



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 2, 2023 – 04:28 PM EDT

PDB ID : 3WDP
Title : Structural analysis of a beta-glucosidase mutant derived from a hyperthermophilic tetrameric structure
Authors : Nakabayashi, M.; Kataoka, M.; Ishikawa, K.
Deposited on : 2013-06-19
Resolution : 1.70 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

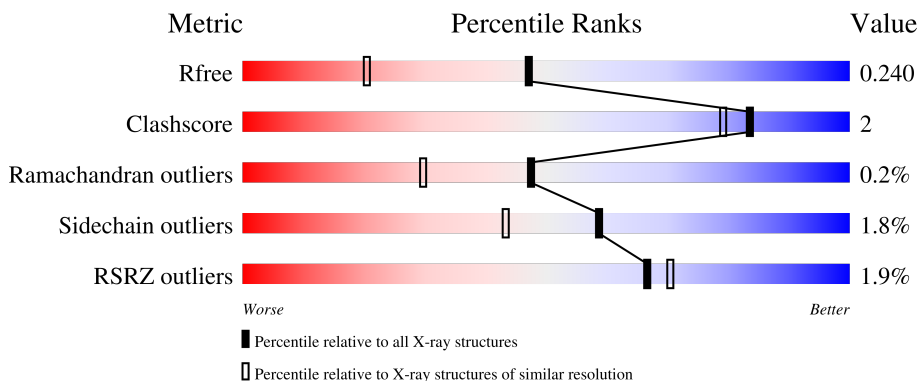
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	P	473	 3% 93% 7%
1	Q	473	 3% 93% 7%
1	R	473	 3% 94% 5%
1	S	473	 3% 92% 7%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 17178 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 Beta-glucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	P	472	3858	2512	631	702	13	0	0	0
1	Q	472	3878	2528	631	706	13	0	3	0
1	R	472	3868	2519	631	704	14	0	2	0
1	S	472	3870	2520	633	704	13	0	2	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	0	MET	-	expression tag	UNP Q51723
P	1	ALA	-	expression tag	UNP Q51723
P	170	ALA	ARG	engineered mutation	UNP Q51723
P	220	ALA	ARG	engineered mutation	UNP Q51723
P	227	PHE	TYR	engineered mutation	UNP Q51723
Q	0	MET	-	expression tag	UNP Q51723
Q	1	ALA	-	expression tag	UNP Q51723
Q	170	ALA	ARG	engineered mutation	UNP Q51723
Q	220	ALA	ARG	engineered mutation	UNP Q51723
Q	227	PHE	TYR	engineered mutation	UNP Q51723
R	0	MET	-	expression tag	UNP Q51723
R	1	ALA	-	expression tag	UNP Q51723
R	170	ALA	ARG	engineered mutation	UNP Q51723
R	220	ALA	ARG	engineered mutation	UNP Q51723
R	227	PHE	TYR	engineered mutation	UNP Q51723
S	0	MET	-	expression tag	UNP Q51723
S	1	ALA	-	expression tag	UNP Q51723
S	170	ALA	ARG	engineered mutation	UNP Q51723
S	220	ALA	ARG	engineered mutation	UNP Q51723
S	227	PHE	TYR	engineered mutation	UNP Q51723

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	P	1	Total C O 6 3 3	0	0
2	P	1	Total C O 6 3 3	0	0
2	P	1	Total C O 6 3 3	0	0
2	P	1	Total C O 6 3 3	0	0
2	Q	1	Total C O 6 3 3	0	0
2	Q	1	Total C O 6 3 3	0	0
2	Q	1	Total C O 6 3 3	0	0
2	R	1	Total C O 6 3 3	0	0
2	R	1	Total C O 6 3 3	0	0
2	R	1	Total C O 6 3 3	0	0
2	S	1	Total C O 6 3 3	0	0

