



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:06 AM GMT

PDB ID : 3H3L
Title : Crystal structure of PUTATIVE SUGAR HYDROLASE (YP_001304206.1)
from Parabacteroides distasonis ATCC 8503 at 1.59 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2009-04-16
Resolution : 1.59 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

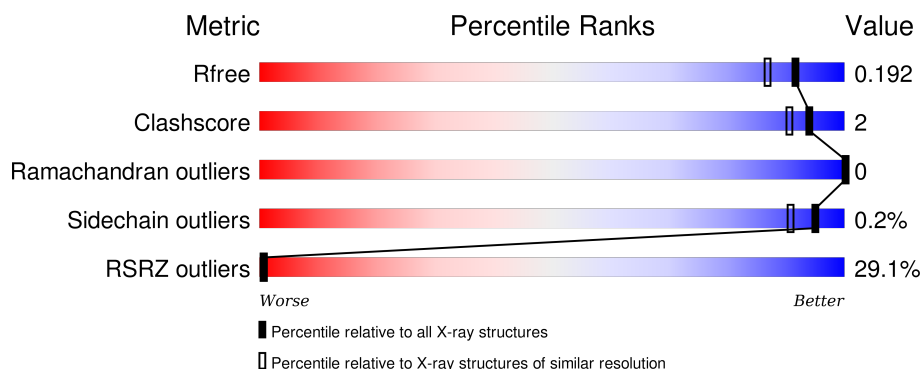
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.59 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	2475 (1.60-1.60)
Clashscore	102246	2732 (1.60-1.60)
Ramachandran outliers	100387	2654 (1.60-1.60)
Sidechain outliers	100360	2653 (1.60-1.60)
RSRZ outliers	91569	2479 (1.60-1.60)

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	241	<div> <div>28%</div> <div>93%</div> <div>• •</div> </div>
1	B	241	<div> <div>21%</div> <div>92%</div> <div>• 5%</div> </div>
1	C	241	<div> <div>31%</div> <div>88%</div> <div>5% 7%</div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6134 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.

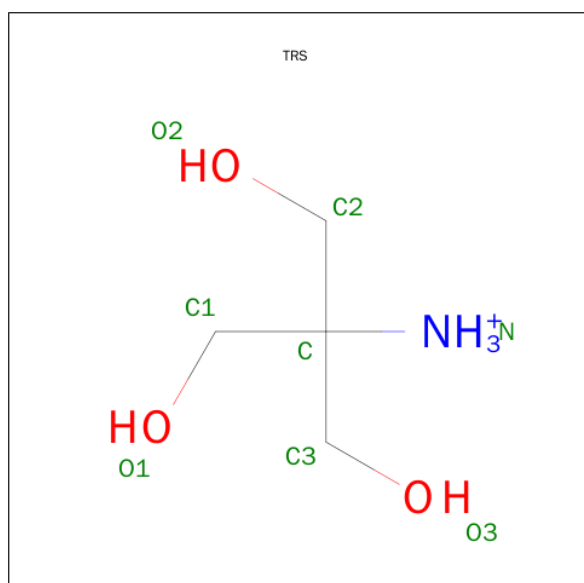
- Molecule 1 is a protein called PUTATIVE SUGAR HYDROLASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	232	Total	C	N	O	S	Se	0	11	0
			1899	1220	314	350	6	9			
1	B	229	Total	C	N	O	S	Se	0	13	0
			1885	1216	309	346	6	8			
1	C	223	Total	C	N	O	S	Se	0	13	0
			1838	1184	297	341	6	10			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	leader sequence	UNP A6LFX0
B	0	GLY	-	leader sequence	UNP A6LFX0
C	0	GLY	-	leader sequence	UNP A6LFX0

- Molecule 2 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: $C_4H_{12}NO_3$).



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

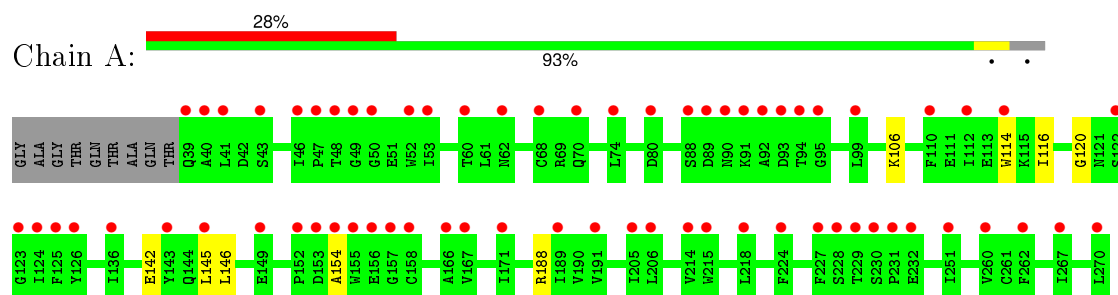
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	178	Total	O	0	0
			178	178		
3	B	169	Total	O	0	0
			169	169		
3	C	141	Total	O	0	0
			141	141		

