



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 19, 2016 – 08:22 AM EDT

PDB ID : 5JMY
Title : NEPRILYSIN COMPLEXED WITH LBQ657
Authors : Schiering, N.; Wiesmann, C.
Deposited on : 2016-04-29
Resolution : 2.00 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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027790
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) : rb-20027790

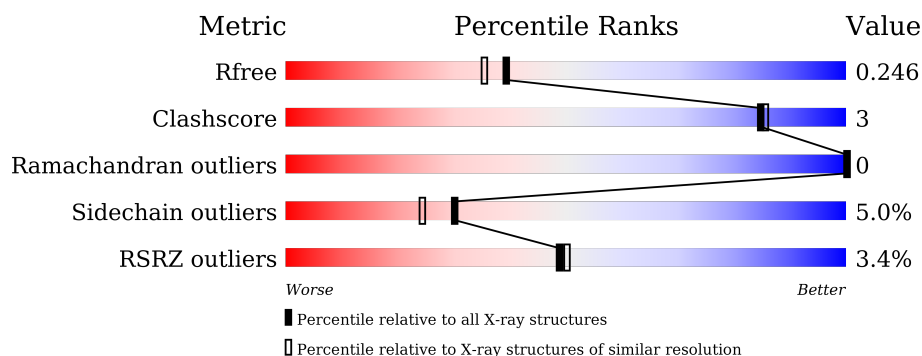
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	698	<div> <div>2%</div> <div> <div></div> <div>89%</div> <div>10%</div> <div>.</div> </div> </div>
1	B	698	<div> <div>5%</div> <div> <div></div> <div>88%</div> <div>11%</div> <div>.</div> </div> </div>

2 Entry composition [i](#)

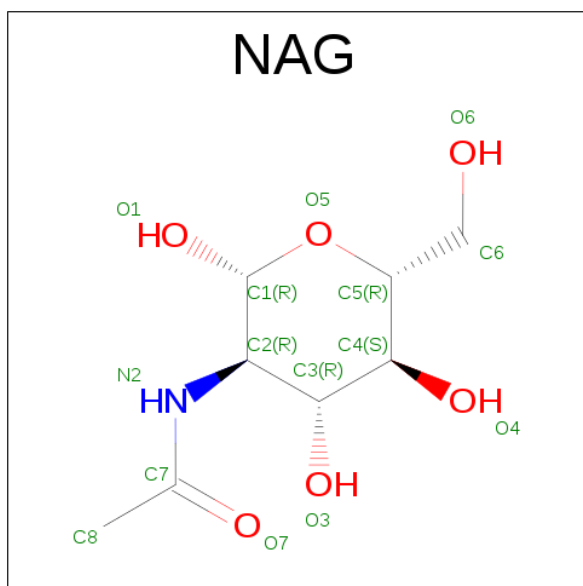
There are 5 unique types of molecules in this entry. The entry contains 12295 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Neprilysin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	696	Total	C	N	O	S	0	2	0
			5612	3549	961	1076	26			
1	B	696	Total	C	N	O	S	0	0	0
			5595	3538	957	1074	26			

- Molecule 2 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

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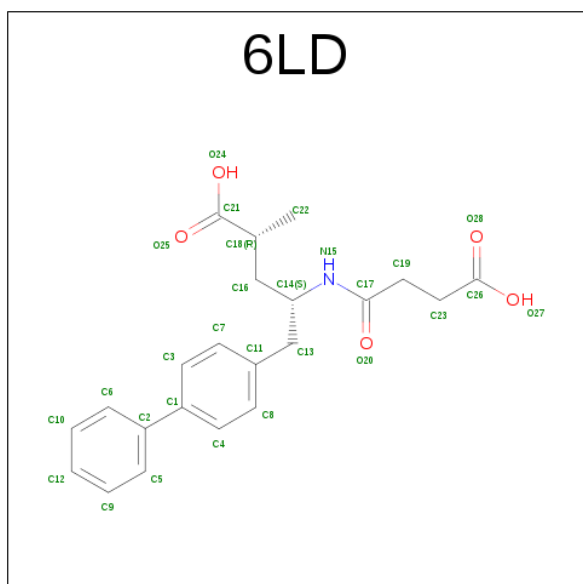
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Zn	0	0
			1	1		
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is Sacubitrilat (three-letter code: 6LD) (formula: C₂₂H₂₅NO₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			28	22	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			28	22	1	5		

