Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:17 PM GMT

PDB ID	:	3WPZ
Title	:	Microbacterium saccharophilum K-1 beta-fructofuranosidase mutant T47S/S 200T/F447P/F470Y/P500S
Authors	:	Yokoi, G.; Mori, M.; Sato, S.; Miyazaki, T.; Nishikawa, A.; Tonozuka, T.
Deposited on	:	2014-01-17
Resolution	:	2.27 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 ①) were used in the production of this report:

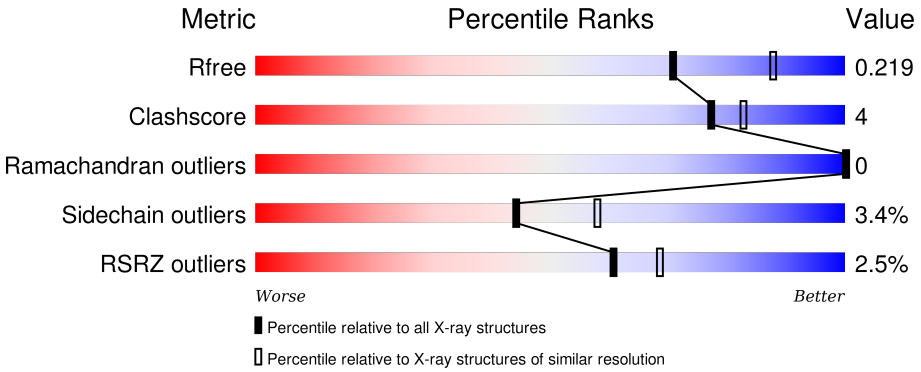
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 2.27 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	5193 (2.30-2.26)
Clashscore	102246	5929 (2.30-2.26)
Ramachandran outliers	100387	5851 (2.30-2.26)
Sidechain outliers	100360	5850 (2.30-2.26)
RSRZ outliers	91569	5204 (2.30-2.26)

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	542	2% 90% 8%
1	B	542	3% 89% 10%
1	C	542	2% 87% 11%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 13190 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-fructofuranosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	538	Total	C	N	O	S	0	0	0
			4173	2640	706	817	10			
1	B	538	Total	C	N	O	S	0	0	0
			4173	2640	706	817	10			
1	C	538	Total	C	N	O	S	0	0	0
			4173	2640	706	817	10			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	47	SER	THR	ENGINEERED MUTATION	UNP Q8VW87
A	200	THR	SER	ENGINEERED MUTATION	UNP Q8VW87
A	447	PRO	PHE	ENGINEERED MUTATION	UNP Q8VW87
A	470	TYR	PHE	ENGINEERED MUTATION	UNP Q8VW87
A	500	SER	PRO	ENGINEERED MUTATION	UNP Q8VW87
B	47	SER	THR	ENGINEERED MUTATION	UNP Q8VW87
B	200	THR	SER	ENGINEERED MUTATION	UNP Q8VW87
B	447	PRO	PHE	ENGINEERED MUTATION	UNP Q8VW87
B	470	TYR	PHE	ENGINEERED MUTATION	UNP Q8VW87
B	500	SER	PRO	ENGINEERED MUTATION	UNP Q8VW87
C	47	SER	THR	ENGINEERED MUTATION	UNP Q8VW87
C	200	THR	SER	ENGINEERED MUTATION	UNP Q8VW87
C	447	PRO	PHE	ENGINEERED MUTATION	UNP Q8VW87
C	470	TYR	PHE	ENGINEERED MUTATION	UNP Q8VW87
C	500	SER	PRO	ENGINEERED MUTATION	UNP Q8VW87

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	237	Total	O	0	0
			237	237		
2	B	233	Total	O	0	0
			233	233		

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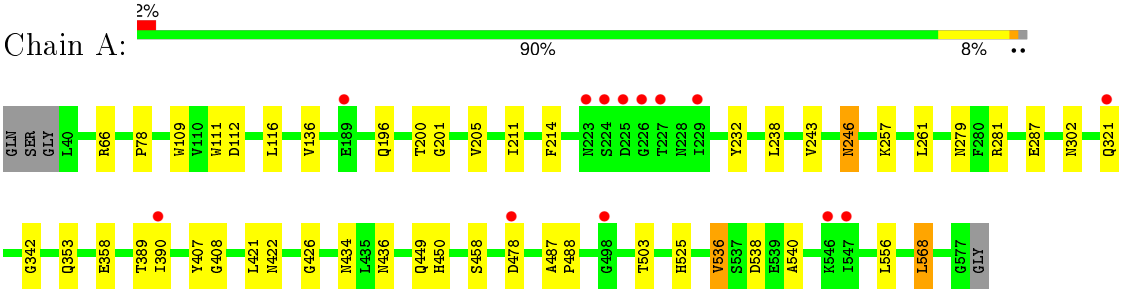
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	201	Total	O	0	0
			201	201		

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.

