



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:36 AM GMT

PDB ID : 2XPK
Title : CELL-PENETRANT, NANOMOLAR O-GLCNACASE INHIBITORS SELECTIVE AGAINST LYSOSOMAL HEXOSAMINIDASES
Authors : Dorfmueller, H.C.; Borodkin, V.S.; Schimpl, M.; Zheng, X.; Kime, R.; Read, K.D.; Van Aalten, D.M.F.
Deposited on : 2010-08-26
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

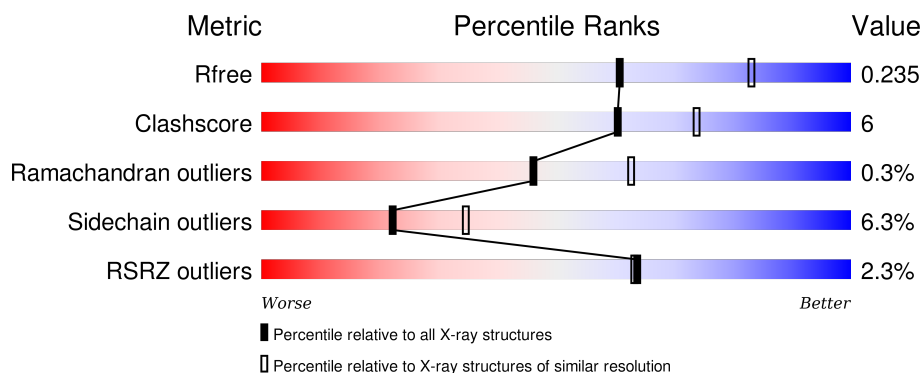
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

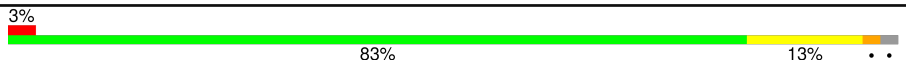

The reported resolution of this entry is 2.40 Å.

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	594	
1	B	594	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 9771 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.

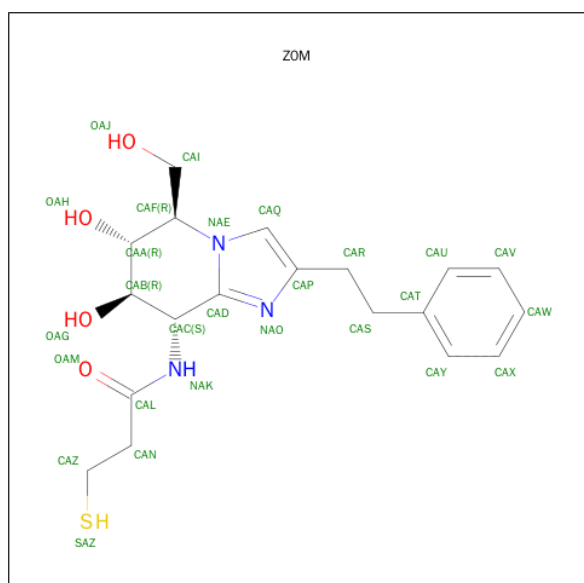
- Molecule 1 is a protein called O-GLCNACASE NAGJ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	585	Total	C	N	O	S	0	0	0
			4627	2911	756	942	18			
1	B	585	Total	C	N	O	S	0	1	0
			4630	2912	757	943	18			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	331	CYS	VAL	ENGINEERED MUTATION	UNP Q0TR53
A	388	ASP	ASN	SEE REMARK 999	UNP Q0TR53
B	331	CYS	VAL	ENGINEERED MUTATION	UNP Q0TR53
B	388	ASP	ASN	SEE REMARK 999	UNP Q0TR53