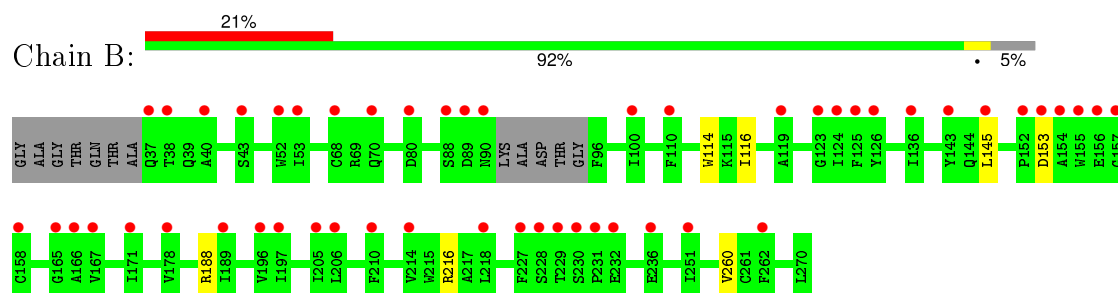
3 Residue-property plots [i](#)

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.

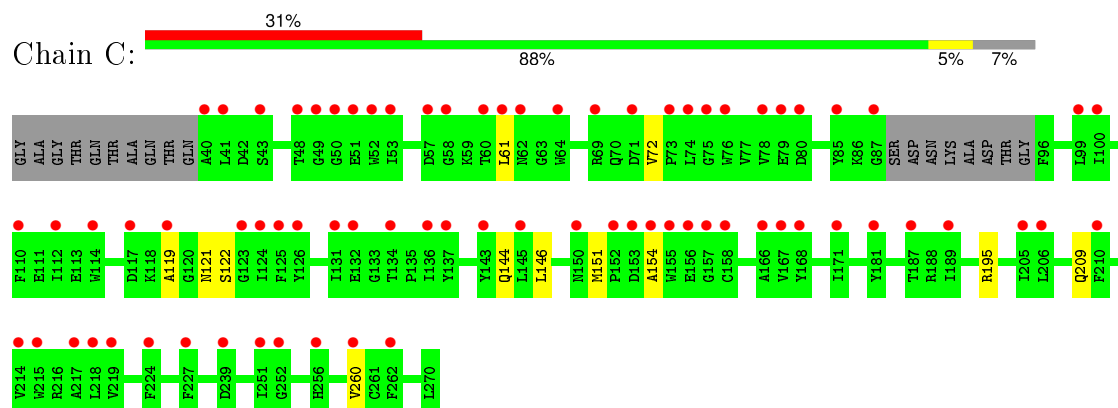
• Molecule 1: PUTATIVE SUGAR HYDROLASE



• Molecule 1: PUTATIVE SUGAR HYDROLASE



• Molecule 1: PUTATIVE SUGAR HYDROLASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	117.26Å 117.26Å 118.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.31 – 1.59 29.31 – 1.59	Depositor EDS
% Data completeness (in resolution range)	96.6 (29.31-1.59) 96.6 (29.31-1.59)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.42 (at 1.59Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.170 , 0.185 0.181 , 0.192	Depositor DCC
R_{free} test set	5358 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	21.8	Xtriage
Anisotropy	0.102	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 49.2	EDS
Estimated twinning fraction	0.019 for -h,l,k 0.013 for -l,-k,-h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 107212 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6134	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.68% 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: TRS

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	0.58	0/1974	0.78	2/2659 (0.1%)
1	B	0.58	0/1968	0.74	3/2650 (0.1%)
1	C	0.60	0/1921	0.78	0/2589
All	All	0.58	0/5863	0.77	5/7898 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	188[A]	ARG	NE-CZ-NH1	6.50	123.55	120.30
1	A	188[B]	ARG	NE-CZ-NH1	6.50	123.55	120.30
1	B	216	ARG	NE-CZ-NH1	5.13	122.86	120.30
1	B	188[A]	ARG	NE-CZ-NH1	5.08	122.84	120.30
1	B	188[B]	ARG	NE-CZ-NH1	5.08	122.84	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	1899	0	1819	5	0
1	B	1885	0	1817	2	0
1	C	1838	0	1755	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	8	0	12	0	0
2	B	8	0	12	0	0
2	C	8	0	12	0	0
3	A	178	0	0	2	0
3	B	169	0	0	0	0
3	C	141	0	0	1	0
All	All	6134	0	5427	20	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 2.

