



Full wwPDB X-ray Structure Validation Report

Nov 27, 2014 – 04:58 PM EST

PDB ID : 4P8Q
Title : Crystal Structure of Human Insulin Regulated Aminopeptidase with Alanine
in Active Site
Authors : Hermans, S.J.; Ascher, D.B.; Hancock, N.C.; Holien, J.K.; Michell, B.; Morton,
C.J.; Parker, M.W.
Deposited on : 2014-03-31
Resolution : 3.02 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

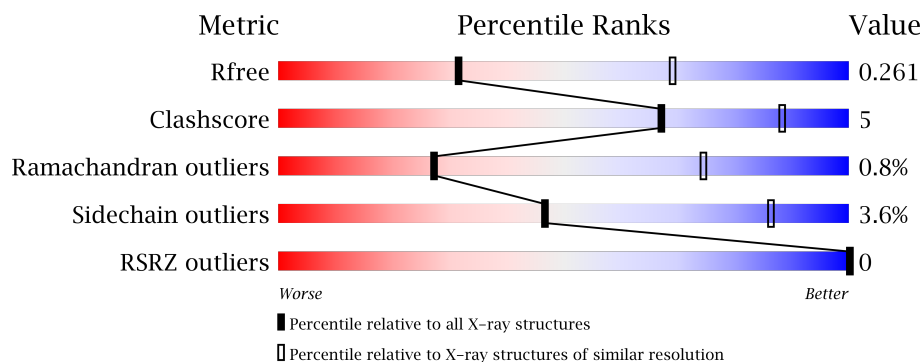
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1439
EDS : stable24195
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.1.3
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable24195

1 Overall quality at a glance



The reported resolution of this entry is 3.02 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}	66092	1332 (3.04-3.00)
Clashscore	79885	1732 (3.04-3.00)
Ramachandran outliers	78287	1669 (3.04-3.00)
Sidechain outliers	78261	1672 (3.04-3.00)
RSRZ outliers	66119	1333 (3.04-3.00)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	872	
1	B	872	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
4	NAG	A	1104	-	X
4	NAG	A	1106	-	X
4	NAG	A	1109	-	X
4	NAG	B	1104	-	X
4	NAG	B	1110	-	X
4	NAG	B	1111	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
4	NAG	B	1112	-	X
5	UNL	A	1112	-	X
5	UNL	B	1113	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 14164 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Leucyl-cystinyl aminopeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	860	Total	C	N	O	S	0	3	0
			6965	4505	1127	1304	29			
1	B	848	Total	C	N	O	S	0	1	0
			6838	4432	1099	1282	25			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	154	SER	-	expression tag	UNP Q9UIQ6
B	154	SER	-	expression tag	UNP Q9UIQ6

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

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

- Molecule 3 is a polymer of unknown type called SUGAR (N-ACETYL-D-GLUCOSAMINE).

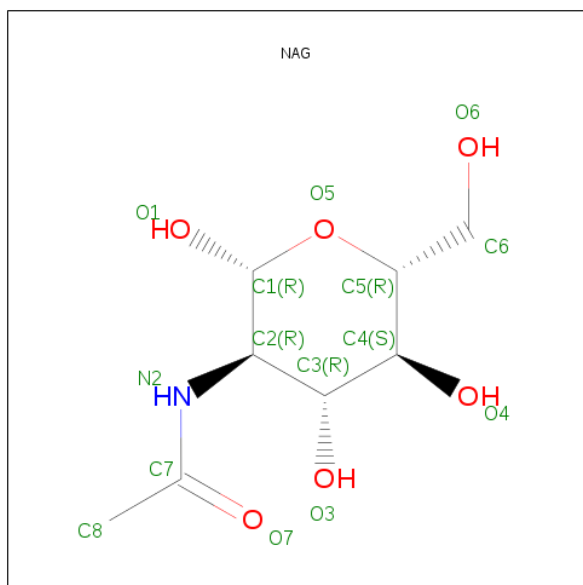
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	2	Total	C	N	O	0	0
			28	16	2	10		
3	A	2	Total	C	N	O	0	0
			28	16	2	10		
3	B	2	Total	C	N	O	0	0
			28	16	2	10		
3	B	2	Total	C	N	O	0	0
			28	16	2	10		

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

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

- Molecule 5 is UNKNOWN LIGAND (three-letter code: UNL) (formula:).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			5	3	1	1		
5	A	1	Total	C	N	O	0	0
			5	3	1	1		

- Molecule 6 is water.