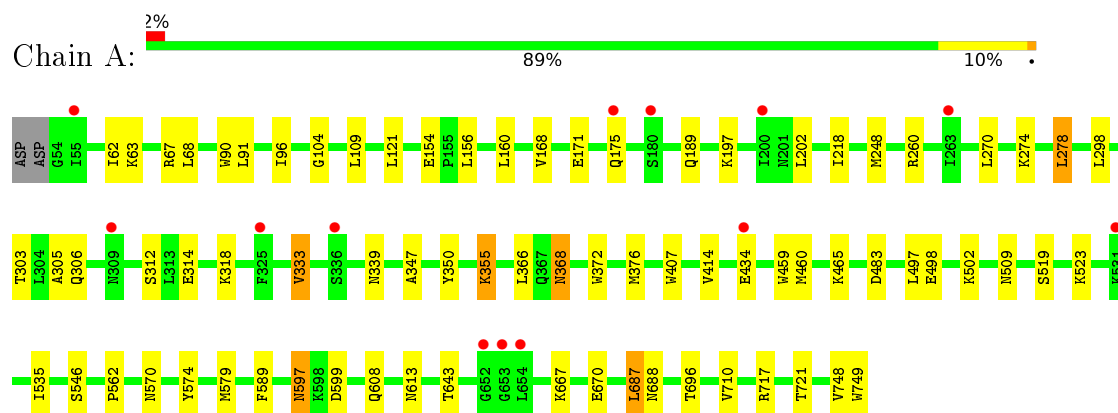
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	514	Total	O	0	0
			514	514		
5	B	376	Total	O	0	0
			376	376		