All (20) 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:C:121[A]:ASN:HB2	1:C:151[A]:MSE:HE3	1.54	0.89
1:C:195[A]:ARG:HG2	1:C:209[A]:GLN:OE1	1.74	0.87
1:C:122:SER:O	3:C:420:HOH:O	2.13	0.67
1:C:146:LEU:HD11	1:C:151[A]:MSE:HG2	1.84	0.60
1:C:146:LEU:CD1	1:C:151[A]:MSE:HG2	2.36	0.55
1:C:195[A]:ARG:CG	1:C:209[A]:GLN:OE1	2.52	0.53
1:C:144:GLN:NE2	1:C:146:LEU:HD13	2.25	0.52
1:C:146:LEU:HD11	1:C:151[A]:MSE:CG	2.39	0.52
1:C:121[A]:ASN:CB	1:C:151[A]:MSE:HE3	2.35	0.52
1:C:119:ALA:O	1:C:151[B]:MSE:SE	2.84	0.45
1:B:114:TRP:CE2	1:B:145:LEU:HD22	2.51	0.45
1:B:116:ILE:HG13	1:B:260:VAL:HG22	1.97	0.45
1:C:61:LEU:HD12	1:C:72:VAL:HG11	1.99	0.45
1:A:142:GLU:OE2	3:A:415:HOH:O	2.20	0.45
1:A:146:LEU:HD21	1:A:154:ALA:HB2	1.98	0.44
1:A:116:ILE:HD11	1:A:120:GLY:C	2.38	0.43
1:C:146:LEU:HD21	1:C:154:ALA:N	2.33	0.43
1:A:114:TRP:CE2	1:A:145:LEU:HD22	2.53	0.43
1:C:122:SER:HB2	1:C:260:VAL:HG21	2.01	0.42
1:A:106[B]:LYS:NZ	3:A:380:HOH:O	2.53	0.41

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	240/241 (100%)	229 (95%)	11 (5%)	0	100	100
1	B	238/241 (99%)	231 (97%)	7 (3%)	0	100	100
1	C	232/241 (96%)	226 (97%)	6 (3%)	0	100	100
All	All	710/723 (98%)	686 (97%)	24 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	200/197 (102%)	200 (100%)	0	100	100
1	B	200/197 (102%)	199 (100%)	1 (0%)	92	85
1	C	196/197 (100%)	196 (100%)	0	100	100
All	All	596/591 (101%)	595 (100%)	1 (0%)	95	91

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	153	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

3 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	TRS	A	2	-	7,7,7	0.73	0	9,9,9	1.25	1 (11%)
2	TRS	B	3	-	7,7,7	0.72	0	9,9,9	1.22	2 (22%)
2	TRS	C	1	-	7,7,7	0.59	0	9,9,9	1.68	3 (33%)

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	TRS	A	2	-	-	0/9/9/9	0/0/0/0
2	TRS	B	3	-	-	0/9/9/9	0/0/0/0
2	TRS	C	1	-	-	0/9/9/9	0/0/0/0

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	2	TRS	C3-C-C1	-2.68	104.98	110.78
2	B	3	TRS	C3-C-C1	-2.58	105.19	110.78
2	C	1	TRS	C2-C-C1	-2.06	106.32	110.78
2	B	3	TRS	C2-C-N	2.29	112.25	108.09
2	C	1	TRS	C3-C-N	2.94	113.44	108.09
2	C	1	TRS	O3-C3-C	3.22	117.70	111.18

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, 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	225/241 (93%)	1.68	67 (29%) 1 0	30, 35, 49, 63	0
1	B	222/241 (92%)	1.52	51 (22%) 1 1	30, 35, 47, 62	0
1	C	216/241 (89%)	1.86	75 (34%) 0 0	30, 35, 44, 58	0
All	All	663/723 (91%)	1.68	193 (29%) 1 1	30, 35, 47, 63	0