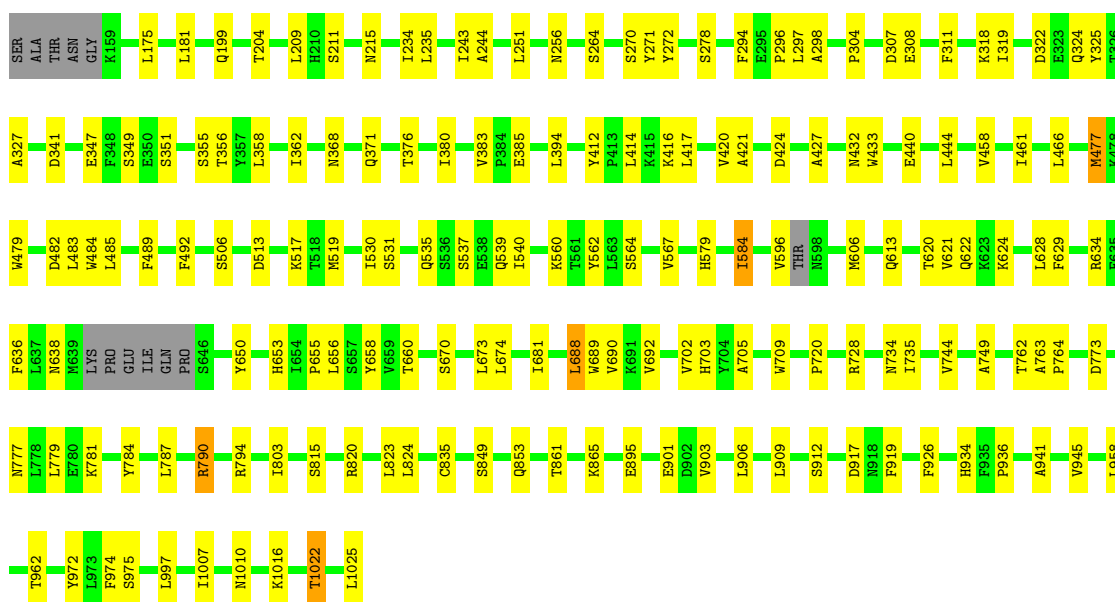
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	45	Total	O	0	0
			45	45		
6	B	10	Total	O	0	0
			10	10		

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.

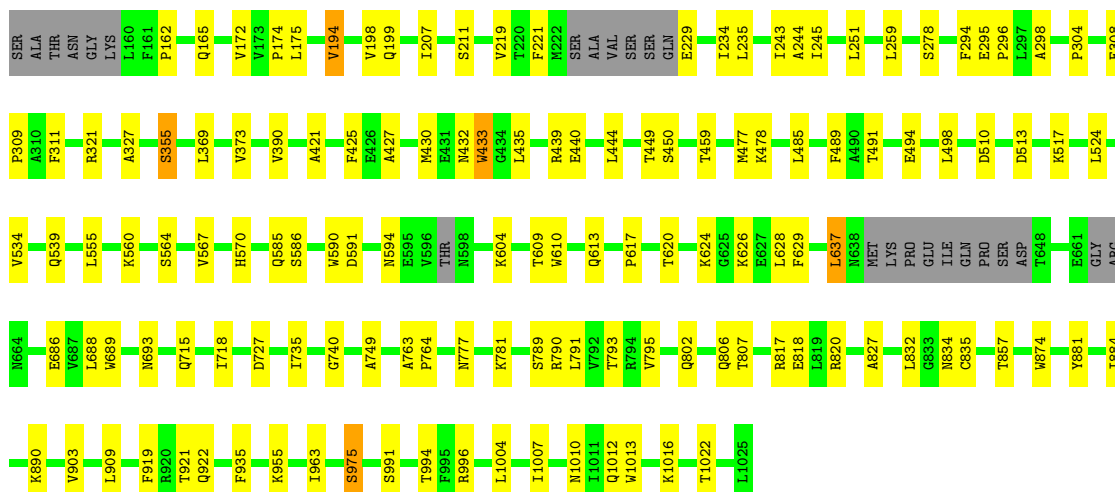
• Molecule 1: Leucyl-cystinyl aminopeptidase