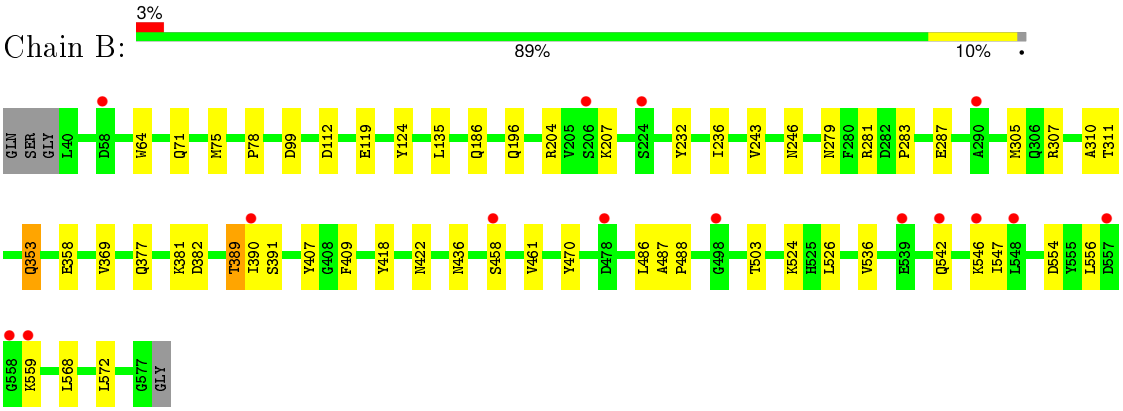
- Molecule 1: Beta-fructofuranosidase

Chain A:



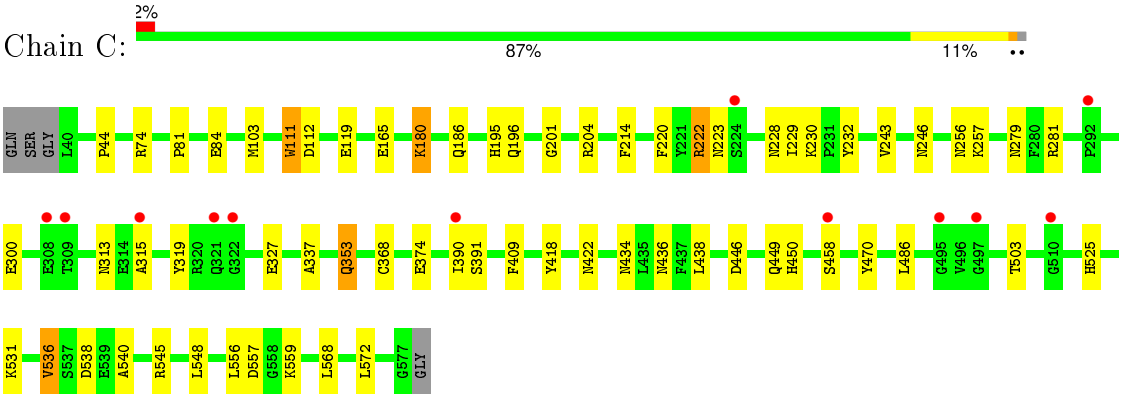
- Molecule 1: Beta-fructofuranosidase

Chain B:



- Molecule 1: Beta-fructofuranosidase

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	57.94Å 86.26Å 85.92Å 63.23° 86.27° 86.68°	Depositor
Resolution (Å)	42.98 – 2.27 42.98 – 2.27	Depositor EDS
% Data completeness (in resolution range)	97.1 (42.98-2.27) 81.9 (42.98-2.27)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.01 (at 2.27Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.158 , 0.211 0.168 , 0.219	Depositor DCC
R_{free} test set	3362 reflections (5.33%)	DCC
Wilson B-factor (Å^2)	26.8	Xtriage
Anisotropy	0.026	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.42 , 49.9	EDS
Estimated twinning fraction	0.018 for -h,-l,-k	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 66460 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	13190	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.37% 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