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	P	1	Total O P 5 4 1	0	0
3	P	1	Total O P 5 4 1	0	0
3	P	1	Total O P 5 4 1	0	0
3	P	1	Total O P 5 4 1	0	0
3	Q	1	Total O P 5 4 1	0	0
3	Q	1	Total O P 5 4 1	0	0
3	Q	1	Total O P 5 4 1	0	0
3	Q	1	Total O P 5 4 1	0	0
3	R	1	Total O P 5 4 1	0	0
3	R	1	Total O P 5 4 1	0	0
3	R	1	Total O P 5 4 1	0	0
3	S	1	Total O P 5 4 1	0	0

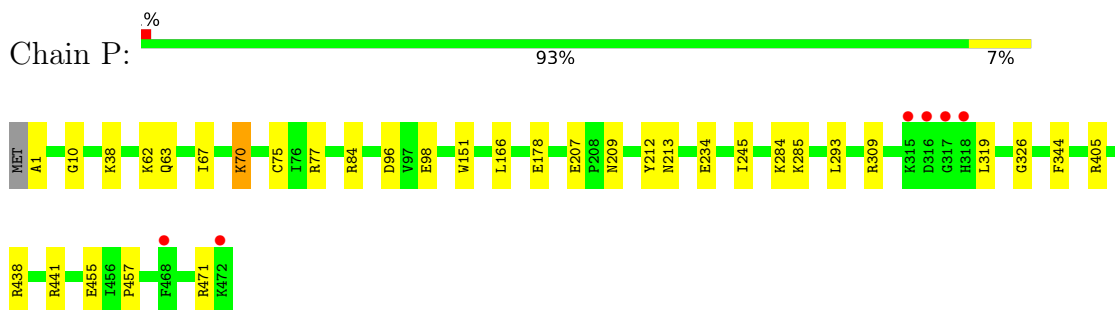
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	P	452	Total 452	O 452	0	0
4	Q	456	Total 456	O 456	0	0
4	R	344	Total 344	O 344	0	0
4	S	326	Total 326	O 326	0	0

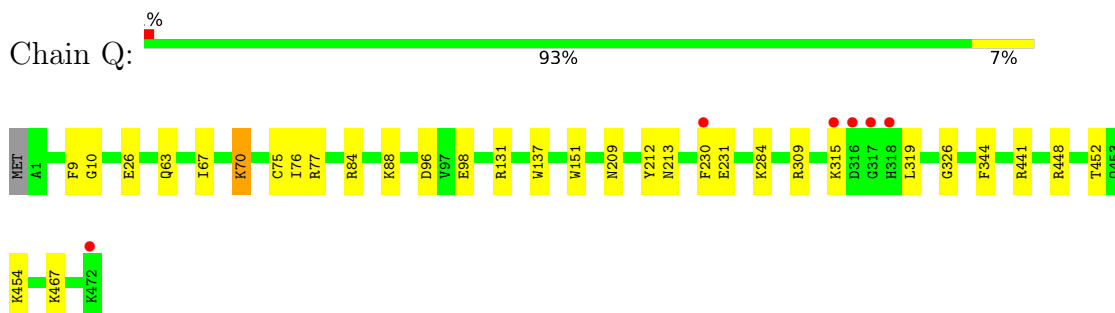
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