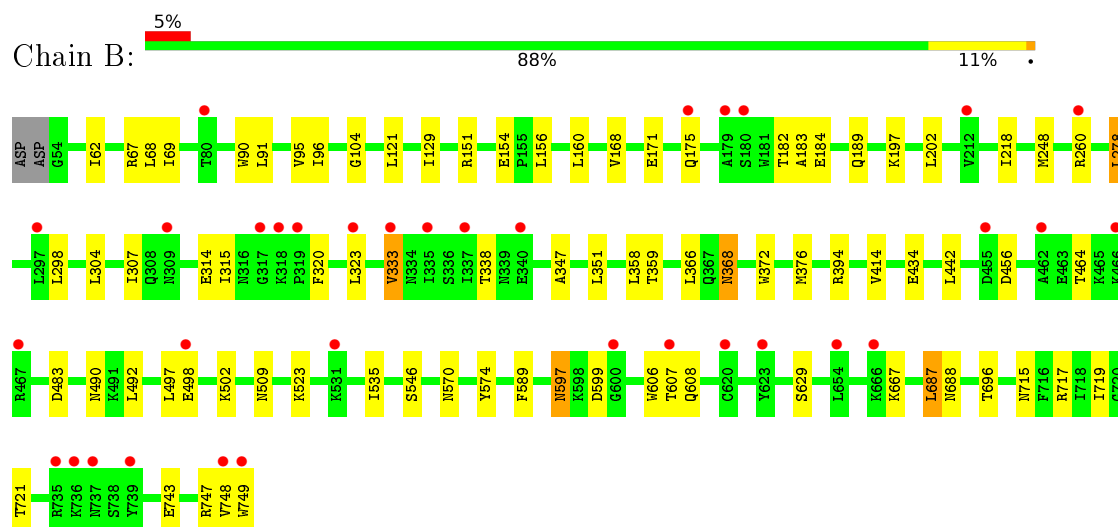
3 Residue-property plots

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: Neprilysin



• Molecule 1: Neprilysin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.74Å 109.14Å 248.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.28 – 2.00 29.08 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.2 (29.28-2.00) 98.2 (29.08-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.11 (at 2.00Å)	Xtriage
Refinement program	BUSTER 2.11.6	Depositor
R, R_{free}	0.186 , 0.228 0.201 , 0.246	Depositor DCC
R_{free} test set	4992 reflections (4.82%)	DCC
Wilson B-factor (Å ²)	32.0	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 58.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12295	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.01% 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: ZN, NAG, 6LD

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	0.52	0/5731	0.65	0/7752
1	B	0.50	0/5713	0.65	0/7727
All	All	0.51	0/11444	0.65	0/15479

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	5612	0	5460	33	0
1	B	5595	0	5446	36	0
2	A	70	0	64	0	0
2	B	70	0	64	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	28	0	0	0	0
4	B	28	0	0	0	0
5	A	514	0	0	1	0
5	B	376	0	0	1	0
All	All	12295	0	11034	66	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 3.