- Molecule 2 is N-[(5R,6R,7R,8S)-6,7-DIHYDROXY-5-(HYDROXYMETHYL)-2-(2-PHENYLETHYL)-5,6,7,8-TETRAHYDROIMIDAZO[1,2-A]PYRIDIN-8-YL]-3-SULFANYLPROPANAMIDE (three-letter code: Z0M) (formula: C₁₉H₂₅N₃O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			27	19	3	4	1		
2	B	1	Total	C	N	O	S	0	0
			27	19	3	4	1		

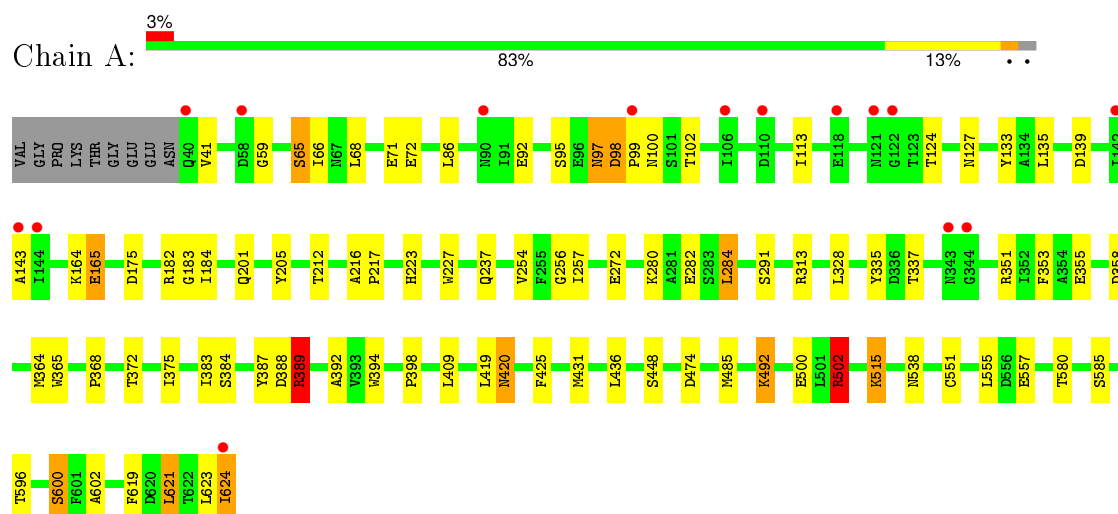
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	245	Total	O	0	0
			245	245		
3	B	215	Total	O	0	0
			215	215		