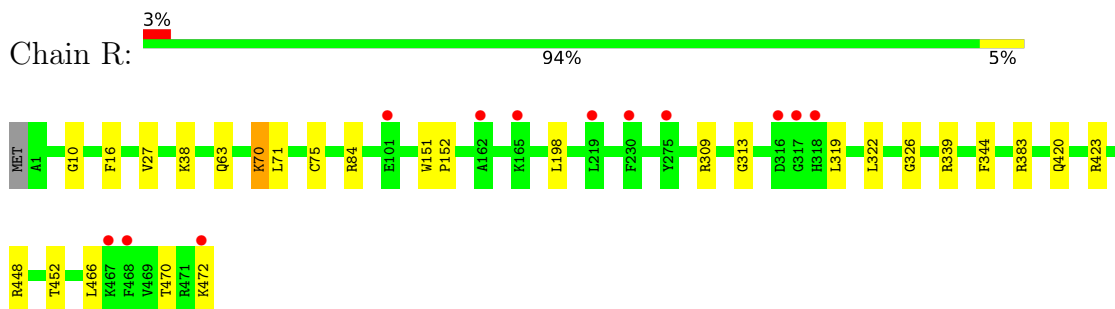
- Molecule 1: Beta-glucosidase



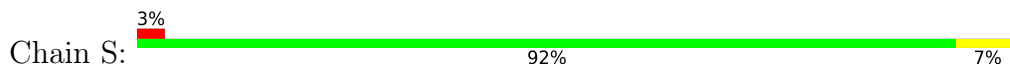
- Molecule 1: Beta-glucosidase

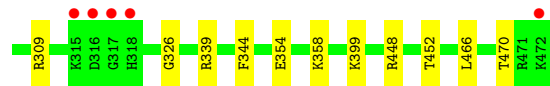
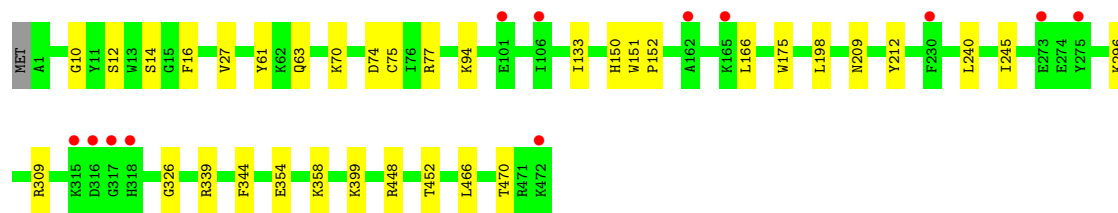


- Molecule 1: Beta-glucosidase



- Molecule 1: Beta-glucosidase





4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	122.15Å 161.15Å 183.82Å 90.00° 108.38° 90.00°	Depositor
Resolution (Å)	47.05 – 1.70 47.05 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.3 (47.05-1.70) 99.3 (47.05-1.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.38 (at 1.70Å)	Xtrriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.212 , 0.233 0.221 , 0.240	Depositor DCC
R_{free} test set	18396 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	16.8	Xtrriage
Anisotropy	0.042	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 50.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.107 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	17178	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.82% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, PO4

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	P	0.63	0/3981	0.76	4/5399 (0.1%)
1	Q	0.63	0/4011	0.75	3/5439 (0.1%)
1	R	0.50	0/3997	0.66	1/5420 (0.0%)
1	S	0.52	0/4000	0.66	2/5425 (0.0%)
All	All	0.57	0/15989	0.71	10/21683 (0.0%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S	74	ASP	CB-CG-OD1	7.53	125.08	118.30
1	Q	441	ARG	NE-CZ-NH2	-6.14	117.23	120.30
1	S	74	ASP	CB-CG-OD2	-5.61	113.25	118.30
1	P	84	ARG	NE-CZ-NH1	-5.53	117.54	120.30
1	Q	84	ARG	NE-CZ-NH1	-5.37	117.61	120.30
1	P	438	ARG	NE-CZ-NH2	-5.29	117.65	120.30
1	Q	131	ARG	NE-CZ-NH2	-5.26	117.67	120.30
1	R	383	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	P	441	ARG	NE-CZ-NH2	-5.13	117.73	120.30
1	P	293	LEU	CB-CG-CD2	5.03	119.56	111.00

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	P	3858	0	3712	17	0
1	Q	3878	0	3733	16	0
1	R	3868	0	3725	23	0
1	S	3870	0	3723	16	0
2	P	24	0	32	1	0
2	Q	18	0	24	0	0
2	R	18	0	24	0	0
2	S	6	0	8	0	0
3	P	20	0	0	1	0
3	Q	20	0	0	1	0
3	R	15	0	0	0	0
3	S	5	0	0	0	0
4	P	452	0	0	8	3
4	Q	456	0	0	4	2
4	R	344	0	0	12	0
4	S	326	0	0	2	0
All	All	17178	0	14981	72	4

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 2.