Chain A:



• Molecule 1: Leucyl-cystinyl aminopeptidase

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	68.32Å 256.05Å 71.13Å 90.00° 115.12° 90.00°	Depositor
Resolution (Å)	48.42 – 3.02 48.42 – 3.02	Depositor EDS
% Data completeness (in resolution range)	99.1 (48.42-3.02) 99.4 (48.42-3.02)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 3.01Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.190 , 0.250 0.200 , 0.261	Depositor DCC
R_{free} test set	2157 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	66.1	Xtriage
Anisotropy	0.150	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 49.8	EDS
Estimated twinning fraction	0.046 for l,-k,h	Xtriage
L-test for twinning	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 42833 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14164	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, UNL, 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	0.46	0/7144	0.72	0/9690
1	B	0.44	0/7009	0.69	0/9517
All	All	0.45	0/14153	0.70	0/19207

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6965	0	6824	83	0
1	B	6838	0	6660	57	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	56	0	50	0	0
3	B	84	0	75	0	0
4	A	84	0	78	1	0
4	B	70	0	65	0	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	45	0	0	0	0
6	B	10	0	0	0	0
All	All	14164	0	13752	138	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

All (138) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:307:ASP:HA	1:A:356:THR:HG21	1.63	0.81
1:A:936:PRO:HA	1:B:903:VAL:HG21	1.64	0.78
1:A:579:HIS:CG	1:A:584:ILE:HD11	2.23	0.74
1:A:564:SER:HB3	1:A:567:VAL:HG23	1.69	0.73
1:B:689:TRP:CD1	1:B:715:GLN:HG3	2.26	0.69
1:B:425:PHE:HB3	1:B:922:GLN:HE22	1.59	0.67
1:A:975:SER:HB3	1:A:1010:ASN:HB3	1.76	0.66
1:A:803:ILE:HG13	1:A:823:LEU:HD22	1.78	0.66
1:A:621:VAL:HG21	1:A:692:VAL:HG21	1.79	0.65
1:A:294:PHE:HA	1:A:298:ALA:HB3	1.76	0.65
1:A:535:GLN:HE21	1:A:539:GLN:HE22	1.45	0.64
1:B:421:ALA:HB1	1:B:440:GLU:HA	1.80	0.64
1:A:204:THR:HG23	1:A:251:LEU:HD12	1.82	0.62
1:B:427:ALA:HB3	1:B:439:ARG:HG2	1.83	0.61
1:A:181:LEU:HB2	1:A:319:ILE:HG22	1.83	0.61
1:B:235:LEU:HB2	1:B:244:ALA:HB3	1.83	0.60
1:A:318:LYS:HB3	1:A:347:GLU:HG3	1.83	0.60
1:A:421:ALA:HB1	1:A:440:GLU:HA	1.82	0.60
1:B:219:VAL:HG11	1:B:234:ILE:HG12	1.83	0.60
1:A:861:THR:O	1:A:865:LYS:HG3	2.02	0.60
1:B:432:ASN:HB2	1:B:435:LEU:O	2.02	0.59
1:B:308:GLU:HB2	1:B:311:PHE:HD2	1.67	0.59
1:B:827:ALA:HA	1:B:832:LEU:HD12	1.83	0.59
1:A:362:ILE:CD1	1:A:420:VAL:HG11	2.34	0.56
1:B:817:ARG:HB3	1:B:820:ARG:HH21	1.71	0.56
1:A:703:HIS:HE1	1:A:744:VAL:HG23	1.71	0.56