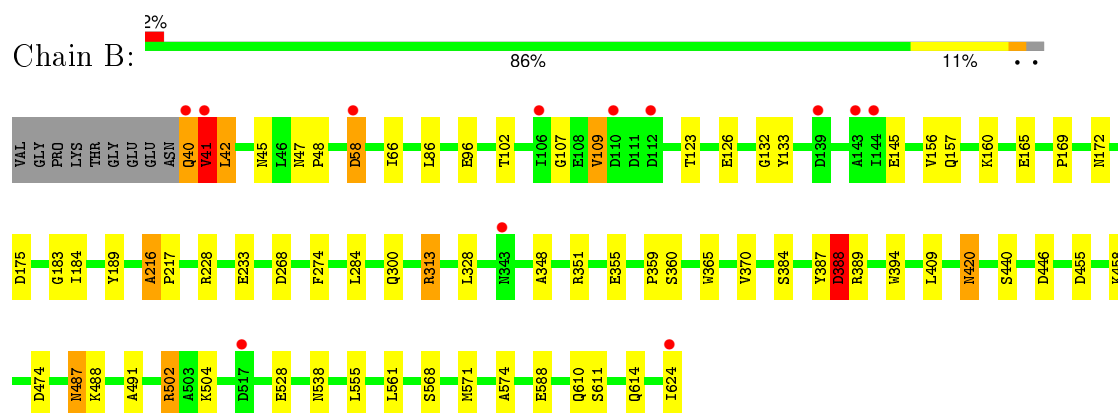
3 Residue-property plots

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: O-GLCNACASE NAGJ



• Molecule 1: O-GLCNACASE NAGJ



4 Data and refinement statistics

Property	Value	Source
Space group	I 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	130.15Å 144.97Å 153.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.02 – 2.40 20.02 – 2.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.02-2.40) 95.1 (20.02-2.40)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.44 (at 2.41Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.196 , 0.242 0.192 , 0.235	Depositor DCC
R_{free} test set	537 reflections (1.01%)	DCC
Wilson B-factor (Å ²)	29.5	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 33.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	2 of 53575 reflections (0.004%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9771	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.39% 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: ZOM

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	0.64	0/4723	0.68	4/6411 (0.1%)
1	B	0.64	0/4732	0.66	0/6424
All	All	0.64	0/9455	0.67	4/12835 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	502	ARG	NE-CZ-NH2	-6.64	116.98	120.30
1	A	389	ARG	NE-CZ-NH1	5.43	123.01	120.30
1	A	284	LEU	CA-CB-CG	-5.34	103.01	115.30
1	A	502	ARG	NE-CZ-NH1	5.02	122.81	120.30

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	4627	0	4412	53	0
1	B	4630	0	4409	53	0
2	A	27	0	25	1	0
2	B	27	0	25	1	0
3	A	245	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	215	0	0	5	0
All	All	9771	0	8871	102	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 6.