All (72) 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:Q:454:LYS:HD3	4:Q:769:HOH:O	1.67	0.94
1:Q:454:LYS:HD3	4:Q:770:HOH:O	1.82	0.79
1:P:245:ILE:HD13	4:P:852:HOH:O	1.83	0.78
1:R:71:LEU:HB3	4:R:782:HOH:O	1.85	0.75
1:Q:454:LYS:CD	4:Q:770:HOH:O	2.33	0.74
1:P:63:GLN:NE2	4:P:710:HOH:O	2.22	0.73
1:R:448:ARG:HG2	4:R:865:HOH:O	1.89	0.70
1:P:62:LYS:NZ	4:P:951:HOH:O	2.24	0.67
1:P:234:GLU:OE1	4:P:850:HOH:O	2.12	0.66
1:R:27:VAL:HG11	1:R:84:ARG:HG2	1.79	0.65
1:P:38:LYS:HD3	4:P:753:HOH:O	1.97	0.63
1:R:71:LEU:CB	4:R:782:HOH:O	2.45	0.63
1:P:207:GLU:OE1	2:P:504:GOL:H11	2.00	0.62
1:P:405:ARG:HD2	4:P:885:HOH:O	2.01	0.60
1:P:63:GLN:HG3	4:P:709:HOH:O	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:420:GLN:NE2	4:R:943:HOH:O	2.31	0.58
1:S:466:LEU:O	1:S:470:THR:HG23	2.02	0.58
1:R:448:ARG:O	1:R:452:THR:HG23	2.04	0.57
1:R:466:LEU:O	1:R:470:THR:HG23	2.06	0.55
1:S:339:ARG:HE	1:S:470:THR:HG21	1.71	0.55
1:S:63:GLN:HG3	4:S:825:HOH:O	2.07	0.55
1:R:448:ARG:CG	4:R:865:HOH:O	2.53	0.53
1:S:309:ARG:O	1:S:326:GLY:HA3	2.08	0.53
1:R:10:GLY:HA3	1:R:75:CYS:O	2.09	0.53
1:P:67:ILE:HG23	1:P:70:LYS:HE2	1.92	0.52
1:R:339:ARG:HD3	1:R:470:THR:HG22	1.92	0.51
1:S:10:GLY:HA3	1:S:75:CYS:O	2.10	0.51
1:S:448:ARG:O	1:S:452:THR:HG23	2.11	0.51
1:S:339:ARG:HD3	1:S:470:THR:HG22	1.92	0.51
1:R:309:ARG:O	1:R:326:GLY:HA3	2.11	0.50
1:R:313:GLY:HA3	1:R:322:LEU:HD11	1.93	0.50
1:Q:70:LYS:O	1:Q:448:ARG:HD3	2.12	0.49
1:R:420:GLN:O	1:R:423:ARG:HG2	2.11	0.49
1:S:198:LEU:HD23	4:S:848:HOH:O	2.12	0.49
1:R:448:ARG:CA	4:R:782:HOH:O	2.60	0.48
1:Q:96:ASP:OD1	1:Q:98:GLU:OE2	2.31	0.48
1:P:209:ASN:HA	1:P:212:TYR:CZ	2.49	0.48
1:R:423:ARG:HB3	4:R:883:HOH:O	2.14	0.48
1:R:63:GLN:NE2	4:R:641:HOH:O	2.37	0.47
1:R:71:LEU:HD22	4:R:782:HOH:O	2.14	0.47
1:R:448:ARG:N	4:R:782:HOH:O	2.48	0.47
1:Q:26[A]:GLU:CG	4:Q:772:HOH:O	2.63	0.46
1:R:27:VAL:HG11	1:R:84:ARG:CG	2.45	0.46
1:Q:230[B]:PHE:CD2	1:Q:231:GLU:N	2.82	0.45
1:Q:209:ASN:HA	1:Q:212:TYR:CZ	2.52	0.45
1:P:10:GLY:HA3	1:P:75:CYS:O	2.17	0.44
1:P:96:ASP:OD1	1:P:98:GLU:OE2	2.36	0.44
1:S:175:TRP:CE2	1:S:240:LEU:HD21	2.51	0.44
1:Q:448:ARG:O	1:Q:452:THR:HG23	2.18	0.43
1:Q:67:ILE:O	1:Q:70:LYS:HD2	2.19	0.43
1:Q:76:ILE:HG13	1:Q:137:TRP:CE2	2.53	0.43
1:Q:67:ILE:HG23	1:Q:70:LYS:HE2	2.00	0.43
1:R:70:LYS:N	1:R:70:LYS:HD3	2.34	0.43
1:R:71:LEU:CA	4:R:782:HOH:O	2.67	0.43
1:S:12:SER:HA	1:S:77:ARG:O	2.19	0.43
1:Q:309:ARG:O	1:Q:326:GLY:HA3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:9:PHE:CE2	1:Q:454:LYS:HE3	2.53	0.42
1:Q:10:GLY:HA3	1:Q:75:CYS:O	2.18	0.42
1:P:213:ASN:OD1	3:P:507:PO4:O1	2.38	0.42
1:R:198:LEU:HD23	4:R:709:HOH:O	2.20	0.42
1:S:16:PHE:HB2	1:S:152:PRO:HG2	2.02	0.42
1:P:209:ASN:HA	1:P:212:TYR:CE2	2.54	0.42
1:P:1:ALA:N	4:P:922:HOH:O	2.38	0.41
1:P:455:GLU:O	1:P:457:PRO:HD3	2.21	0.41
1:S:209:ASN:HA	1:S:212:TYR:CZ	2.56	0.41
1:S:245:ILE:HD11	1:S:296:LYS:HD2	2.02	0.41
1:S:354:GLU:HG2	1:S:358:LYS:HE2	2.02	0.41
1:R:16:PHE:HB2	1:R:152:PRO:HG2	2.03	0.40
1:S:14:SER:HB3	1:S:150:HIS:CE1	2.56	0.40
1:P:309:ARG:O	1:P:326:GLY:HA3	2.22	0.40
1:Q:213:ASN:OD1	3:Q:507:PO4:O1	2.39	0.40
1:S:61:TYR:CG	1:S:133:ILE:HG12	2.57	0.40