1:A:895:GLU:HB2	1:A:926:PHE:HZ	1.71	0.56
1:A:613:GLN:OE1	1:A:650:TYR:HA	2.05	0.55
1:B:626:LYS:HG3	1:B:686:GLU:HG2	1.88	0.55
1:B:534:VAL:HG13	1:B:539:GLN:HB3	1.89	0.55
1:A:211:SER:HB3	1:A:243:ILE:HG12	1.89	0.54
1:B:975:SER:HB3	1:B:1010:ASN:HB3	1.88	0.54
1:A:477[B]:MET:HE1	1:A:584:ILE:HG22	1.89	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:369:LEU:HD22	1:B:390:VAL:HG23	1.90	0.53
1:A:606:MET:HG3	1:A:653:HIS:HB2	1.90	0.53
1:A:720:PRO:HB2	1:A:728:ARG:HD3	1.90	0.53
1:A:492:PHE:HZ	1:A:560:LYS:HD3	1.74	0.53
1:B:294:PHE:HA	1:B:298:ALA:HB3	1.91	0.53
1:A:308:GLU:HB2	1:A:311:PHE:HD2	1.73	0.52
1:A:622:GLN:HG3	1:A:705:ALA:HB2	1.90	0.52
1:A:562:TYR:CD1	1:A:655:PRO:HB3	2.44	0.52
1:B:440:GLU:HG2	1:B:444:LEU:HD11	1.90	0.52
1:A:735:ILE:HG12	1:A:749:ALA:HA	1.91	0.52
1:A:688:LEU:HD12	1:A:689:TRP:HD1	1.73	0.52
1:A:270:SER:OG	1:A:271:TYR:N	2.39	0.52
1:B:321:ARG:HG2	1:B:327:ALA:HB2	1.92	0.51
1:A:656:LEU:HD11	1:A:674:LEU:HB2	1.93	0.51
1:A:941:ALA:O	1:A:945:VAL:HG23	2.10	0.51
1:B:449:THR:O	1:B:857:THR:HG21	2.10	0.51
1:A:934[A]:HIS:HD2	1:A:936:PRO:HD2	1.75	0.51
1:B:309:PRO:HA	1:B:355:SER:HB3	1.93	0.51
1:A:355:SER:HB2	1:A:358:LEU:HD12	1.92	0.51
1:A:934[A]:HIS:CD2	1:A:936:PRO:HD2	2.45	0.51
1:A:958:LEU:HG	1:A:997:LEU:HD11	1.93	0.51
1:B:740:GLY:HA2	1:B:1013:TRP:CD1	2.46	0.50
1:A:215:ASN:OD1	4:A:1104:NAG:H2	2.11	0.50
1:B:777:ASN:O	1:B:781:LYS:HG2	2.12	0.50
1:B:478:LYS:HD2	1:B:585:GLN:HE21	1.76	0.50
1:B:564:SER:HB3	1:B:567:VAL:HG23	1.94	0.49
1:A:901:GLU:HG2	1:A:936:PRO:HG2	1.94	0.49
1:A:417:LEU:HD21	1:A:466:LEU:HD11	1.95	0.49
1:B:221:PHE:HE2	1:B:251:LEU:HD21	1.78	0.49
1:A:702:VAL:H	1:A:734:ASN:ND2	2.11	0.48
1:B:610:TRP:HZ3	1:B:617:PRO:HD3	1.78	0.48
1:B:789:SER:O	1:B:793:THR:HG23	2.13	0.48
1:A:628:LEU:HB3	1:A:681:ILE:HB	1.94	0.48
1:B:921:THR:HG21	1:B:955:LYS:HD3	1.96	0.48
1:A:634:ARG:HD3	1:A:636:PHE:HB2	1.95	0.48
1:A:537:SER:HA	1:A:540:ILE:HD12	1.96	0.48
1:A:513:ASP:O	1:A:517:LYS:HG2	2.14	0.47
1:A:371:GLN:HB2	1:A:394:LEU:HD21	1.96	0.47
1:A:380:ILE:HG12	1:A:394:LEU:HB2	1.97	0.47
1:B:1004:LEU:HA	1:B:1007:ILE:HD12	1.96	0.47
1:B:624:LYS:HB2	1:B:629:PHE:HE2	1.79	0.46
1:A:777:ASN:O	1:A:781:LYS:HG2	2.15	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:881:TYR:O	1:B:890:LYS:HE2	2.15	0.46
1:B:524:LEU:HA	1:B:637:LEU:HD11	1.96	0.46
1:A:362:ILE:HD13	1:A:420:VAL:HG11	1.97	0.46
1:A:794:ARG:HH11	1:A:1025:LEU:HA	1.80	0.46
1:A:272:TYR:CZ	1:A:298:ALA:HB2	2.51	0.46
1:A:906:LEU:HA	1:A:909:LEU:HD12	1.98	0.46
1:A:849:SER:OG	1:A:853:GLN:HB2	2.16	0.45
1:A:790:ARG:HH22	1:A:1022:THR:HA	1.82	0.45
1:A:477[B]:MET:HE2	1:A:482:ASP:HB3	1.99	0.45
