



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:12 PM GMT

PDB ID : 4KXB
Title : Crystal structure of human aminopeptidase A complexed with bestatin
Authors : Yang, Y.; Liu, C.; Lin, Y.Y.; Li, F.
Deposited on : 2013-05-24
Resolution : 2.40 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

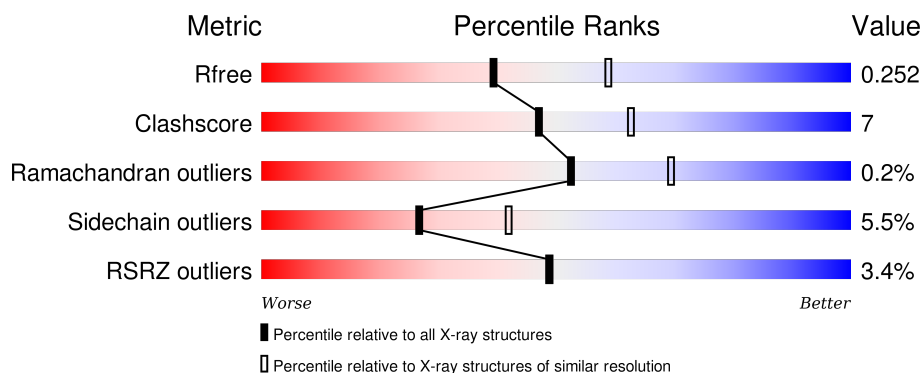
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

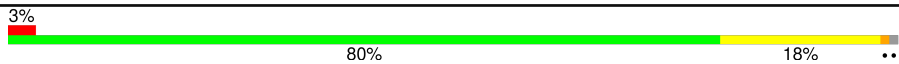
The reported resolution of this entry is 2.40 Å.

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}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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 on the lower 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 $\leq 5\%$. 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	888	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7839 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 Glutamyl aminopeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	875	Total	C	N	O	S	0	2	0
			7159	4584	1192	1358	25			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	213	ARG	GLN	NATURAL VARIANT	UNP Q07075
A	218	ALA	VAL	NATURAL VARIANT	UNP Q07075
A	958	HIS	-	EXPRESSION TAG	UNP Q07075
A	959	HIS	-	EXPRESSION TAG	UNP Q07075
A	960	HIS	-	EXPRESSION TAG	UNP Q07075
A	961	HIS	-	EXPRESSION TAG	UNP Q07075
A	962	HIS	-	EXPRESSION TAG	UNP Q07075
A	963	HIS	-	EXPRESSION TAG	UNP Q07075

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	2	Total	C	N	O	0	0
			28	16	2	10		
3	A	2	Total	C	N	O	0	0
			28	16	2	10		
3	A	2	Total	C	N	O	0	0
			28	16	2	10		
3	A	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

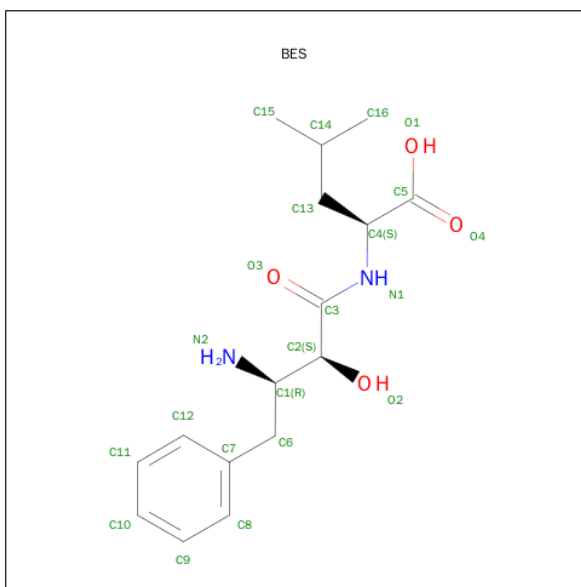


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	3	Total	C	N	O	0	0
			42	24	3	15		
5	A	3	Total	C	N	O	0	0
			42	24	3	15		

- Molecule 6 is 2-(3-AMINO-2-HYDROXY-4-PHENYL-BUTYRYLAMINO)-4-METHYL-PENTANOIC ACID (three-letter code: BES) (formula: $C_{16}H_{24}N_2O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			22	16	2	4		