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	0.54	0/4288	0.70	1/5833 (0.0%)
1	B	0.54	0/4288	0.69	0/5833
1	C	0.52	0/4288	0.69	1/5833 (0.0%)
All	All	0.53	0/12864	0.69	2/17499 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	66	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	C	222	ARG	NE-CZ-NH2	-5.07	117.77	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4173	0	3929	28	0
1	B	4173	0	3929	28	0
1	C	4173	0	3929	38	0
2	A	237	0	0	2	0
2	B	233	0	0	1	0
2	C	201	0	0	3	0
All	All	13190	0	11787	91	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 4.

All (91) 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:434:ASN:H	1:A:449:GLN:HE22	1.18	0.87
1:A:536:VAL:HG13	1:A:540:ALA:HB3	1.63	0.80
1:B:353:GLN:HE22	1:C:436:ASN:ND2	1.83	0.74
1:A:353:GLN:HE21	1:B:436:ASN:HD22	1.37	0.72
1:A:302:ASN:HD22	1:A:342:GLY:HA2	1.56	0.70
1:C:545:ARG:HG2	2:C:781:HOH:O	1.92	0.70
1:C:434:ASN:H	1:C:449:GLN:HE22	1.37	0.70
1:A:434:ASN:H	1:A:449:GLN:NE2	1.92	0.68
1:C:165:GLU:N	1:C:165:GLU:OE1	2.28	0.67
1:B:377:GLN:HE22	1:B:461:VAL:H	1.43	0.65
1:A:390:ILE:CD1	1:A:458:SER:HA	2.33	0.58
1:B:119:GLU:HB3	1:B:204:ARG:NH2	2.19	0.58
1:C:422:ASN:HD21	1:C:503:THR:H	1.51	0.58
1:C:279:ASN:HD22	1:C:281:ARG:HH12	1.51	0.58
1:C:449:GLN:HE21	1:C:450:HIS:H	1.53	0.57
1:B:389:THR:HG22	1:B:407:TYR:O	2.06	0.55
1:A:390:ILE:HD13	1:A:458:SER:HA	1.88	0.55
1:A:525:HIS:NE2	1:A:538:ASP:OD1	2.34	0.55
1:B:119:GLU:HB2	1:B:287:GLU:HB2	1.89	0.54
1:B:353:GLN:HE22	1:C:436:ASN:HD22	1.52	0.54
1:C:434:ASN:H	1:C:449:GLN:NE2	2.06	0.54
1:B:279:ASN:HD22	1:B:281:ARG:HH12	1.57	0.53
1:A:434:ASN:N	1:A:449:GLN:HE22	1.96	0.52
1:B:305:MET:HE2	1:B:310:ALA:HA	1.91	0.52
1:C:319:TYR:OH	1:C:327:GLU:OE1	2.24	0.51
1:C:536:VAL:HG13	1:C:540:ALA:HB3	1.91	0.51
1:B:554:ASP:HB3	1:B:559:LYS:HD2	1.92	0.51
1:B:78:PRO:HA	1:B:436:ASN:HD21	1.75	0.51
1:A:279:ASN:HD22	1:A:281:ARG:HH12	1.59	0.50
1:C:545:ARG:CD	2:C:781:HOH:O	2.59	0.50
1:B:422:ASN:HD21	1:B:503:THR:H	1.60	0.49
1:C:180:LYS:HD2	1:C:256:ASN:HD21	1.77	0.49
1:B:390:ILE:HD13	1:B:458:SER:HA	1.95	0.48
1:C:409:PHE:HB3	1:C:418:TYR:HB3	1.95	0.48
1:C:195:HIS:HB2	1:C:220:PHE:HB2	1.95	0.48
1:C:201:GLY:HA3	1:C:214:PHE:O	2.13	0.48
1:A:449:GLN:HE21	1:A:450:HIS:H	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:71:GLN:O	1:B:75:MET:HG3	2.14	0.47
1:C:119:GLU:HB3	1:C:204:ARG:NH2	2.28	0.47
1:A:422:ASN:HD21	1:A:503:THR:H	1.61	0.47
1:A:116:LEU:HG	1:A:205:VAL:HB	1.96	0.47
1:C:525:HIS:NE2	1:C:538:ASP:OD1	2.31	0.47
1:B:377:GLN:NE2	1:B:461:VAL:H	2.13	0.46