All (66) 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:202:LEU:HD23	1:A:218:ILE:HD11	1.70	0.72
1:B:202:LEU:HD23	1:B:218:ILE:HD11	1.72	0.71
1:A:305:ALA:HB2	1:A:339:ASN:HB3	1.77	0.67
1:B:168:VAL:H	1:B:368:ASN:HD21	1.44	0.65
1:B:183:ALA:HB2	1:B:315:ILE:HG21	1.79	0.64
1:A:168:VAL:H	1:A:368:ASN:HD21	1.43	0.64
1:A:333:VAL:HG11	1:A:523:LYS:HB3	1.79	0.62
1:B:333:VAL:HG11	1:B:523:LYS:HB3	1.79	0.62
1:A:67:ARG:HH22	1:A:688:ASN:HD21	1.47	0.62
1:A:407:TRP:CZ2	1:B:95:VAL:HG11	2.34	0.61
1:B:502:LYS:H	1:B:509:ASN:HD21	1.50	0.59
1:A:502:LYS:H	1:A:509:ASN:HD21	1.52	0.58
1:A:67:ARG:HH22	1:A:688:ASN:ND2	2.03	0.56
1:B:589:PHE:HB3	1:B:749:TRP:CZ2	2.41	0.56
1:A:589:PHE:HB3	1:A:749:TRP:CZ2	2.41	0.56
1:A:96:ILE:HD11	1:A:696:THR:HG23	1.90	0.53
1:B:67:ARG:HH22	1:B:688:ASN:ND2	2.07	0.52
1:B:121:LEU:HD13	1:B:414:VAL:HG21	1.92	0.52
1:B:67:ARG:HH22	1:B:688:ASN:HD21	1.57	0.51
1:A:67:ARG:HH12	1:A:688:ASN:ND2	2.09	0.51
1:B:67:ARG:HH12	1:B:688:ASN:ND2	2.09	0.51
1:A:278:LEU:HD11	1:A:366:LEU:HD23	1.94	0.50
1:A:535:ILE:HD13	1:A:546:SER:HB2	1.94	0.50
1:A:62:ILE:HG13	1:B:62:ILE:HG13	1.94	0.50
1:B:67:ARG:HH12	1:B:688:ASN:HD22	1.60	0.50
1:A:597:ASN:ND2	1:A:599:ASP:H	2.10	0.50
1:B:570:ASN:O	1:B:574:TYR:HD1	1.94	0.49
1:B:597:ASN:ND2	1:B:599:ASP:H	2.11	0.49
1:A:372:TRP:CE2	1:A:376:MET:HG3	2.48	0.48
1:B:372:TRP:CE2	1:B:376:MET:HG3	2.48	0.48
1:A:347:ALA:HB1	1:A:350:TYR:HB3	1.95	0.48
1:B:278:LEU:HD11	1:B:366:LEU:HD23	1.93	0.48
1:B:96:ILE:HD11	1:B:696:THR:HG23	1.95	0.48
1:A:121:LEU:HD13	1:A:414[A]:VAL:HG21	1.96	0.48
1:A:570:ASN:O	1:A:574:TYR:HD1	1.96	0.48
1:B:464:THR:HG23	1:B:607:THR:HG23	1.96	0.47
1:A:460:MET:HE3	1:A:465:LYS:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:LEU:HD22	1:A:687:LEU:HD13	1.96	0.47
1:A:67:ARG:HH12	1:A:688:ASN:HD22	1.63	0.47
1:B:535:ILE:HD13	1:B:546:SER:HB2	1.97	0.47
1:A:597:ASN:HD22	1:A:597:ASN:C	2.18	0.46
1:B:314:GLU:HB3	1:B:359:THR:HG22	1.97	0.46
1:B:597:ASN:HD22	1:B:597:ASN:C	2.18	0.46
1:A:90:TRP:CZ2	1:A:104:GLY:HA2	2.51	0.45
1:B:315:ILE:HD11	1:B:358:LEU:HD23	1.98	0.45
1:B:715:ASN:O	1:B:719:ILE:HD12	2.16	0.45
1:B:304:LEU:HD13	1:B:323:LEU:HA	1.99	0.45
1:A:459:TRP:HB2	1:A:613:ASN:HB3	1.99	0.45
1:B:68:LEU:HD22	1:B:687:LEU:HD13	2.00	0.44
1:A:303:THR:H	1:A:306:GLN:HE21	1.64	0.44
1:A:270:LEU:HB2	5:A:1264:HOH:O	2.18	0.44
1:B:90:TRP:CZ2	1:B:104:GLY:HA2	2.52	0.43
1:B:717:ARG:O	1:B:721:THR:HG23	2.19	0.43
1:B:464:THR:HG22	1:B:606:TRP:HA	2.01	0.42
1:B:248:MET:HG2	1:B:372:TRP:CE2	2.54	0.42
1:B:304:LEU:HA	1:B:307:ILE:HD12	2.01	0.42
1:A:248:MET:HG2	1:A:372:TRP:CE2	2.55	0.42
1:B:490:ASN:HB2	5:B:1145:HOH:O	2.19	0.42
1:A:109:LEU:HD11	1:A:562:PRO:HD2	2.02	0.41
1:B:184:GLU:HG3	1:B:320:PHE:CE1	2.56	0.41
1:A:63:LYS:HD2	1:B:69:ILE:CG2	2.50	0.41
1:B:347:ALA:O	1:B:351:LEU:HG	2.20	0.41
1:A:312:SER:O	1:A:355:LYS:HG3	2.20	0.41
1:A:643:THR:HA	1:A:710:VAL:O	2.21	0.41
1:B:129:ILE:HD11	1:B:492:LEU:HD23	2.02	0.40
1:A:717:ARG:O	1:A:721:THR:HG23	2.21	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	696/698 (100%)	677 (97%)	19 (3%)	0	100	100
1	B	694/698 (99%)	672 (97%)	22 (3%)	0	100	100
All	All	1390/1396 (100%)	1349 (97%)	41 (3%)	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 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	607/607 (100%)	578 (95%)	29 (5%)	31	26
1	B	605/607 (100%)	574 (95%)	31 (5%)	29	23
All	All	1212/1214 (100%)	1152 (95%)	60 (5%)	30	24

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	91	LEU
1	A	154	GLU
1	A	156	LEU
1	A	160	LEU
1	A	171	GLU
1	A	175	GLN
1	A	189	GLN
1	A	197	LYS
1	A	260	ARG
1	A	274	LYS
1	A	278	LEU
1	A	298	LEU
1	A	314	GLU
1	A	318	LYS
1	A	333	VAL
1	A	355	LYS
1	A	368	ASN
1	A	434	GLU

