Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 04:58 AM GMT

PDB ID	:	2OXE
Title	:	Structure of the Human Pancreatic Lipase-related Protein 2
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Deposited on	:	2007-02-20
Resolution	:	2.80 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

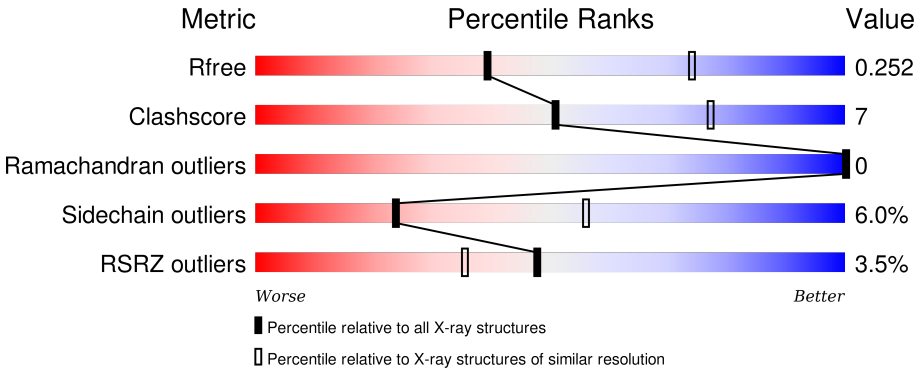
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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 <=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	466	4% 79% 12% • 7%
1	B	466	2% 76% 15% • 8%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	A	500	-	-	-	X
2	NAG	B	500	X	-	-	-
2	NAG	B	501	-	-	-	X

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 6886 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 Pancreatic lipase-related protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	435	Total	C	N	O	S	0	2	0
			3353	2118	561	653	21			
1	B	431	Total	C	N	O	S	0	2	0
			3328	2098	560	649	21			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	ALA	-	CLONING ARTIFACT	UNP P54317
A	17	ALA	-	CLONING ARTIFACT	UNP P54317
A	470	GLU	-	CLONING ARTIFACT	UNP P54317
A	471	PHE	-	CLONING ARTIFACT	UNP P54317
A	472	VAL	-	CLONING ARTIFACT	UNP P54317
A	473	GLU	-	CLONING ARTIFACT	UNP P54317
A	474	HIS	-	CLONING ARTIFACT	UNP P54317
A	475	HIS	-	CLONING ARTIFACT	UNP P54317
A	476	HIS	-	CLONING ARTIFACT	UNP P54317
A	477	HIS	-	CLONING ARTIFACT	UNP P54317
A	478	HIS	-	CLONING ARTIFACT	UNP P54317
A	479	HIS	-	CLONING ARTIFACT	UNP P54317
A	480	HIS	-	CLONING ARTIFACT	UNP P54317
A	481	HIS	-	CLONING ARTIFACT	UNP P54317
B	16	ALA	-	CLONING ARTIFACT	UNP P54317
B	17	ALA	-	CLONING ARTIFACT	UNP P54317
B	470	GLU	-	CLONING ARTIFACT	UNP P54317
B	471	PHE	-	CLONING ARTIFACT	UNP P54317
B	472	VAL	-	CLONING ARTIFACT	UNP P54317
B	473	GLU	-	CLONING ARTIFACT	UNP P54317
B	474	HIS	-	CLONING ARTIFACT	UNP P54317
B	475	HIS	-	CLONING ARTIFACT	UNP P54317
B	476	HIS	-	CLONING ARTIFACT	UNP P54317
B	477	HIS	-	CLONING ARTIFACT	UNP P54317
B	478	HIS	-	CLONING ARTIFACT	UNP P54317

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Chain	Residue	Modelled	Actual	Comment	Reference
B	479	HIS	-	CLONING ARTIFACT	UNP P54317
B	480	HIS	-	CLONING ARTIFACT	UNP P54317
B	481	HIS	-	CLONING ARTIFACT	UNP P54317

- Molecule 2 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	5	Total C N O 61 34 2 25	0	0
2	B	5	Total C N O 61 34 2 25	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	3	Total Cl 3 3	0	0
4	A	2	Total Cl 2 2	0	0

- Molecule 5 is water.