1:B:381:LYS:NZ	1:B:382:ASP:OD2	2.49	0.46
1:A:568:LEU:HD13	2:A:712:HOH:O	2.15	0.46
1:C:390:ILE:HD13	1:C:458:SER:HA	1.98	0.46
1:A:436:ASN:ND2	2:A:652:HOH:O	2.48	0.46
1:C:446:ASP:HB3	1:C:449:GLN:HB2	1.98	0.45
1:B:305:MET:CE	1:B:311:THR:H	2.30	0.45
1:C:557:ASP:OD2	1:C:559:LYS:HE2	2.17	0.45
1:C:300:GLU:OE1	1:C:374:GLU:HG2	2.16	0.45
1:B:470:TYR:HA	1:B:486:LEU:HA	1.99	0.45
1:C:222:ARG:HG3	1:C:228:ASN:HD22	1.82	0.44
1:A:449:GLN:NE2	1:A:450:HIS:H	2.15	0.44
1:C:545:ARG:CG	2:C:781:HOH:O	2.59	0.44
1:C:449:GLN:NE2	1:C:450:HIS:H	2.16	0.44
1:B:487:ALA:HB1	1:B:488:PRO:CD	2.47	0.44
1:B:487:ALA:HB1	1:B:488:PRO:HD2	2.00	0.44
1:C:44:PRO:O	1:C:74:ARG:NH1	2.50	0.44
1:C:313:ASN:OD1	1:C:315:ALA:N	2.47	0.44
1:B:207:LYS:HA	1:B:526:LEU:HD11	1.99	0.44
1:A:112:ASP:OD2	1:A:200:THR:OG1	2.27	0.44
1:A:238:LEU:HB2	1:A:261:LEU:HD11	1.99	0.43
1:A:116:LEU:HD11	1:A:211:ILE:HG12	2.00	0.43
1:A:246:ASN:C	1:A:246:ASN:HD22	2.21	0.43
2:B:724:HOH:O	1:C:438:LEU:HD23	2.18	0.43
1:B:547:ILE:HG21	1:B:572:LEU:HD11	2.01	0.43
1:A:487:ALA:HB1	1:A:488:PRO:HD2	2.00	0.43
1:B:124:TYR:HA	1:B:524:LYS:O	2.18	0.43
1:A:302:ASN:ND2	1:A:342:GLY:HA2	2.30	0.42
1:A:407:TYR:HA	1:A:426:GLY:O	2.19	0.42
1:C:81:PRO:HG2	1:C:84:GLU:HG3	2.01	0.42
1:B:390:ILE:CD1	1:B:458:SER:HA	2.49	0.42
1:A:109:TRP:O	1:A:136:VAL:HA	2.19	0.42
1:C:103:MET:SD	1:C:486:LEU:HG	2.59	0.42
1:C:353:GLN:HA	1:C:353:GLN:OE1	2.20	0.42
1:C:390:ILE:CD1	1:C:458:SER:HA	2.50	0.42
1:C:223:ASN:OD1	1:C:229:ILE:HD11	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:470:TYR:HA	1:C:486:LEU:HA	2.03	0.41
1:A:408:GLY:HA3	1:A:421:LEU:HD12	2.03	0.41
1:B:409:PHE:HB3	1:B:418:TYR:HB3	2.02	0.41
1:A:201:GLY:HA3	1:A:214:PHE:O	2.21	0.41
1:A:78:PRO:HA	1:A:436:ASN:HD21	1.86	0.41
1:B:112:ASP:HB2	1:B:135:LEU:HG	2.03	0.41
1:C:220:PHE:HB3	1:C:222:ARG:HD3	2.03	0.41
1:C:337:ALA:O	1:C:368:CYS:HA	2.21	0.41
1:C:548:LEU:HD21	1:C:572:LEU:HD13	2.02	0.40
1:C:111:TRP:O	1:C:112:ASP:C	2.59	0.40
1:A:111:TRP:O	1:A:112:ASP:C	2.59	0.40
1:B:236:ILE:HG23	1:B:283:PRO:HG3	2.01	0.40
1:B:64:TRP:O	1:B:369:VAL:HG21	2.21	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	536/542 (99%)	518 (97%)	18 (3%)	0	100	100
1	B	536/542 (99%)	509 (95%)	27 (5%)	0	100	100
1	C	536/542 (99%)	518 (97%)	18 (3%)	0	100	100
All	All	1608/1626 (99%)	1545 (96%)	63 (4%)	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	436/438 (100%)	423 (97%)	13 (3%)	48 63
1	B	436/438 (100%)	420 (96%)	16 (4%)	41 54
1	C	436/438 (100%)	421 (97%)	15 (3%)	44 58
All	All	1308/1314 (100%)	1264 (97%)	44 (3%)	44 58