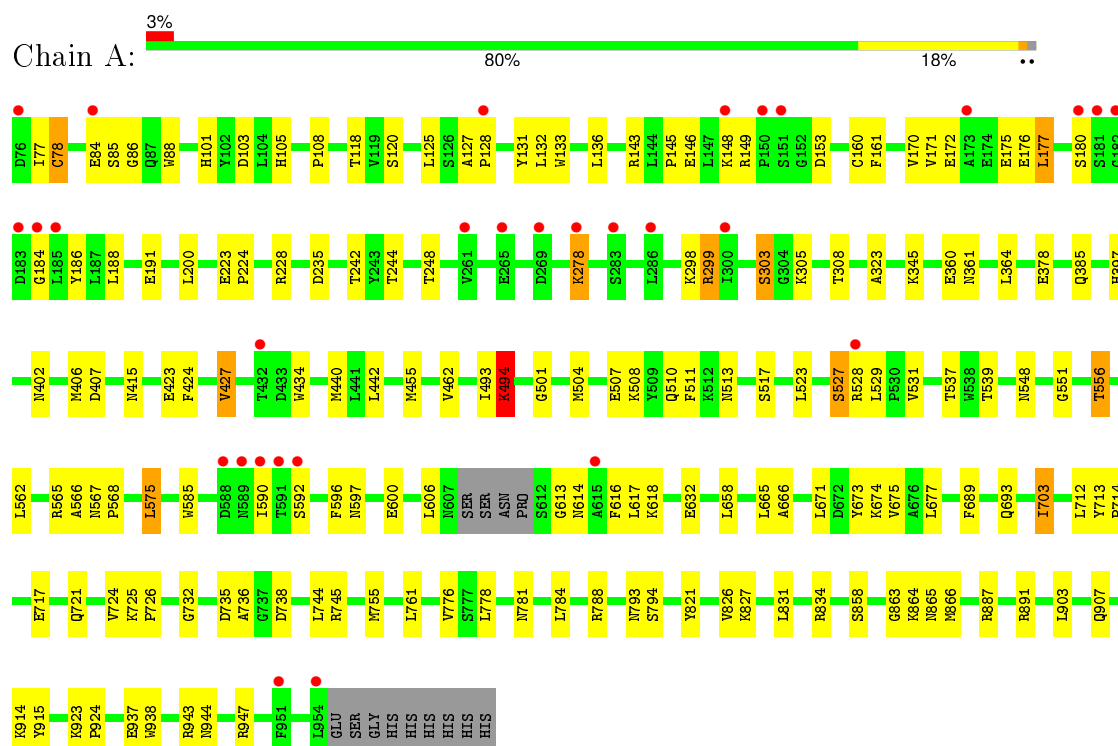
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	445	Total	O	0	2
			447	447		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Glutamyl aminopeptidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 64 2 2	Depositor
Cell constants a, b, c, α , β , γ	141.85Å 141.85Å 237.06Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	33.73 – 2.40 33.73 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.0 (33.73-2.40) 99.0 (33.73-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.54 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.171 , 0.252 0.175 , 0.252	Depositor DCC
R_{free} test set	2822 reflections (5.40%)	DCC
Wilson B-factor (Å ²)	42.8	Xtriage
Anisotropy	0.521	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 51.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Outliers	0 of 55096 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7839	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.69% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BES, ZN, NAG

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	0.41	0/7344	0.57	0/9985

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	7159	0	6952	107	0
2	A	1	0	0	0	0
3	A	112	0	100	1	0
4	A	14	0	13	0	0
5	A	84	0	74	1	0
6	A	22	0	22	0	0
7	A	447	0	0	18	0
All	All	7839	0	7161	108	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 7.