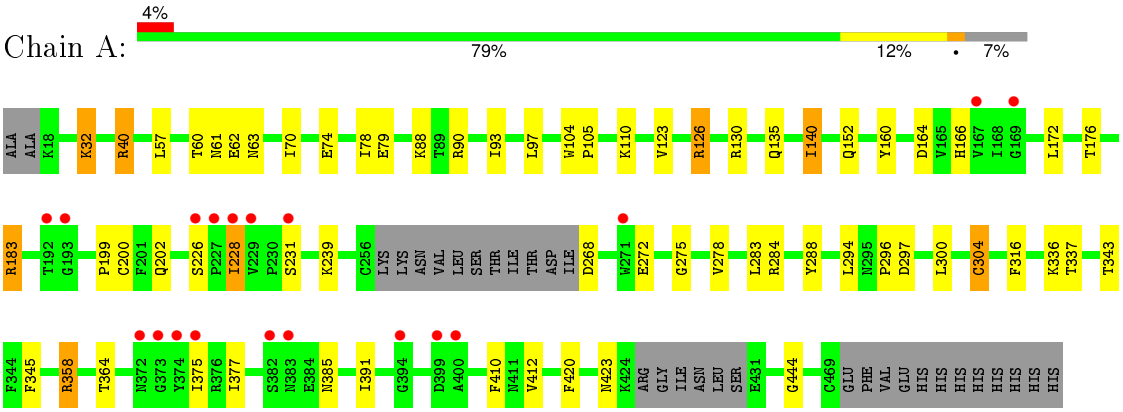
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	44	Total O 44 44	0	0
5	B	32	Total O 32 32	0	0

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.

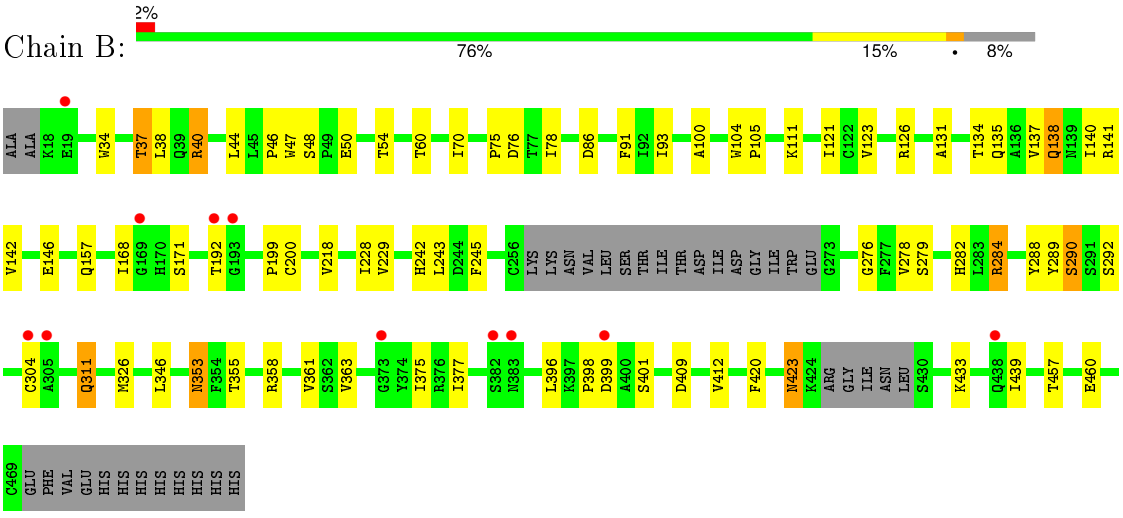
- Molecule 1: Pancreatic lipase-related protein 2

Chain A:



- Molecule 1: Pancreatic lipase-related protein 2

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α, β, γ	216.92Å 216.92Å 123.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.88 – 2.80 29.88 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.3 (29.88-2.80) 99.3 (29.88-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	3.48 (at 2.80Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.222 , 0.261 0.217 , 0.252	Depositor DCC
R_{free} test set	1811 reflections (5.28%)	DCC
Wilson B-factor (Å^2)	65.9	Xtriage
Anisotropy	0.121	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 54.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 36116 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	6886	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 14.21% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: CA, CL, NAG, MAN

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	0.40	0/3438	0.54	0/4667
1	B	0.40	0/3411	0.53	0/4628
All	All	0.40	0/6849	0.53	0/9295

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
2	B	1	0

There are no bond length outliers.