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	196	GLN
1	A	232	TYR
1	A	243	VAL
1	A	246	ASN
1	A	257	LYS
1	A	287	GLU
1	A	321	GLN
1	A	358	GLU
1	A	389	THR
1	A	478	ASP
1	A	536	VAL
1	A	556	LEU
1	A	568	LEU
1	B	99	ASP
1	B	186	GLN
1	B	196	GLN
1	B	232	TYR
1	B	243	VAL
1	B	246	ASN
1	B	307	ARG
1	B	353	GLN
1	B	358	GLU
1	B	389	THR
1	B	391	SER
1	B	536	VAL
1	B	542	GLN
1	B	546	LYS
1	B	556	LEU
1	B	568	LEU
1	C	111	TRP
1	C	180	LYS

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Mol	Chain	Res	Type
1	C	186	GLN
1	C	196	GLN
1	C	230	LYS
1	C	232	TYR
1	C	243	VAL
1	C	246	ASN
1	C	257	LYS
1	C	353	GLN
1	C	391	SER
1	C	531	LYS
1	C	536	VAL
1	C	556	LEU
1	C	568	LEU

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

Mol	Chain	Res	Type
1	A	186	GLN
1	A	191	GLN
1	A	228	ASN
1	A	246	ASN
1	A	279	ASN
1	A	422	ASN
1	A	436	ASN
1	A	449	GLN
1	B	246	ASN
1	B	279	ASN
1	B	306	GLN
1	B	321	GLN
1	B	377	GLN
1	B	419	GLN
1	B	422	ASN
1	B	436	ASN
1	C	52	GLN
1	C	228	ASN
1	C	246	ASN
1	C	256	ASN
1	C	279	ASN
1	C	306	GLN
1	C	422	ASN
1	C	436	ASN
1	C	449	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

There are no ligands in this entry.

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, 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	538/542 (99%)	-0.16	13 (2%)	62	70	18, 26, 48, 73	0
1	B	538/542 (99%)	-0.11	15 (2%)	56	65	19, 27, 45, 73	2 (0%)
1	C	538/542 (99%)	-0.07	12 (2%)	65	72	18, 31, 50, 68	1 (0%)
All	All	1614/1626 (99%)	-0.12	40 (2%)	61	68	18, 28, 48, 73	3 (0%)

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	478	ASP	4.3
1	A	226	GLY	3.9
1	B	458	SER	3.9
1	C	309	THR	3.3
1	C	497	GLY	3.2
1	A	224	SER	3.1
1	C	315	ALA	3.0
1	A	223	ASN	3.0
1	B	558	GLY	3.0
1	C	322	GLY	2.9
1	A	547	ILE	2.8
1	B	498	GLY	2.8
1	A	225	ASP	2.8
1	B	224	SER	2.7
1	B	559	LYS	2.7
1	C	458	SER	2.7
1	C	390	ILE	2.6
1	B	557	ASP	2.6
1	B	548	LEU	2.5
1	A	227	THR	2.4
1	C	292	PRO	2.4
1	C	224	SER	2.4
1	C	510	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	546	LYS	2.4
1	B	542	GLN	2.4
1	A	189	GLU	2.4
1	B	539	GLU	2.3
1	C	308	GLU	2.3
1	A	390	ILE	2.2
1	A	478	ASP	2.2
1	B	390	ILE	2.2
1	B	58	ASP	2.2
1	A	321	GLN	2.2
1	A	498	GLY	2.1
1	C	495	GLY	2.1
1	B	290	ALA	2.1
1	B	546	LYS	2.1
1	A	229	ILE	2.1
1	B	206	SER	2.0
1	C	321	GLN	2.0

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

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.