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:840:HOH:O	4:P:840:HOH:O[2_555]	2.04	0.16
4:P:800:HOH:O	4:P:800:HOH:O[2_555]	2.05	0.15
4:P:732:HOH:O	4:Q:824:HOH:O[3_555]	2.14	0.06
4:Q:861:HOH:O	4:Q:861:HOH:O[2_555]	2.14	0.06

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	P	470/473 (99%)	463 (98%)	6 (1%)	1 (0%)	47 30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Q	473/473 (100%)	462 (98%)	10 (2%)	1 (0%)	47	30
1	R	472/473 (100%)	463 (98%)	8 (2%)	1 (0%)	47	30
1	S	472/473 (100%)	464 (98%)	7 (2%)	1 (0%)	47	30
All	All	1887/1892 (100%)	1852 (98%)	31 (2%)	4 (0%)	47	30

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	P	151	TRP
1	Q	151	TRP
1	R	151	TRP
1	S	151	TRP

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	P	398/399 (100%)	389 (98%)	9 (2%)	50	33
1	Q	401/399 (100%)	392 (98%)	9 (2%)	52	34
1	R	400/399 (100%)	395 (99%)	5 (1%)	69	56
1	S	400/399 (100%)	394 (98%)	6 (2%)	65	51
All	All	1599/1596 (100%)	1570 (98%)	29 (2%)	59	43

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	P	70	LYS
1	P	77	ARG
1	P	166	LEU
1	P	178	GLU
1	P	284	LYS
1	P	285	LYS
1	P	319	LEU