There are no bond angle outliers.

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	500	NAG	C1

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	3353	0	3108	45	0
1	B	3328	0	3095	43	0
2	A	61	0	52	0	0
2	B	61	0	52	2	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	2	0	0	0	0
4	B	3	0	0	0	0
5	A	44	0	0	0	0
5	B	32	0	0	0	0
All	All	6886	0	6307	90	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 (90) 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:140:ILE:HD11	1:A:172:LEU:HB3	1.27	1.15
1:A:358:ARG:HG2	1:A:358:ARG:HH11	1.34	0.91
1:A:183:ARG:CG	1:A:183:ARG:HH21	1.85	0.89
1:A:183:ARG:HH21	1:A:183:ARG:HG2	1.39	0.87
1:B:361:VAL:HG11	1:B:377:ILE:HD13	1.67	0.77
1:A:60:THR:HB	1:A:63:ASN:OD1	1.84	0.77
1:B:218:VAL:H	1:B:242:HIS:HD2	1.32	0.76
1:A:40:ARG:NH2	1:A:200:CYS:O	2.22	0.72
1:B:284:ARG:HG2	1:B:288:TYR:CZ	2.26	0.70
1:A:358:ARG:CG	1:A:358:ARG:HH11	2.05	0.70
1:A:140:ILE:CD1	1:A:172:LEU:HB3	2.16	0.69
1:A:60:THR:HG22	1:A:62:GLU:H	1.58	0.67
1:A:140:ILE:HG12	1:A:176:THR:OG1	1.97	0.65
1:A:410:PHE:CE2	1:A:412:VAL:HG12	2.37	0.60
1:A:140:ILE:HD12	1:A:172:LEU:HD22	1.85	0.58
1:A:239:LYS:HE2	1:A:343:THR:OG1	2.04	0.58
1:B:37:THR:HG23	1:B:40:ARG:HG2	1.85	0.58
1:B:218:VAL:H	1:B:242:HIS:CD2	2.18	0.56
1:A:284:ARG:HG2	1:A:288:TYR:CZ	2.41	0.55
1:B:218:VAL:N	1:B:242:HIS:HD2	2.03	0.55
1:B:228:ILE:HG22	1:B:229:VAL:HG23	1.87	0.55
1:A:183:ARG:NH2	1:A:183:ARG:HG2	2.12	0.55
1:B:46:PRO:HD3	1:B:138:GLN:HG3	1.88	0.55
1:B:34:TRP:CZ3	1:B:141:ARG:HD3	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:ARG:CG	1:A:183:ARG:NH2	2.56	0.54
1:B:377:ILE:HD11	1:B:439:ILE:HD13	1.90	0.54
1:B:37:THR:HG23	1:B:40:ARG:CG	2.37	0.53
1:B:142:VAL:O	1:B:146:GLU:HG3	2.09	0.52
1:A:97:LEU:HD23	1:A:130[A]:ARG:HG3	1.92	0.52
1:A:183:ARG:HH21	1:A:183:ARG:HG3	1.74	0.52
1:A:304:CYS:HB3	1:A:345:PHE:HD1	1.73	0.52
1:B:375:ILE:HD12	1:B:420:PHE:CE1	2.45	0.51
1:B:361:VAL:CG1	1:B:377:ILE:HD13	2.39	0.51
1:B:353:ASN:HB2	1:B:355:THR:HG23	1.92	0.51
1:B:423:ASN:HA	1:B:460:GLU:HG3	1.92	0.51
1:B:111:LYS:HE3	1:B:290:SER:HB3	1.92	0.51
1:B:34:TRP:CE3	1:B:141:ARG:HD3	2.46	0.50
1:B:423:ASN:N	1:B:423:ASN:HD22	2.10	0.50
1:B:104:TRP:CG	1:B:105:PRO:HD3	2.48	0.49
1:A:90:ARG:HG2	1:A:166:HIS:HB3	1.95	0.49
1:B:70:ILE:HB	1:B:78:ILE:HD13	1.94	0.49
1:A:377:ILE:HD12	1:A:391:ILE:HD13	1.95	0.49
1:A:126:ARG:O	1:A:130[A]:ARG:HD2	2.13	0.48
1:A:70:ILE:HB	1:A:78:ILE:HD13	1.94	0.48
1:B:171:SER:HB3	1:B:282:HIS:CE1	2.48	0.48