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Mol	Chain	Res	Type
1	A	483	ASP
1	A	497	LEU
1	A	498	GLU
1	A	519	SER
1	A	579	MET
1	A	597	ASN
1	A	608	GLN
1	A	667	LYS
1	A	670	GLU
1	A	687	LEU
1	A	748	VAL
1	B	91	LEU
1	B	151	ARG
1	B	154	GLU
1	B	156	LEU
1	B	160	LEU
1	B	171	GLU
1	B	175	GLN
1	B	182	THR
1	B	189	GLN
1	B	197	LYS
1	B	260	ARG
1	B	278	LEU
1	B	298	LEU
1	B	333	VAL
1	B	338	THR
1	B	368	ASN
1	B	394	ARG
1	B	434	GLU
1	B	442	LEU
1	B	456	ASP
1	B	483	ASP
1	B	497	LEU
1	B	498	GLU
1	B	597	ASN
1	B	608	GLN
1	B	629	SER
1	B	667	LYS
1	B	687	LEU
1	B	743	GLU
1	B	747	ARG
1	B	748	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	105	ASN
1	A	257	GLN
1	A	306	GLN
1	A	368	ASN
1	A	490	ASN
1	A	509	ASN
1	A	550	ASN
1	A	597	ASN
1	A	619	GLN
1	A	656	GLN
1	A	662	GLN
1	A	688	ASN
1	B	105	ASN
1	B	213	ASN
1	B	257	GLN
1	B	368	ASN
1	B	452	GLN
1	B	509	ASN
1	B	550	ASN
1	B	551	GLN
1	B	597	ASN
1	B	619	GLN
1	B	656	GLN
1	B	662	GLN
1	B	688	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 carbohydrates in this entry.

5.6 Ligand geometry

Of 14 ligands modelled in this entry, 2 are monoatomic - leaving 12 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$
2	NAG	A	801	1	14,14,15	0.29	0	15,19,21	0.52	0
2	NAG	A	802	1	14,14,15	0.27	0	15,19,21	0.76	1 (6%)
2	NAG	A	803	1,2	14,14,15	0.21	0	15,19,21	0.51	0
2	NAG	A	804	2	14,14,15	0.29	0	15,19,21	0.77	1 (6%)
2	NAG	A	805	1	14,14,15	0.29	0	15,19,21	0.51	0
4	6LD	A	807	3	23,29,29	1.20	1 (4%)	30,38,38	1.23	3 (10%)
2	NAG	B	801	1	14,14,15	0.29	0	15,19,21	0.72	1 (6%)
2	NAG	B	802	1	14,14,15	0.28	0	15,19,21	0.72	1 (6%)
2	NAG	B	803	1,2	14,14,15	0.28	0	15,19,21	0.45	0
2	NAG	B	804	2	14,14,15	0.27	0	15,19,21	0.85	1 (6%)
2	NAG	B	805	1	14,14,15	0.32	0	15,19,21	0.43	0
4	6LD	B	807	3	23,29,29	1.06	0	30,38,38	1.18	3 (10%)

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
2	NAG	A	801	1	-	0/6/23/26	0/1/1/1
2	NAG	A	802	1	-	0/6/23/26	0/1/1/1
2	NAG	A	803	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	804	2	-	0/6/23/26	0/1/1/1
2	NAG	A	805	1	-	0/6/23/26	0/1/1/1
4	6LD	A	807	3	-	0/19/25/25	0/2/2/2
2	NAG	B	801	1	-	0/6/23/26	0/1/1/1
2	NAG	B	802	1	-	0/6/23/26	0/1/1/1
2	NAG	B	803	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	804	2	-	0/6/23/26	0/1/1/1
2	NAG	B	805	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	6LD	B	807	3	-	0/19/25/25	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	807	6LD	C10-C6	2.05	1.42	1.38