1:B:211:SER:HB3	1:B:243:ILE:HG12	1.97	0.45
1:B:245:ILE:HD13	1:B:259:LEU:HD21	1.98	0.45
1:A:688:LEU:HD12	1:A:689:TRP:CD1	2.51	0.45
1:B:735:ILE:HG12	1:B:749:ALA:HA	1.98	0.45
1:B:807:THR:O	1:B:820:ARG:HD3	2.17	0.45
1:A:412:TYR:CE2	1:A:414:LEU:HB2	2.53	0.44
1:B:513:ASP:O	1:B:517:LYS:HG2	2.16	0.44
1:A:762:THR:HG22	1:A:815:SER:OG	2.16	0.44
1:A:297:LEU:HD11	1:A:540:ILE:HD13	1.98	0.44
1:B:174:PRO:HA	1:B:198:VAL:HG12	1.99	0.44
1:B:874:TRP:HZ2	1:B:909:LEU:HD11	1.83	0.44
1:A:440:GLU:HG2	1:A:444:LEU:HD11	1.99	0.44
1:A:820:ARG:HG3	1:A:824:LEU:HD12	1.99	0.43
1:B:459:THR:HG22	1:B:498:LEU:HD11	2.01	0.43
1:A:477[B]:MET:SD	1:A:584:ILE:HG22	2.58	0.43
1:A:624:LYS:HB2	1:A:629:PHE:HE2	1.83	0.43
1:B:791:LEU:O	1:B:795:VAL:HG23	2.18	0.43
1:A:319:ILE:HD11	1:A:327:ALA:HB1	2.01	0.43
1:B:295:GLU:HA	1:B:296:PRO:HA	1.84	0.43
1:A:211:SER:HB2	1:A:304:PRO:HB3	2.01	0.42
1:A:479:TRP:CE3	1:A:479:TRP:HA	2.54	0.42
1:A:620:THR:HG23	1:A:703:HIS:HD2	1.83	0.42
1:A:763:ALA:HB3	1:A:764:PRO:HD3	2.01	0.42
1:B:591:ASP:HA	1:B:594:ASN:HD22	1.83	0.42
1:B:604:LYS:HD3	1:B:604:LYS:HA	1.80	0.42
1:A:380:ILE:CG1	1:A:394:LEU:HB2	2.50	0.42
1:A:383:VAL:HG22	1:A:385:GLU:HG2	2.01	0.42
1:B:763:ALA:HB3	1:B:764:PRO:HD3	2.01	0.42
1:B:1012:GLN:HG2	1:B:1016:LYS:HE3	2.01	0.42
1:B:194:VAL:HG21	1:B:304:PRO:HD2	2.01	0.42
1:A:424:ASP:HB3	1:A:427:ALA:HB2	2.02	0.42
1:B:802:GLN:O	1:B:806:GLN:HG2	2.20	0.42
1:A:458:VAL:HA	1:A:461:ILE:HG22	2.02	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:484:TRP:CE3	1:A:530:ILE:HD12	2.55	0.42
1:A:779:LEU:HD13	1:A:787:LEU:HB3	2.02	0.42
1:A:974:PHE:HB2	1:A:1007:ILE:HG12	2.02	0.41
1:B:609:THR:O	1:B:613:GLN:HG2	2.21	0.41
1:B:172:VAL:HG21	1:B:207:ILE:HG23	2.02	0.41
1:B:485:LEU:HD22	1:B:586:SER:HA	2.02	0.41
1:B:991:SER:HB2	1:B:994:THR:H	1.85	0.41
1:A:579:HIS:CD2	1:A:584:ILE:HD11	2.55	0.41
1:A:660:THR:HG22	1:A:690:VAL:HA	2.03	0.41
1:A:235:LEU:HB2	1:A:244:ALA:HB3	2.01	0.41
1:A:322:ASP:HB2	1:A:325:TYR:CD2	2.56	0.41
1:A:912:SER:HG	1:A:919:PHE:HD2	1.68	0.41
1:A:175:LEU:HD11	1:A:199:GLN:HB2	2.01	0.41
1:A:477[B]:MET:CE	1:A:584:ILE:HG22	2.51	0.41
1:B:590:TRP:HB3	1:B:604:LYS:CB	2.51	0.41
1:B:491:THR:O	1:B:494:GLU:HB3	2.21	0.40
1:A:903:VAL:HG12	1:B:935:PHE:CE1	2.56	0.40
1:B:295:GLU:HB2	1:B:430:MET:SD	2.61	0.40
1:A:658:TYR:CZ	1:A:670:SER:HB3	2.57	0.40
1:B:175:LEU:HD11	1:B:199:GLN:HB2	2.04	0.40
1:A:322:ASP:HB3	1:A:324:GLN:OE1	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	857/872 (98%)	794 (93%)	57 (7%)	6 (1%)	30	77
1	B	839/872 (96%)	770 (92%)	61 (7%)	8 (1%)	22	69
All	All	1696/1744 (97%)	1564 (92%)	118 (7%)	14 (1%)	27	74