All (108) 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:907:GLN:HB3	7:A:1543:HOH:O	1.42	1.13
1:A:865:ASN:HB2	7:A:1516:HOH:O	1.68	0.94
1:A:177:LEU:HB3	1:A:186:TYR:OH	1.68	0.94
1:A:78:CYS:HA	1:A:160:CYS:SG	2.11	0.91
1:A:378:GLU:HG3	7:A:1478:HOH:O	1.72	0.88
1:A:613:GLY:HA3	7:A:1544:HOH:O	1.73	0.87
1:A:101:HIS:HD2	1:A:242:THR:HG23	1.48	0.79
1:A:101:HIS:CD2	1:A:242:THR:HG23	2.18	0.78
1:A:78:CYS:CB	1:A:160:CYS:HG	1.97	0.76
1:A:501:GLY:HA3	1:A:523:LEU:HD23	1.69	0.75
1:A:161:PHE:CZ	1:A:170:VAL:HB	2.22	0.75
1:A:423:GLU:O	1:A:427:VAL:HG12	1.86	0.75
1:A:761:LEU:HD22	1:A:793:ASN:HD21	1.50	0.74
1:A:78:CYS:CA	1:A:160:CYS:SG	2.75	0.74
1:A:565:ARG:CZ	1:A:937:GLU:HG3	2.17	0.73
1:A:118:THR:HG22	1:A:191:GLU:HG2	1.69	0.73
1:A:551:GLY:O	1:A:632:GLU:OE1	2.08	0.71
1:A:493:ILE:HD11	1:A:531:VAL:HG22	1.71	0.71
1:A:128:PRO:HB3	1:A:176:GLU:OE1	1.91	0.71
1:A:149:ARG:HE	1:A:177:LEU:HD21	1.55	0.70
1:A:717:GLU:HG2	1:A:755:MET:O	1.91	0.69
1:A:793:ASN:HB3	7:A:1506:HOH:O	1.94	0.67
1:A:732:GLY:O	1:A:745:ARG:HD2	1.95	0.66
1:A:511:PHE:CZ	7:A:1413:HOH:O	2.47	0.65
1:A:146:GLU:HA	7:A:1518:HOH:O	1.98	0.63
1:A:616:PHE:HE2	1:A:618:LYS:HG3	1.62	0.63
1:A:361:ASN:HB2	1:A:364:LEU:O	1.99	0.63
1:A:527:SER:HB3	1:A:529:LEU:HD12	1.81	0.62
1:A:78:CYS:SG	1:A:160:CYS:HB2	2.39	0.62
1:A:244:THR:HG22	1:A:278:LYS:HA	1.80	0.61
1:A:891:ARG:NH2	7:A:1435:HOH:O	2.32	0.61
1:A:548:ASN:HB2	1:A:556:THR:HG22	1.82	0.61
1:A:944:ASN:HB3	7:A:1496:HOH:O	1.99	0.60
1:A:143:ARG:HB3	1:A:191:GLU:HB2	1.83	0.59
1:A:736:ALA:O	1:A:745:ARG:NH1	2.28	0.59
1:A:133:TRP:HB3	1:A:170:VAL:HG22	1.87	0.57
1:A:788:ARG:HD2	7:A:1144:HOH:O	2.04	0.56
1:A:78:CYS:CA	1:A:160:CYS:HG	2.15	0.56
1:A:689:PHE:HA	1:A:744:LEU:HD13	1.89	0.55
1:A:298:LYS:HA	1:A:308:THR:HG22	1.89	0.54
1:A:133:TRP:CB	1:A:170:VAL:HG22	2.39	0.53
1:A:125:LEU:HD21	1:A:127:ALA:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:914:LYS:HD3	1:A:915:TYR:CE2	2.45	0.52
1:A:735:ASP:OD1	1:A:781:ASN:HB2	2.10	0.51
1:A:937:GLU:HG2	7:A:1469:HOH:O	2.11	0.51
1:A:493:ILE:HD11	1:A:531:VAL:CG2	2.41	0.51
1:A:537:THR:HA	1:A:575:LEU:HD23	1.93	0.51
1:A:78:CYS:SG	1:A:160:CYS:CB	2.99	0.50
1:A:78:CYS:HG	1:A:160:CYS:HG	1.40	0.49
1:A:161:PHE:CE1	1:A:170:VAL:HB	2.46	0.49
1:A:180:SER:HB2	1:A:184:GLY:O	2.12	0.49
1:A:732:GLY:O	1:A:745:ARG:CD	2.60	0.49
1:A:131:TYR:CE2	1:A:172:GLU:HB3	2.47	0.49
1:A:303:SER:HB2	1:A:305:LYS:HE3	1.96	0.48
1:A:863:GLY:HA2	1:A:866:MET:HB2	1.94	0.48