All (102) 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:351:ARG:HD2	3:A:2093:HOH:O	1.57	1.03
1:B:41:VAL:HG23	1:B:42:LEU:HA	1.34	1.03
1:A:165:GLU:OE1	1:A:165:GLU:HA	1.83	0.78
1:B:41:VAL:CG2	1:B:42:LEU:HA	2.15	0.73
1:B:387:TYR:HB3	1:B:389:ARG:HH11	1.54	0.72
1:A:502:ARG:O	1:A:502:ARG:HD3	1.89	0.71
1:B:474:ASP:OD2	1:B:538:ASN:ND2	2.25	0.69
1:B:109:VAL:HG11	1:B:126:GLU:HG2	1.76	0.68
1:B:47:ASN:HD21	1:B:446:ASP:HB2	1.59	0.67
1:B:58:ASP:N	1:B:58:ASP:OD2	2.28	0.67
1:B:487:ASN:O	1:B:488:LYS:HB2	1.94	0.66
1:B:502:ARG:HD3	1:B:502:ARG:O	1.95	0.66
1:B:487:ASN:HD21	1:B:491:ALA:H	1.44	0.64
1:A:41:VAL:CG1	1:A:59:GLY:HA3	2.28	0.63
1:A:420:ASN:H	1:A:420:ASN:HD22	1.46	0.63
1:B:42:LEU:N	1:B:42:LEU:HD22	2.16	0.61
1:A:182:ARG:HG2	1:A:448:SER:HB2	1.83	0.61
1:A:515:LYS:HG2	1:A:515:LYS:O	2.01	0.60
1:A:183:GLY:C	1:A:184:ILE:HD12	2.22	0.60
1:A:500:GLU:OE1	3:A:2178:HOH:O	2.16	0.59
1:A:358:ASP:O	1:A:389:ARG:NH2	2.34	0.59
1:A:502:ARG:C	1:A:502:ARG:HD3	2.24	0.58
1:B:66:ILE:HG22	1:B:102:THR:HB	1.85	0.58
1:B:274:PHE:CE2	1:B:313:ARG:HD2	2.38	0.58
1:A:216:ALA:N	1:A:217:PRO:HD3	2.20	0.56
1:B:487:ASN:ND2	1:B:491:ALA:H	2.02	0.56
1:A:223:HIS:HD2	1:A:256:GLY:O	1.87	0.56
1:B:183:GLY:C	1:B:184:ILE:HD12	2.25	0.56
1:A:65:SER:HB2	1:A:92:GLU:HB3	1.86	0.56
1:B:157:GLN:OE1	1:B:160:LYS:HE2	2.07	0.55
1:A:68:LEU:HG	1:A:71:GLU:HG3	1.89	0.54
1:B:384:SER:O	1:B:388:ASP:HA	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:348:ALA:HA	1:B:351:ARG:HH21	1.72	0.52
1:A:68:LEU:HG	1:A:71:GLU:CG	2.39	0.52
1:B:40:GLN:CD	1:B:40:GLN:N	2.63	0.52
1:A:596:THR:O	1:A:600:SER:HB3	2.10	0.52
1:A:227:TRP:O	1:A:280:LYS:NZ	2.42	0.52
1:A:165:GLU:OE1	1:A:165:GLU:CA	2.57	0.52
1:B:502:ARG:C	1:B:502:ARG:HD3	2.31	0.52
1:A:254:VAL:HG22	1:A:291:SER:HB3	1.92	0.51
1:B:41:VAL:HG11	1:B:169:PRO:HA	1.93	0.50
1:A:474:ASP:OD2	1:A:538:ASN:ND2	2.41	0.50
1:B:45:ASN:O	3:B:2002:HOH:O	2.19	0.50
1:A:557:GLU:HG2	1:A:602:ALA:HB3	1.94	0.50
1:B:274:PHE:CZ	1:B:313:ARG:HD2	2.48	0.49
1:B:42:LEU:CD2	1:B:42:LEU:N	2.76	0.49
1:B:455:ASP:HB3	1:B:458:LYS:HB2	1.94	0.48
1:B:156:VAL:O	1:B:160:LYS:HG3	2.14	0.47
1:A:98:ASP:C	1:A:98:ASP:OD2	2.50	0.47
1:B:359:PRO:HA	1:B:389:ARG:HH21	1.80	0.47
1:B:420:ASN:H	1:B:420:ASN:HD22	1.63	0.47
1:B:387:TYR:O	1:B:389:ARG:NH1	2.49	0.46
1:B:133:TYR:CE2	1:B:175:ASP:HB3	2.49	0.46