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	835	CYS
1	A	638	ASN
1	A	972	TYR
1	B	433	TRP
1	B	693	ASN
1	B	835	CYS
1	A	784	TYR
1	A	917	ASP
1	B	162	PRO
1	B	450	SER
1	B	718	ILE
1	B	373	VAL
1	B	884	ILE
1	A	296	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	765/781 (98%)	734 (96%)	31 (4%)	41	83
1	B	746/781 (96%)	721 (97%)	25 (3%)	49	87
All	All	1511/1562 (97%)	1455 (96%)	56 (4%)	47	86

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	209	LEU
1	A	234	ILE
1	A	256	ASN
1	A	264	SER
1	A	278	SER
1	A	341	ASP
1	A	349	SER
1	A	351	SER
1	A	368	ASN
1	A	376	THR
1	A	416	LYS
1	A	432	ASN

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Mol	Chain	Res	Type
1	A	433	TRP
1	A	477[A]	MET
1	A	477[B]	MET
1	A	483	LEU
1	A	485	LEU
1	A	489	PHE
1	A	506	SER
1	A	519	MET
1	A	531	SER
1	A	584	ILE
1	A	596	VAL
1	A	673	LEU
1	A	688	LEU
1	A	709	TRP
1	A	773	ASP
1	A	790	ARG
1	A	962	THR
1	A	1016	LYS
1	A	1022	THR
1	B	165	GLN
1	B	194	VAL
1	B	229	GLU
1	B	278	SER
1	B	355	SER
1	B	433	TRP
1	B	477	MET
1	B	489	PHE
1	B	510	ASP
1	B	555	LEU
1	B	560	LYS
1	B	570	HIS
1	B	620	THR
1	B	628	LEU
1	B	637	LEU
1	B	688	LEU
1	B	727	ASP
1	B	790	ARG
1	B	818	GLU
1	B	834	ASN
1	B	919	PHE
1	B	963	ILE
1	B	975	SER

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Mol	Chain	Res	Type
1	B	996	ARG
1	B	1022	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	486	ASN
1	A	535	GLN
1	A	733	ASN
1	A	734	ASN
1	B	469	GLN
1	B	585	GLN
1	B	771	GLN
1	B	922	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

10 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	1102	1,3	12,14,15	0.37	0	15,19,21	0.51	0
3	NAG	A	1103	3	12,14,15	0.34	0	15,19,21	0.36	0
3	NAG	A	1107	1,3	12,14,15	0.34	0	15,19,21	0.37	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	A	1108	3	12,14,15	0.35	0	15,19,21	0.38	0
3	NAG	B	1102	1,3	12,14,15	0.36	0	15,19,21	0.41	0
3	NAG	B	1103	3	12,14,15	0.36	0	15,19,21	0.41	0
3	NAG	B	1105	1,3	12,14,15	0.35	0	15,19,21	0.42	0
3	NAG	B	1106	3	12,14,15	0.32	0	15,19,21	0.31	0
3	NAG	B	1108	1,3	12,14,15	0.35	0	15,19,21	0.36	0
3	NAG	B	1109	3	12,14,15	0.40	0	15,19,21	0.39	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	1102	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	1103	3	-	0/6/23/26	0/1/1/1
3	NAG	A	1107	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	1108	3	-	0/6/23/26	0/1/1/1
3	NAG	B	1102	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	1103	3	-	0/6/23/26	0/1/1/1
3	NAG	B	1105	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	1106	3	-	0/6/23/26	0/1/1/1
3	NAG	B	1108	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	1109	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.6 Ligand geometry ⓘ