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Mol	Chain	Res	Type
1	P	344	PHE
1	P	471	ARG
1	Q	63	GLN
1	Q	70	LYS
1	Q	77	ARG
1	Q	88	LYS
1	Q	284	LYS
1	Q	315	LYS
1	Q	319	LEU
1	Q	344	PHE
1	Q	467	LYS
1	R	38	LYS
1	R	70	LYS
1	R	319	LEU
1	R	344	PHE
1	R	472	LYS
1	S	27	VAL
1	S	70	LYS
1	S	94	LYS
1	S	166	LEU
1	S	344	PHE
1	S	399	LYS

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

Mol	Chain	Res	Type
1	P	213	ASN
1	Q	213	ASN
1	Q	268	HIS
1	Q	355	ASN
1	Q	462	HIS
1	R	355	ASN
1	S	415	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](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

23 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	GOL	R	501	-	5,5,5	0.24	0	5,5,5	0.55	0
3	PO4	P	506	-	4,4,4	0.58	0	6,6,6	0.79	0
3	PO4	Q	506	-	4,4,4	0.71	0	6,6,6	0.76	0
3	PO4	R	504	-	4,4,4	0.70	0	6,6,6	0.77	0
3	PO4	Q	504	-	4,4,4	0.84	0	6,6,6	0.34	0
3	PO4	P	505	-	4,4,4	0.93	0	6,6,6	0.61	0
2	GOL	P	502	-	5,5,5	0.29	0	5,5,5	0.51	0
2	GOL	R	502	-	5,5,5	0.23	0	5,5,5	0.76	0
2	GOL	P	504	-	5,5,5	0.49	0	5,5,5	0.75	0
3	PO4	R	505	-	4,4,4	0.83	0	6,6,6	0.40	0
2	GOL	S	501	-	5,5,5	0.41	0	5,5,5	0.77	0
2	GOL	Q	503	-	5,5,5	0.40	0	5,5,5	0.87	0
3	PO4	R	506	-	4,4,4	0.87	0	6,6,6	0.37	0
2	GOL	P	503	-	5,5,5	0.76	0	5,5,5	0.84	0
3	PO4	S	502	-	4,4,4	0.73	0	6,6,6	0.91	0
3	PO4	P	507	-	4,4,4	0.75	0	6,6,6	0.84	0
3	PO4	Q	507	-	4,4,4	0.75	0	6,6,6	0.81	0
2	GOL	P	501	-	5,5,5	0.29	0	5,5,5	0.67	0
3	PO4	P	508	-	4,4,4	0.84	0	6,6,6	0.49	0
3	PO4	Q	505	-	4,4,4	0.76	0	6,6,6	0.58	0
2	GOL	Q	501	-	5,5,5	0.32	0	5,5,5	0.86	0
2	GOL	Q	502	-	5,5,5	0.35	0	5,5,5	0.22	0
2	GOL	R	503	-	5,5,5	0.40	0	5,5,5	0.36	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
2	GOL	R	503	-	-	2/4/4/4	-
2	GOL	Q	503	-	-	4/4/4/4	-
2	GOL	R	502	-	-	2/4/4/4	-
2	GOL	P	504	-	-	0/4/4/4	-
2	GOL	Q	501	-	-	0/4/4/4	-
2	GOL	P	503	-	-	0/4/4/4	-
2	GOL	S	501	-	-	0/4/4/4	-
2	GOL	R	501	-	-	0/4/4/4	-
2	GOL	Q	502	-	-	2/4/4/4	-
2	GOL	P	501	-	-	0/4/4/4	-
2	GOL	P	502	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	Q	502	GOL	C1-C2-C3-O3
2	Q	503	GOL	O1-C1-C2-C3
2	Q	503	GOL	C1-C2-C3-O3
2	R	502	GOL	O1-C1-C2-C3
2	R	503	GOL	O1-C1-C2-O2
2	R	503	GOL	O1-C1-C2-C3
2	Q	502	GOL	O2-C2-C3-O3
2	Q	503	GOL	O2-C2-C3-O3
2	Q	503	GOL	O1-C1-C2-O2
2	R	502	GOL	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	P	504	GOL	1	0
3	P	507	PO4	1	0