1:A:619:PHE:CD2	1:A:621:LEU:HD22	2.51	0.46
1:A:436:LEU:HD11	1:A:551:CYS:HB3	1.97	0.46
1:A:133:TYR:CE2	1:A:175:ASP:HB3	2.51	0.46
1:A:389:ARG:HH11	1:A:389:ARG:HG2	1.81	0.45
1:A:135:LEU:HA	1:A:143:ALA:O	2.17	0.45
3:A:2238:HOH:O	1:B:488:LYS:HE2	2.16	0.45
1:A:97:ASN:ND2	1:A:97:ASN:C	2.70	0.45
1:B:488:LYS:HA	1:B:488:LYS:HD2	1.60	0.44
1:A:41:VAL:HG12	1:A:59:GLY:HA3	1.98	0.44
1:B:504:LYS:NZ	1:B:528:GLU:OE1	2.51	0.44
1:A:98:ASP:CG	1:A:99:PRO:N	2.68	0.44
1:A:337:THR:HB	1:A:368:PRO:HA	2.00	0.44
1:A:164:LYS:O	1:A:165:GLU:HB2	2.17	0.44
1:A:183:GLY:HA3	1:A:212:THR:O	2.18	0.43
1:A:624:ILE:HB	1:B:189:TYR:HE2	1.82	0.43
1:A:384:SER:O	1:A:388:ASP:N	2.51	0.43
1:A:201:GLN:HB3	1:A:205:TYR:CZ	2.54	0.43
1:B:574:ALA:HA	3:B:2183:HOH:O	2.18	0.43
1:A:485:MET:O	1:A:492:LYS:HA	2.19	0.43
1:A:515:LYS:HG2	1:B:300:GLN:OE1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:624:ILE:HB	1:B:189:TYR:CE2	2.54	0.43
1:A:335:TYR:CD2	2:A:1625:ZOM:HAZ1	2.53	0.43
1:A:398:PRO:O	1:A:431:MET:HG2	2.18	0.43
1:B:611:SER:HA	1:B:614:GLN:HE21	1.82	0.42
1:B:41:VAL:CB	1:B:42:LEU:HA	2.49	0.42
1:A:387:TYR:HB3	1:A:389:ARG:HD2	2.01	0.42
1:A:254:VAL:HG22	1:A:291:SER:CB	2.49	0.42
1:A:515:LYS:CG	1:B:300:GLN:OE1	2.67	0.42
1:B:47:ASN:ND2	3:B:2130:HOH:O	2.53	0.41
1:B:216:ALA:N	1:B:217:PRO:CD	2.83	0.41
1:B:107:GLY:O	1:B:145:GLU:HA	2.21	0.41
1:A:353:PHE:HD2	1:A:387:TYR:HH	1.66	0.41
1:B:48:PRO:HB3	1:B:446:ASP:HA	2.02	0.41
1:A:389:ARG:HG2	1:A:389:ARG:NH1	2.35	0.41
1:B:133:TYR:CZ	1:B:175:ASP:HB3	2.55	0.41
1:B:228:ARG:HB2	3:B:2038:HOH:O	2.20	0.41
1:A:282:GLU:HG2	3:A:2066:HOH:O	2.21	0.41
1:B:370:VAL:HG11	2:B:1625:ZOM:CAQ	2.51	0.41
1:A:375:ILE:HG22	1:A:419:LEU:HD11	2.03	0.41
1:A:420:ASN:HD22	1:A:420:ASN:N	2.13	0.41
1:B:420:ASN:ND2	3:B:2115:HOH:O	2.53	0.41
1:A:364:MET:HA	1:A:392:ALA:O	2.21	0.41
1:B:132:GLY:HA2	1:B:175:ASP:O	2.21	0.41
1:B:561:LEU:HD22	1:B:610:GLN:HA	2.02	0.41
1:B:109:VAL:CG1	1:B:126:GLU:HG2	2.49	0.40
1:B:568:SER:HA	1:B:571:MET:HE2	2.03	0.40
1:A:337:THR:HG23	1:A:383:ILE:HD11	2.04	0.40
3:A:2241:HOH:O	1:B:488:LYS:HG2	2.20	0.40
1:A:66:ILE:HG22	1:A:102:THR:HB	2.02	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	583/594 (98%)	565 (97%)	17 (3%)	1 (0%)	52	69
1	B	584/594 (98%)	556 (95%)	25 (4%)	3 (0%)	34	48
All	All	1167/1188 (98%)	1121 (96%)	42 (4%)	4 (0%)	46	63