1:B:44:LEU:HD23	1:B:134:THR:HG22	1.95	0.48
1:B:398:PRO:O	1:B:399:ASP:HB2	2.14	0.48
1:A:140:ILE:CD1	1:A:172:LEU:HD22	2.44	0.47
1:A:60:THR:HG22	1:A:61:ASN:N	2.30	0.47
1:A:93:ILE:HG12	1:A:123:VAL:HB	1.97	0.47
1:B:86:ASP:N	1:B:86:ASP:OD1	2.45	0.47
1:B:137:VAL:O	1:B:140:ILE:HG12	2.15	0.47
1:A:375:ILE:HD12	1:A:420:PHE:CE1	2.50	0.47
1:B:47:TRP:CH2	1:B:131:ALA:HB2	2.50	0.46
2:B:500:NAG:H61	2:B:501:NAG:HN2	1.81	0.45
1:B:276:GLY:O	1:B:279:SER:HB3	2.16	0.45
1:A:336:LYS:HG3	1:A:337:THR:HG23	1.99	0.45
1:A:377:ILE:HD12	1:A:391:ILE:CD1	2.46	0.45
1:B:93:ILE:HG12	1:B:123:VAL:HB	1.98	0.45
1:A:377:ILE:HB	1:A:391:ILE:HD12	1.97	0.45
1:B:311:GLN:HA	1:B:311:GLN:HE21	1.82	0.45
1:B:48:SER:OG	1:B:50:GLU:HG2	2.17	0.45
1:A:160:TYR:CE2	1:A:164:ASP:HB2	2.52	0.45
1:A:275:GLY:O	1:A:278:VAL:HG12	2.18	0.44
1:B:100:ALA:HA	1:B:105:PRO:HG2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:363:VAL:O	1:B:401:SER:HA	2.16	0.44
1:B:75:PRO:HB3	1:B:157:GLN:HG2	1.98	0.44
1:B:168:ILE:HG23	1:B:192:THR:HB	1.99	0.44
2:B:500:NAG:H61	2:B:501:NAG:N2	2.32	0.44
1:A:60:THR:CG2	1:A:61:ASN:N	2.81	0.43
1:B:289:TYR:O	1:B:292:SER:HB3	2.18	0.43
1:A:375:ILE:HG23	1:A:420:PHE:CE1	2.54	0.43
1:A:278:VAL:HA	1:A:283:LEU:HD21	2.01	0.43
1:A:32:LYS:HG2	1:A:32:LYS:H	1.59	0.42
1:B:199:PRO:O	1:B:200:CYS:HB2	2.19	0.42
1:B:91:PHE:HA	1:B:121:ILE:O	2.20	0.42
1:A:358:ARG:NH1	1:A:358:ARG:CG	2.72	0.42
1:B:433:LYS:HG2	1:B:457:THR:O	2.21	0.41
1:A:104:TRP:CG	1:A:105:PRO:HD3	2.54	0.41
1:A:375:ILE:HD12	1:A:420:PHE:HE1	1.86	0.41
1:A:304:CYS:HB3	1:A:345:PHE:CD1	2.55	0.41
1:B:245:PHE:CG	1:B:326:MET:HG3	2.55	0.41
1:A:316:PHE:CE2	1:A:444:GLY:HA2	2.54	0.41
1:A:294:LEU:O	1:A:296:PRO:HD3	2.20	0.41
1:A:202:GLN:HG2	1:A:228:ILE:HD13	2.03	0.41
1:A:199:PRO:O	1:A:200:CYS:HB2	2.21	0.41
1:B:37:THR:CG2	1:B:40:ARG:HG3	2.51	0.40
1:B:375:ILE:HG12	1:B:396:LEU:HD22	2.03	0.40
1:A:297:ASP:HB2	1:A:300:LEU:HD21	2.03	0.40
1:B:37:THR:CG2	1:B:40:ARG:CG	2.99	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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	431/466 (92%)	403 (94%)	28 (6%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	427/466 (92%)	410 (96%)	17 (4%)	0	100 100
All	All	858/932 (92%)	813 (95%)	45 (5%)	0	100 100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	359/400 (90%)	337 (94%)	22 (6%)	23 55
1	B	358/400 (90%)	337 (94%)	21 (6%)	24 57
All	All	717/800 (90%)	674 (94%)	43 (6%)	24 56