1:A:761:LEU:HD22	1:A:793:ASN:ND2	2.25	0.48
1:A:385:GLN:HA	1:A:434:TRP:CZ3	2.49	0.48
1:A:86:GLY:HA3	1:A:88:TRP:CZ3	2.49	0.47
1:A:299:ARG:HD2	1:A:323:ALA:HB1	1.97	0.47
1:A:597:ASN:HB3	1:A:600:GLU:HG2	1.95	0.47
1:A:703:ILE:HD12	1:A:713:TYR:CE2	2.49	0.47
1:A:455:MET:HE3	1:A:566:ALA:HB1	1.96	0.47
1:A:736:ALA:H	1:A:745:ARG:NH1	2.12	0.47
1:A:527:SER:C	1:A:529:LEU:H	2.18	0.47
1:A:402:ASN:HD22	1:A:402:ASN:N	2.13	0.46
1:A:666:ALA:HA	1:A:671:LEU:O	2.15	0.46
1:A:673:TYR:HH	1:A:938:TRP:HE1	1.63	0.46
1:A:149:ARG:HE	1:A:177:LEU:CD2	2.25	0.45
1:A:717:GLU:O	1:A:721:GLN:HB2	2.17	0.45
1:A:713:TYR:HB3	1:A:714:PRO:HD3	1.99	0.45
1:A:827:LYS:HE2	7:A:1485:HOH:O	2.16	0.45
1:A:131:TYR:CD2	1:A:172:GLU:HB3	2.52	0.45
1:A:834:ARG:HD2	7:A:1132:HOH:O	2.16	0.45
1:A:493:ILE:O	1:A:494:LYS:HB2	2.16	0.44
1:A:424:PHE:CG	1:A:440:MET:HG2	2.52	0.44
1:A:703:ILE:HG22	7:A:1363:HOH:O	2.17	0.44
1:A:671:LEU:HD11	1:A:675:VAL:HG11	2.00	0.44
1:A:223:GLU:HA	1:A:224:PRO:HA	1.72	0.43
1:A:442:LEU:HD13	1:A:693:GLN:HG3	2.01	0.43
1:A:108:PRO:HD2	1:A:248:THR:O	2.18	0.43
1:A:360:GLU:HG3	1:A:397:HIS:HB3	2.00	0.43
1:A:943:ARG:HH22	1:A:947:ARG:NH1	2.16	0.43
1:A:78:CYS:HG	1:A:160:CYS:CB	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:616:PHE:CE2	1:A:618:LYS:HG3	2.49	0.43
1:A:105:HIS:HE1	1:A:248:THR:OG1	2.01	0.43
1:A:858:SER:O	1:A:864:LYS:HA	2.19	0.43
1:A:228:ARG:HH21	1:A:235:ASP:HB3	1.84	0.43
3:A:1004:NAG:H83	7:A:1123:HOH:O	2.18	0.42
1:A:424:PHE:CD2	1:A:440:MET:HG2	2.53	0.42
1:A:725:LYS:HB3	1:A:726:PRO:HD3	2.01	0.42
1:A:407:ASP:HA	1:A:513:ASN:HB3	2.00	0.42
1:A:674:LYS:HD3	5:A:1007:NAG:H62	2.01	0.42
1:A:887:ARG:NH1	7:A:1266:HOH:O	2.52	0.42
1:A:153:ASP:HB3	7:A:1525:HOH:O	2.19	0.42
1:A:776:VAL:HG23	7:A:1370:HOH:O	2.19	0.42
1:A:120:SER:HA	1:A:188:LEU:O	2.19	0.42
1:A:133:TRP:HB3	1:A:170:VAL:HG13	2.01	0.41
1:A:784:LEU:O	1:A:788:ARG:HG3	2.19	0.41
1:A:923:LYS:HA	1:A:923:LYS:HD2	1.85	0.41
1:A:385:GLN:HA	1:A:434:TRP:HZ3	1.85	0.41
1:A:826:VAL:HG21	1:A:831:LEU:HD12	2.03	0.41
1:A:161:PHE:CZ	1:A:170:VAL:CB	3.01	0.41
1:A:585:TRP:CZ3	1:A:606:LEU:HD22	2.56	0.41
1:A:145:PRO:HG2	1:A:171:VAL:HG11	2.02	0.41
1:A:923:LYS:HB2	1:A:924:PRO:HD3	2.03	0.40
1:A:504:MET:O	1:A:508:LYS:HB2	2.22	0.40
1:A:567:ASN:HA	1:A:568:PRO:HD3	1.90	0.40
1:A:562:LEU:HA	1:A:562:LEU:HD12	1.89	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	873/888 (98%)	832 (95%)	39 (4%)	2 (0%)	52	69