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	807	6LD	C11-C13-C14	-3.67	106.49	114.36
4	B	807	6LD	O20-C17-C19	-3.34	116.17	121.97
4	B	807	6LD	C11-C13-C14	-2.97	107.99	114.36
4	A	807	6LD	C16-C14-N15	-2.68	103.04	110.58
4	A	807	6LD	C19-C23-C26	2.06	116.79	112.78
2	B	802	NAG	C1-O5-C5	2.42	115.69	112.14
2	B	801	NAG	C1-O5-C5	2.45	115.74	112.14
4	B	807	6LD	C19-C17-N15	2.47	120.00	115.85
2	A	804	NAG	C1-O5-C5	2.53	115.87	112.14
2	A	802	NAG	C1-O5-C5	2.64	116.03	112.14
2	B	804	NAG	C1-O5-C5	2.75	116.18	112.14

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	696/698 (99%)	-0.07	13 (1%)	70 70	19, 34, 60, 83	0
1	B	696/698 (99%)	0.37	34 (4%)	33 35	22, 45, 73, 88	0
All	All	1392/1396 (99%)	0.15	47 (3%)	49 50	19, 40, 70, 88	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	333	VAL	5.7
1	B	323	LEU	5.2
1	B	317	GLY	4.1
1	B	600	GLY	3.9
1	B	179	ALA	3.7
1	B	80	THR	3.4
1	A	434	GLU	3.3
1	B	260	ARG	3.2
1	A	309	ASN	3.1
1	B	319	PRO	3.1
1	B	297	LEU	3.1
1	B	175	GLN	3.0
1	B	212	VAL	3.0
1	B	739	TYR	3.0
1	B	318	LYS	2.9
1	B	180	SER	2.9
1	B	748	VAL	2.9
1	B	736	LYS	2.9
1	B	666	LYS	2.8
1	B	309	ASN	2.7
1	B	749	TRP	2.6
1	B	623	TYR	2.6
1	B	607	THR	2.6
1	B	620	CYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	263	ILE	2.5
1	B	462	ALA	2.5
1	B	737	ASN	2.5
1	B	531	LYS	2.4
1	B	335	ILE	2.4
1	B	735	ARG	2.4
1	A	653	GLY	2.4
1	B	467	ARG	2.4
1	A	55	ILE	2.3
1	A	654	LEU	2.3
1	B	455	ASP	2.3
1	A	200	ILE	2.3
1	A	531	LYS	2.3
1	A	180	SER	2.2
1	A	652	GLY	2.2
1	A	325	PHE	2.2
1	B	340	GLU	2.2
1	B	498	GLU	2.2
1	B	654	LEU	2.2
1	A	175	GLN	2.1
1	B	466	LYS	2.1
1	B	337	ILE	2.0
1	A	336	SER	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 carbohydrates in this entry.

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
2	NAG	B	803	14/15	0.75	0.21	1.22	73,82,87,92	0
2	NAG	B	802	14/15	0.86	0.28	0.96	62,65,79,79	0
2	NAG	A	802	14/15	0.94	0.15	0.81	51,53,60,61	0
4	6LD	A	807	28/28	0.95	0.12	-0.04	17,22,34,38	0
4	6LD	B	807	28/28	0.95	0.12	-0.64	18,27,35,39	0
2	NAG	A	803	14/15	0.96	0.09	-0.94	27,34,38,41	0
3	ZN	A	806	1/1	1.00	0.07	-1.32	24,24,24,24	0
3	ZN	B	806	1/1	0.99	0.07	-2.19	31,31,31,31	0
2	NAG	B	804	14/15	0.78	0.25	-	95,97,100,103	0
2	NAG	A	804	14/15	0.90	0.13	-	43,48,53,54	0
2	NAG	A	805	14/15	0.86	0.24	-	67,73,78,79	0
2	NAG	B	805	14/15	0.82	0.24	-	79,80,81,82	0
2	NAG	B	801	14/15	0.80	0.29	-	64,74,80,83	0
2	NAG	A	801	14/15	0.92	0.17	-	49,55,57,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.