Of 15 ligands modelled in this entry, 2 are unknown and 2 are monoatomic - leaving 11 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	1104	1	12,14,15	0.28	0	15,19,21	0.50	0
4	NAG	A	1105	1	12,14,15	0.37	0	15,19,21	0.52	0
4	NAG	A	1106	1	12,14,15	0.34	0	15,19,21	0.40	0
4	NAG	A	1109	1	12,14,15	0.35	0	15,19,21	0.61	0
4	NAG	A	1110	1	12,14,15	0.26	0	15,19,21	0.60	0
4	NAG	A	1111	1	12,14,15	0.32	0	15,19,21	0.28	0
4	NAG	B	1104	1	12,14,15	0.37	0	15,19,21	0.48	0
4	NAG	B	1107	1	12,14,15	0.33	0	15,19,21	0.36	0
4	NAG	B	1110	1	12,14,15	0.33	0	15,19,21	0.39	0
4	NAG	B	1111	1	12,14,15	0.34	0	15,19,21	0.36	0
4	NAG	B	1112	1	12,14,15	0.43	0	15,19,21	0.59	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	1104	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1105	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1106	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1109	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1110	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1111	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1104	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1107	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1110	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1111	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1112	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	860/872 (98%)	-0.24	0 100 100	29, 60, 93, 124	0
1	B	848/872 (97%)	-0.14	0 100 100	35, 71, 100, 126	0
All	All	1708/1744 (97%)	-0.19	0 100 100	29, 66, 97, 126	0

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	NAG	A	1103	14/15	0.37	37.86	122,123,124,125	0
3	NAG	A	1107	14/15	0.35	6.05	119,127,132,134	0
3	NAG	B	1102	14/15	0.44	4.77	133,135,138,139	0
3	NAG	B	1106	14/15	0.36	1.45	106,108,109,109	0
3	NAG	A	1102	14/15	0.28	1.42	107,113,117,120	0
3	NAG	B	1103	14/15	0.44	1.26	139,140,140,140	0
3	NAG	B	1105	14/15	0.23	0.20	94,98,103,103	0
3	NAG	B	1108	14/15	0.18	-0.35	92,98,102,107	0
3	NAG	A	1108	14/15	0.48	-	133,138,139,139	0
3	NAG	B	1109	14/15	0.46	-	109,115,116,117	0

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	NAG	B	1110	14/15	0.28	41.40	119,121,122,123	0
4	NAG	A	1109	14/15	0.32	16.42	101,106,108,109	0
5	UNL	A	1112	5/-	0.61	15.52	53,59,80,82	5
5	UNL	B	1113	5/-	0.45	6.32	36,57,66,85	5
4	NAG	B	1111	14/15	0.47	4.22	112,113,114,114	0
4	NAG	B	1112	14/15	0.42	3.59	118,121,123,123	0
4	NAG	B	1104	14/15	0.34	2.91	124,127,130,131	0
4	NAG	A	1104	14/15	0.27	2.77	123,130,131,131	0
4	NAG	A	1106	14/15	0.26	2.51	110,112,114,115	0
4	NAG	A	1110	14/15	0.27	1.50	107,111,112,112	0
4	NAG	A	1105	14/15	0.31	1.44	110,116,118,118	0
2	ZN	A	1101	1/1	0.23	0.89	53,53,53,53	1
4	NAG	B	1107	14/15	0.22	0.70	89,95,98,98	0
4	NAG	A	1111	14/15	0.20	0.03	95,96,101,101	0
2	ZN	B	1101	1/1	0.20	-0.92	54,54,54,54	1

6.5 Other polymers ⓘ

There are no such residues in this entry.