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	85	SER
1	A	494	LYS

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	787/797 (99%)	744 (94%)	43 (6%)	27	42

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	77	ILE
1	A	78	CYS
1	A	84	GLU
1	A	103	ASP
1	A	132	LEU
1	A	136	LEU
1	A	148	LYS
1	A	175	GLU
1	A	177	LEU
1	A	200	LEU
1	A	278	LYS
1	A	299	ARG
1	A	303	SER
1	A	345	LYS
1	A	406	MET
1	A	415	ASN
1	A	427	VAL
1	A	462	VAL
1	A	494	LYS
1	A	507	GLU
1	A	510	GLN
1	A	517	SER
1	A	527	SER

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Mol	Chain	Res	Type
1	A	528	ARG
1	A	539	THR
1	A	556	THR
1	A	575	LEU
1	A	590	ILE
1	A	592	SER
1	A	596	PHE
1	A	614	ASN
1	A	617	LEU
1	A	658	LEU
1	A	665	LEU
1	A	677	LEU
1	A	703	ILE
1	A	712	LEU
1	A	724	VAL
1	A	738	ASP
1	A	778	LEU
1	A	794	SER
1	A	821	TYR
1	A	903	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	101	HIS
1	A	105	HIS
1	A	317	HIS
1	A	402	ASN
1	A	415	ASN
1	A	510	GLN
1	A	550	ASN
1	A	570	GLN
1	A	792	GLN
1	A	793	ASN
1	A	874	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 ⓘ

14 carbohydrates 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$
3	NAG	A	1002	1,3	14,14,15	0.52	0	15,19,21	1.12	1 (6%)
3	NAG	A	1003	3	14,14,15	0.41	0	15,19,21	1.29	1 (6%)
3	NAG	A	1004	1,3	14,14,15	0.51	0	15,19,21	1.72	5 (33%)
3	NAG	A	1005	3	14,14,15	0.69	1 (7%)	15,19,21	2.30	2 (13%)
5	NAG	A	1007	1,5	14,14,15	0.54	0	15,19,21	1.08	1 (6%)
5	NAG	A	1008	5	14,14,15	0.55	0	15,19,21	1.33	1 (6%)
5	NAG	A	1009	5	14,14,15	0.50	0	15,19,21	1.30	1 (6%)
5	NAG	A	1010	1,5	14,14,15	0.48	0	15,19,21	0.94	1 (6%)
5	NAG	A	1011	5	14,14,15	0.71	0	15,19,21	1.49	3 (20%)
5	NAG	A	1012	5	14,14,15	0.66	0	15,19,21	2.02	4 (26%)
3	NAG	A	1013	1,3	14,14,15	0.66	0	15,19,21	2.18	3 (20%)
3	NAG	A	1014	3	14,14,15	0.45	0	15,19,21	1.51	2 (13%)
3	NAG	A	1015	1,3	14,14,15	0.49	0	15,19,21	0.79	0
3	NAG	A	1016	3	14,14,15	0.53	0	15,19,21	0.73	0

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
3	NAG	A	1002	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	1003	3	-	0/6/23/26	0/1/1/1
3	NAG	A	1004	1,3	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	1005	3	-	0/6/23/26	0/1/1/1
5	NAG	A	1007	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	1008	5	-	0/6/23/26	0/1/1/1
5	NAG	A	1009	5	-	0/6/23/26	0/1/1/1
5	NAG	A	1010	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	1011	5	-	0/6/23/26	0/1/1/1
5	NAG	A	1012	5	-	0/6/23/26	0/1/1/1
3	NAG	A	1013	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	1014	3	-	0/6/23/26	0/1/1/1
3	NAG	A	1015	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	1016	3	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1005	NAG	C1-C2	2.03	1.55	1.52