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

Mol	Chain	Res	Type
1	A	32	LYS
1	A	40	ARG
1	A	57	LEU
1	A	74	GLU
1	A	79	GLU
1	A	88	LYS
1	A	110	LYS
1	A	126	ARG
1	A	135	GLN
1	A	140	ILE
1	A	152	GLN
1	A	183	ARG
1	A	226	SER
1	A	228	ILE
1	A	231	SER
1	A	268	ASP
1	A	272	GLU
1	A	304	CYS

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Mol	Chain	Res	Type
1	A	358	ARG
1	A	364	THR
1	A	385	ASN
1	A	423	ASN
1	B	37	THR
1	B	38	LEU
1	B	40	ARG
1	B	54	THR
1	B	60	THR
1	B	76	ASP
1	B	126	ARG
1	B	135	GLN
1	B	138	GLN
1	B	243	LEU
1	B	278	VAL
1	B	284	ARG
1	B	290	SER
1	B	304	CYS
1	B	311	GLN
1	B	346	LEU
1	B	353	ASN
1	B	358	ARG
1	B	409	ASP
1	B	412	VAL
1	B	423	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	152	GLN
1	A	423	ASN
1	B	152	GLN
1	B	242	HIS
1	B	311	GLN
1	B	385	ASN
1	B	423	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

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	$\#\|Z\| > 2$
2	NAG	A	500	1,2	14,14,15	0.53	0	15,19,21	2.35	4 (26%)
2	NAG	A	501	2	14,14,15	0.47	0	15,19,21	1.75	4 (26%)
2	MAN	A	502	2	11,11,12	0.93	1 (9%)	14,15,17	2.10	2 (14%)
2	MAN	A	503	2	11,11,12	0.58	0	14,15,17	1.35	2 (14%)
2	MAN	A	504	2	11,11,12	0.53	0	14,15,17	2.19	2 (14%)
2	NAG	B	500	1,2	14,14,15	0.73	0	15,19,21	1.04	1 (6%)
2	NAG	B	501	2	14,14,15	0.46	0	15,19,21	1.10	1 (6%)
2	MAN	B	502	2	11,11,12	0.48	0	14,15,17	2.33	5 (35%)
2	MAN	B	503	2	11,11,12	0.61	0	14,15,17	0.95	1 (7%)
2	MAN	B	504	2	11,11,12	0.68	0	14,15,17	1.04	2 (14%)

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	500	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	501	2	-	0/6/23/26	0/1/1/1
2	MAN	A	502	2	-	0/2/19/22	0/1/1/1
2	MAN	A	503	2	-	0/2/19/22	0/1/1/1
2	MAN	A	504	2	-	0/2/19/22	0/1/1/1
2	NAG	B	500	1,2	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	B	501	2	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MAN	B	502	2	-	0/2/19/22	1/1/1/1
2	MAN	B	503	2	-	0/2/19/22	0/1/1/1
2	MAN	B	504	2	-	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	502	MAN	C2-C3	2.38	1.55	1.52