3	Q	507	PO4	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	P	472/473 (99%)	-0.08	6 (1%) 77 81	9, 15, 28, 65	0
1	Q	472/473 (99%)	-0.09	6 (1%) 77 81	9, 15, 28, 62	0
1	R	472/473 (99%)	0.18	12 (2%) 57 61	13, 21, 37, 59	0
1	S	472/473 (99%)	0.21	12 (2%) 57 61	13, 20, 36, 72	0
All	All	1888/1892 (99%)	0.06	36 (1%) 66 70	9, 18, 34, 72	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	S	317	GLY	6.0
1	S	472	LYS	5.7
1	P	316	ASP	5.0
1	S	316	ASP	4.9
1	R	317	GLY	4.6
1	Q	318	HIS	4.4
1	P	318	HIS	4.0
1	Q	316	ASP	4.0
1	R	101	GLU	4.0
1	P	472	LYS	3.8
1	Q	315	LYS	3.7
1	Q	472	LYS	3.6
1	P	317	GLY	3.3
1	R	275	TYR	3.3
1	R	472	LYS	3.3
1	S	106	ILE	3.3
1	P	468	PHE	3.2
1	S	101	GLU	3.2
1	P	315	LYS	3.0
1	S	275	TYR	2.9
1	Q	317	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
1	R	468	PHE	2.6
1	R	318	HIS	2.6
1	Q	230[A]	PHE	2.6
1	S	165	LYS	2.5
1	S	318	HIS	2.5
1	S	162	ALA	2.4
1	R	467	LYS	2.4
1	S	315	LYS	2.3
1	R	165	LYS	2.2
1	R	219	LEU	2.2
1	R	316	ASP	2.1
1	S	230	PHE	2.1
1	S	273	GLU	2.0
1	R	162	ALA	2.0
1	R	230	PHE	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 monosaccharides 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. 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	B-factors(Å ²)	Q<0.9
3	PO4	R	505	5/5	0.70	0.20	44,45,50,51	0
3	PO4	R	506	5/5	0.78	0.21	66,66,69,71	0
2	GOL	P	503	6/6	0.80	0.16	19,26,30,32	0
2	GOL	P	504	6/6	0.80	0.18	20,26,27,32	0
2	GOL	Q	502	6/6	0.81	0.21	18,27,31,33	0
2	GOL	Q	503	6/6	0.81	0.15	18,22,25,27	0
3	PO4	R	504	5/5	0.84	0.30	37,39,41,42	0
2	GOL	R	503	6/6	0.84	0.18	30,34,36,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	PO4	P	508	5/5	0.84	0.28	55,56,58,61	0
3	PO4	Q	505	5/5	0.85	0.23	45,46,48,52	0
3	PO4	P	505	5/5	0.86	0.21	43,44,46,51	0
3	PO4	P	507	5/5	0.86	0.16	22,24,27,30	0
3	PO4	Q	506	5/5	0.86	0.21	28,29,33,35	0
2	GOL	R	502	6/6	0.87	0.17	23,28,32,35	0
2	GOL	P	501	6/6	0.87	0.12	13,16,17,21	0
2	GOL	P	502	6/6	0.88	0.15	29,32,36,36	0
3	PO4	Q	507	5/5	0.90	0.17	23,23,27,30	0
2	GOL	R	501	6/6	0.90	0.11	19,20,21,21	0
2	GOL	S	501	6/6	0.91	0.12	19,19,20,20	0
3	PO4	P	506	5/5	0.91	0.20	28,28,32,33	0
2	GOL	Q	501	6/6	0.92	0.11	13,15,17,20	0
3	PO4	Q	504	5/5	0.92	0.23	50,50,51,52	0
3	PO4	S	502	5/5	0.93	0.24	36,38,40,40	0

6.5 Other polymers [i](#)

There are no such residues in this entry.