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1013	NAG	C4-C3-C2	-3.42	105.91	111.23
3	A	1002	NAG	C3-C4-C5	-2.22	106.32	110.20
3	A	1004	NAG	O7-C7-C8	-2.19	118.03	122.06
5	A	1007	NAG	O7-C7-C8	-2.07	118.26	122.06
5	A	1012	NAG	O7-C7-C8	-2.02	118.36	122.06
3	A	1014	NAG	C4-C3-C2	-2.01	108.10	111.23
5	A	1011	NAG	C3-C2-N2	2.05	115.46	110.56
5	A	1011	NAG	C1-O5-C5	2.43	115.34	112.25
5	A	1012	NAG	O7-C7-N2	2.52	127.00	121.86
3	A	1004	NAG	C8-C7-N2	2.53	120.95	116.11
5	A	1010	NAG	C1-O5-C5	2.59	115.54	112.25
3	A	1004	NAG	C2-N2-C7	2.78	126.62	123.04
3	A	1004	NAG	O4-C4-C3	3.07	117.25	110.34
3	A	1004	NAG	C1-O5-C5	3.11	116.19	112.25
5	A	1012	NAG	C1-O5-C5	3.18	116.29	112.25
5	A	1011	NAG	C2-N2-C7	3.21	127.16	123.04
3	A	1003	NAG	C1-O5-C5	3.68	116.92	112.25
5	A	1009	NAG	C1-O5-C5	3.80	117.07	112.25
5	A	1008	NAG	C4-C3-C2	3.84	117.21	111.23
3	A	1014	NAG	C1-O5-C5	4.72	118.24	112.25
3	A	1013	NAG	O4-C4-C3	4.86	121.28	110.34
3	A	1013	NAG	C1-O5-C5	5.22	118.88	112.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1012	NAG	C2-N2-C7	5.28	129.82	123.04
3	A	1005	NAG	C2-N2-C7	5.60	130.24	123.04
3	A	1005	NAG	C1-O5-C5	6.02	119.89	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1004	NAG	1	0
5	A	1007	NAG	1	0

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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	$\# Z > 2$
4	NAG	A	1006	1	14,14,15	0.52	0	15,19,21	1.05	1 (6%)
6	BES	A	1017	2	19,22,22	0.74	0	19,29,29	0.60	0

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
4	NAG	A	1006	1	-	0/6/23/26	0/1/1/1
6	BES	A	1017	2	-	0/20/24/24	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	A	1006	NAG	C2-N2-C7	2.34	126.04	123.04

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	875/888 (98%)	-0.25	30 (3%)	49 49	25, 60, 110, 151	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	185	LEU	5.2
1	A	184	GLY	4.9
1	A	183	ASP	4.1
1	A	951	PHE	3.6
1	A	182	GLY	3.6
1	A	300	ILE	3.5
1	A	432	THR	3.3
1	A	591	THR	3.2
1	A	128	PRO	3.2
1	A	265	GLU	3.1
1	A	278	LYS	2.9
1	A	615	ALA	2.9
1	A	181	SER	2.9
1	A	151	SER	2.9
1	A	180	SER	2.8
1	A	528	ARG	2.8
1	A	173	ALA	2.8
1	A	76	ASP	2.6
1	A	84	GLU	2.6
1	A	269	ASP	2.5
1	A	590	ILE	2.5
1	A	283	SER	2.4
1	A	592	SER	2.3
1	A	150	PRO	2.3
1	A	261	VAL	2.3
1	A	954	LEU	2.2
1	A	589	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	148	LYS	2.0
1	A	286	LEU	2.0
1	A	588	ASP	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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
5	NAG	A	1010	14/15	0.96	0.14	1.68	66,84,118,158	0
5	NAG	A	1007	14/15	0.90	0.13	-0.21	72,107,123,133	0
3	NAG	A	1002	14/15	0.94	0.21	-	65,93,115,132	0
5	NAG	A	1008	14/15	0.96	0.24	-	124,140,164,170	0
3	NAG	A	1005	14/15	0.77	0.37	-	94,168,179,187	0
3	NAG	A	1015	14/15	0.96	0.10	-	53,80,90,100	0
5	NAG	A	1012	14/15	0.85	0.23	-	126,146,163,169	0
3	NAG	A	1013	14/15	0.96	0.27	-	59,83,105,109	0
3	NAG	A	1016	14/15	0.87	0.28	-	101,127,148,158	0
3	NAG	A	1014	14/15	0.87	0.44	-	108,136,150,155	0
3	NAG	A	1003	14/15	0.88	0.35	-	101,138,154,159	0
3	NAG	A	1004	14/15	0.94	0.20	-	79,105,132,137	0
5	NAG	A	1009	14/15	0.86	0.23	-	129,159,171,179	0
5	NAG	A	1011	14/15	0.93	0.21	-	99,108,133,134	0

6.4 Ligands [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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
6	BES	A	1017	22/22	0.95	0.19	0.74	61,74,81,94	0
2	ZN	A	1001	1/1	0.99	0.10	-1.66	74,74,74,74	0
4	NAG	A	1006	14/15	0.72	0.34	-	114,148,167,173	0

6.5 Other polymers [i](#)

There are no such residues in this entry.