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	388	ASP
1	A	139	ASP
1	B	216	ALA
1	B	41	VAL

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	500/507 (99%)	465 (93%)	35 (7%)	19	29
1	B	501/507 (99%)	473 (94%)	28 (6%)	26	41
All	All	1001/1014 (99%)	938 (94%)	63 (6%)	22	35

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	SER
1	A	72	GLU
1	A	86	LEU
1	A	95	SER
1	A	97	ASN
1	A	98	ASP
1	A	100	ASN
1	A	113	ILE
1	A	124	THR
1	A	127	ASN
1	A	165	GLU
1	A	237	GLN

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Mol	Chain	Res	Type
1	A	257	ILE
1	A	272	GLU
1	A	284	LEU
1	A	313	ARG
1	A	328	LEU
1	A	355	GLU
1	A	365	TRP
1	A	372	THR
1	A	389	ARG
1	A	394	TRP
1	A	409	LEU
1	A	420	ASN
1	A	425	PHE
1	A	492	LYS
1	A	502	ARG
1	A	515	LYS
1	A	555	LEU
1	A	580	THR
1	A	585	SER
1	A	600	SER
1	A	621	LEU
1	A	623	LEU
1	A	624	ILE
1	B	40	GLN
1	B	41	VAL
1	B	42	LEU
1	B	58	ASP
1	B	86	LEU
1	B	96	GLU
1	B	109	VAL
1	B	123	THR
1	B	165	GLU
1	B	172	ASN
1	B	233	GLU
1	B	268	ASP
1	B	284	LEU
1	B	313	ARG
1	B	328	LEU
1	B	355	GLU
1	B	360	SER
1	B	365	TRP
1	B	388	ASP

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Mol	Chain	Res	Type
1	B	394	TRP
1	B	409	LEU
1	B	420	ASN
1	B	440	SER
1	B	487	ASN
1	B	502	ARG
1	B	555	LEU
1	B	588	GLU
1	B	624	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	97	ASN
1	A	100	ASN
1	A	223	HIS
1	A	309	GLN
1	A	420	ASN
1	A	610	GLN
1	B	47	ASN
1	B	420	ASN
1	B	487	ASN
1	B	542	ASN
1	B	610	GLN
1	B	614	GLN

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

2 ligands 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	Z0M	A	1625	-	24,29,29	1.29	4 (16%)	23,40,40	1.47	2 (8%)
2	Z0M	B	1625	-	24,29,29	1.05	2 (8%)	23,40,40	1.39	2 (8%)

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	Z0M	A	1625	-	-	0/13/34/34	0/2/3/3
2	Z0M	B	1625	-	-	0/13/34/34	0/2/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1625	Z0M	CAQ-NAE	-3.27	1.33	1.38
2	B	1625	Z0M	CAQ-NAE	-3.08	1.33	1.38
2	A	1625	Z0M	CAN-CAL	2.02	1.55	1.51
2	B	1625	Z0M	CAD-CAC	2.09	1.56	1.51
2	A	1625	Z0M	CAD-CAC	2.10	1.56	1.51
2	A	1625	Z0M	CAR-CAP	2.81	1.57	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1625	Z0M	CAQ-NAE-CAD	-4.86	106.32	109.31
2	B	1625	Z0M	CAQ-NAE-CAD	-4.02	106.84	109.31
2	B	1625	Z0M	CAR-CAP-CAQ	-2.98	124.94	129.55
2	A	1625	Z0M	CAR-CAP-CAQ	-2.67	125.42	129.55

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
2	A	1625	ZOM	1	0
2	B	1625	ZOM	1	0

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	585/594 (98%)	-0.32	15 (2%) 59 58	16, 34, 79, 105	0
1	B	585/594 (98%)	-0.28	12 (2%) 67 66	17, 34, 80, 107	0
All	All	1170/1188 (98%)	-0.30	27 (2%) 64 63	16, 34, 80, 107	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	41	VAL	4.7
1	B	112	ASP	4.6
1	B	624	ILE	4.0
1	A	110	ASP	3.3
1	A	144	ILE	3.3
1	A	343	ASN	3.2
1	B	139	ASP	3.1
1	B	110	ASP	3.1
1	B	40	GLN	3.0
1	B	144	ILE	2.7
1	A	142	ILE	2.6
1	A	121	ASN	2.5
1	A	122	GLY	2.5
1	A	99	PRO	2.4
1	A	624	ILE	2.4
1	A	118	GLU	2.4
1	B	106	ILE	2.4
1	A	106	ILE	2.4
1	A	90	ASN	2.3
1	B	343	ASN	2.3
1	B	143	ALA	2.3
1	A	58	ASP	2.2
1	B	517	ASP	2.2
1	A	344	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	40	GLN	2.1
1	B	58	ASP	2.1
1	A	143	ALA	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	Z0M	A	1625	27/27	0.96	0.11	0.07	21,25,40,42	0
2	Z0M	B	1625	27/27	0.97	0.09	-0.38	19,23,38,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.