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	501	NAG	C4-C3-C2	-3.03	106.52	111.23
2	B	502	MAN	C3-C4-C5	-3.00	104.97	110.20
2	A	500	NAG	C4-C3-C2	-2.85	106.81	111.23
2	B	504	MAN	O5-C1-C2	-2.12	107.42	110.86
2	B	504	MAN	C3-C4-C5	2.00	113.69	110.20
2	B	502	MAN	O5-C1-C2	2.05	114.17	110.86
2	A	501	NAG	O4-C4-C5	2.10	114.80	109.24
2	B	502	MAN	O5-C5-C6	2.23	112.18	107.35
2	B	503	MAN	C1-O5-C5	2.35	115.23	112.25
2	B	501	NAG	C1-O5-C5	2.36	115.24	112.25
2	A	500	NAG	C3-C2-N2	2.39	116.28	110.56
2	B	500	NAG	C2-N2-C7	2.61	126.39	123.04
2	A	504	MAN	C3-C4-C5	2.72	114.94	110.20
2	A	503	MAN	C3-C4-C5	2.87	115.19	110.20
2	A	500	NAG	C2-N2-C7	2.88	126.73	123.04
2	A	501	NAG	O4-C4-C3	3.20	117.54	110.34
2	A	503	MAN	C1-O5-C5	3.32	116.46	112.25
2	A	502	MAN	C2-C3-C4	3.57	117.11	111.04
2	A	501	NAG	C1-O5-C5	4.00	117.33	112.25
2	B	502	MAN	O3-C3-C4	4.33	120.08	110.34
2	B	502	MAN	C1-O5-C5	5.90	119.74	112.25
2	A	502	MAN	C1-C2-C3	6.48	117.21	109.54
2	A	504	MAN	C1-O5-C5	7.18	121.36	112.25
2	A	500	NAG	C1-O5-C5	7.21	121.39	112.25

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	500	NAG	C1

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	502	MAN	C1-C2-C3-C4-C5-O5

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	500	NAG	2	0
2	B	501	NAG	2	0

5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 7 are monoatomic - leaving 0 for Mogul analysis.

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.

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, 95^{th} 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	435/466 (93%)	0.12	19 (4%)	38	26	40, 64, 109, 158	0
1	B	431/466 (92%)	0.06	11 (2%)	59	47	40, 67, 100, 134	0
All	All	866/932 (92%)	0.09	30 (3%)	48	35	40, 65, 104, 158	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	394	GLY	5.5
1	B	305	ALA	4.4
1	A	228	ILE	4.2
1	A	229	VAL	4.2
1	A	383	ASN	4.0
1	A	372	ASN	4.0
1	B	169	GLY	3.8
1	A	192	THR	3.5
1	A	271	TRP	3.4
1	A	227	PRO	3.2
1	A	231	SER	3.1
1	A	399	ASP	3.1
1	A	167	VAL	3.1
1	B	399	ASP	2.8
1	B	304	CYS	2.7
1	A	374	TYR	2.7
1	A	382	SER	2.6
1	A	193	GLY	2.6
1	A	169	GLY	2.6
1	B	192	THR	2.5
1	A	226	SER	2.4
1	A	375	ILE	2.3
1	B	373	GLY	2.3
1	A	373	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	193	GLY	2.3
1	A	400	ALA	2.3
1	B	19	GLU	2.2
1	B	438	GLN	2.1
1	B	383	ASN	2.1
1	B	382	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)

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, 95^{th} 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
2	NAG	A	500	14/15	0.91	0.31	3.60	66,72,76,81	0
2	NAG	B	501	14/15	0.78	0.36	2.79	93,96,100,104	0
2	MAN	B	504	11/12	0.81	0.46	-	113,113,114,114	0
2	MAN	B	503	11/12	0.69	0.56	-	115,116,116,116	0
2	MAN	A	503	11/12	0.82	0.38	-	108,109,109,110	0
2	MAN	B	502	11/12	0.83	0.30	-	107,110,111,113	0
2	MAN	A	502	11/12	0.77	0.23	-	100,103,105,106	0
2	NAG	A	501	14/15	0.87	0.33	-	86,89,92,96	0
2	MAN	A	504	11/12	0.80	0.39	-	106,107,108,108	0
2	NAG	B	500	14/15	0.84	0.35	-	72,79,82,88	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, 95^{th} 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
3	CA	A	600	1/1	0.95	0.18	-0.06	40,40,40,40	0
3	CA	B	600	1/1	0.95	0.17	-0.26	67,67,67,67	0
4	CL	B	5	1/1	0.94	0.07	-	65,65,65,65	0
4	CL	B	2	1/1	0.94	0.23	-	77,77,77,77	0
4	CL	A	1	1/1	0.90	0.17	-	59,59,59,59	0
4	CL	A	3	1/1	0.98	0.16	-	57,57,57,57	0
4	CL	B	4	1/1	0.98	0.14	-	59,59,59,59	0

6.5 Other polymers (i)

There are no such residues in this entry.