG:O	1:B:408:TYR:HD2	2.04	0.40
1:A:124:GLU:HA	1:A:127:LYS:HG2	2.03	0.40
1:A:234:TRP:HA	1:A:234:TRP:CE3	2.56	0.40
1:A:347:ILE:O	1:A:351:VAL:HG23	2.22	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	381/441 (86%)	367 (96%)	12 (3%)	2 (0%)	24	48
1	B	381/441 (86%)	359 (94%)	19 (5%)	3 (1%)	16	37
All	All	762/882 (86%)	726 (95%)	31 (4%)	5 (1%)	18	41

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	417	PRO
1	B	431	CYS
1	B	432	LEU
1	A	46	ARG
1	B	214	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 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	342/386 (89%)	315 (92%)	27 (8%)	11	28
1	B	342/386 (89%)	312 (91%)	30 (9%)	9	23
All	All	684/772 (89%)	627 (92%)	57 (8%)	10	26

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	89	ILE
1	A	106	THR
1	A	126	VAL
1	A	140	ARG
1	A	155	ILE
1	A	182	GLN
1	A	183	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	189	GLU
1	A	193	SER
1	A	204	ILE
1	A	216	GLU
1	A	237	VAL
1	A	245	VAL
1	A	258	HIS
1	A	279	THR
1	A	316	ILE
1	A	320	LYS
1	A	327	VAL
1	A	331	GLN
1	A	357	LEU
1	A	358	LEU
1	A	380	CYS
1	A	398	VAL
1	A	404	LEU
1	A	421	ASP
1	A	430	VAL
1	A	432	LEU
1	B	76	ILE
1	B	89	ILE
1	B	97	VAL
1	B	101	VAL
1	B	106	THR
1	B	126	VAL
1	B	173	ARG
1	B	180	MET
1	B	183	LYS
1	B	193	SER
1	B	204	ILE
1	B	215	LYS
1	B	227	ARG
1	B	237	VAL
1	B	245	VAL
1	B	252	THR
1	B	266	THR
1	B	271	GLN
1	B	279	THR
1	B	289	LYS
1	B	296	ILE
1	B	301	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	331	GLN
1	B	346	VAL
1	B	348	GLU
1	B	355	VAL
1	B	356	SER
1	B	399	THR
1	B	401	GLU
1	B	425	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	HIS
1	A	258	HIS
1	A	402	HIS
1	B	47	HIS
1	B	61	ASN
1	B	67	GLN
1	B	78	ASN
1	B	164	HIS
1	B	352	HIS
1	B	394	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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

6.1 Protein, DNA and RNA chains

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	385/441 (87%)	0.27	13 (3%) 48 44	3, 25, 59, 97	0
1	B	385/441 (87%)	0.36	20 (5%) 33 29	5, 28, 61, 103	0
All	All	770/882 (87%)	0.31	33 (4%) 40 36	3, 26, 61, 103	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	432	LEU	7.6
1	B	433	SER	6.6
1	A	432	LEU	5.5
1	A	433	SER	3.6
1	B	405	ARG	3.1
1	A	398	VAL	2.9
1	B	417	PRO	2.9
1	B	348	GLU	2.8
1	B	422	ARG	2.8
1	B	415	GLU	2.7
1	B	328	LYS	2.7
1	B	379	ASP	2.7
1	A	431	CYS	2.7
1	A	149	ASP	2.7
1	A	401	GLU	2.6
1	B	401	GLU	2.6
1	A	325	ASN	2.6
1	A	327	VAL	2.5
1	B	430	VAL	2.5
1	B	254	HIS	2.4
1	B	398	VAL	2.4
1	A	289	LYS	2.4
1	A	39	SER	2.3
1	B	423	ILE	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	399	THR	2.2
1	B	225	GLU	2.2
1	B	108	GLU	2.1
1	A	425	MET	2.1
1	B	419	PRO	2.1
1	B	150	HIS	2.1
1	B	202	ASP	2.1
1	A	415	GLU	2.1
1	B	329	GLU	2.0

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

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

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.