All (193) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	155	TRP	15.5
1	A	155	TRP	12.3
1	C	155	TRP	12.3
1	A	93	ASP	9.8
1	C	49	GLY	9.2
1	A	94	THR	8.4
1	A	49	GLY	7.9
1	B	231	PRO	7.8
1	B	89	ASP	7.8
1	B	88	SER	7.7
1	A	90	ASN	7.6
1	A	154	ALA	7.4
1	B	154	ALA	7.2
1	A	229	THR	7.0
1	A	39[A]	GLN	7.0
1	C	48	THR	6.9
1	C	124	ILE	6.7
1	C	74	LEU	6.7
1	C	152	PRO	6.5
1	C	60	THR	6.5
1	B	227	PHE	6.4
1	B	156	GLU	6.1
1	A	152	PRO	6.1

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Mol	Chain	Res	Type	RSRZ
1	A	157	GLY	6.0
1	C	87	GLY	5.8
1	A	231	PRO	5.8
1	A	227	PHE	5.8
1	B	37	GLN	5.7
1	C	119	ALA	5.7
1	B	152	PRO	5.6
1	B	229	THR	5.6
1	C	251	ILE	5.5
1	C	62	ASN	5.5
1	B	124	ILE	5.3
1	A	48	THR	5.3
1	C	154	ALA	5.2
1	B	125	PHE	5.1
1	A	40	ALA	5.1
1	C	181	TYR	5.0
1	A	91	LYS	4.9
1	C	125	PHE	4.7
1	A	92	ALA	4.7
1	B	167	VAL	4.6
1	C	58	GLY	4.6
1	A	153	ASP	4.6
1	B	143	TYR	4.6
1	B	90	ASN	4.6
1	A	95	GLY	4.5
1	A	124	ILE	4.5
1	B	171	ILE	4.5
1	B	251	ILE	4.5
1	C	50	GLY	4.4
1	C	43[A]	SER	4.4
1	C	189	ILE	4.4
1	A	156	GLU	4.3
1	C	71	ASP	4.3
1	C	157	GLY	4.2
1	C	153	ASP	4.2
1	C	75	GLY	4.2
1	A	52	TRP	4.2
1	B	230	SER	4.2
1	C	143	TYR	4.1
1	B	145	LEU	4.0
1	C	61	LEU	4.0
1	A	126	TYR	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	74	LEU	3.9
1	A	60	THR	3.9
1	B	126	TYR	3.9
1	C	150	ASN	3.9
1	B	189	ILE	3.8
1	B	153	ASP	3.8
1	B	53[A]	ILE	3.8
1	B	38	THR	3.8
1	A	167	VAL	3.8
1	C	117[A]	ASP	3.7
1	C	167	VAL	3.7
1	C	145	LEU	3.7
1	A	171	ILE	3.6
1	C	112	ILE	3.6
1	C	80	ASP	3.6
1	B	157	GLY	3.5
1	A	145	LEU	3.5
1	C	214	VAL	3.5
1	C	40	ALA	3.5
1	B	100	ILE	3.5
1	A	251	ILE	3.4
1	C	123	GLY	3.4
1	C	136	ILE	3.4
1	C	76	TRP	3.3
1	A	143	TYR	3.3
1	C	156	GLU	3.3
1	B	210	PHE	3.3
1	C	262	PHE	3.2
1	C	114	TRP	3.2
1	C	110	PHE	3.1
1	C	57	ASP	3.1
1	C	78	VAL	3.1
1	A	47	PRO	3.1
1	C	171	ILE	3.1
1	A	125	PHE	3.0
1	B	123	GLY	3.0
1	C	79	GLU	3.0
1	C	187	THR	3.0
1	A	136	ILE	3.0
1	A	189	ILE	3.0
1	A	158	CYS	2.9
1	A	218	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	214	VAL	2.9
1	A	114	TRP	2.9
1	B	218	LEU	2.9
1	A	206	LEU	2.9
1	C	99	LEU	2.9
1	B	136	ILE	2.9
1	A	262	PHE	2.9
1	C	85	TYR	2.9
1	A	80[A]	ASP	2.9
1	B	119	ALA	2.9
1	C	166	ALA	2.9
1	C	206	LEU	2.8
1	B	214	VAL	2.8
1	C	73	PRO	2.8
1	A	123	GLY	2.8
1	C	168	TYR	2.8
1	B	70	GLN	2.8
1	A	191	VAL	2.7
1	B	232[A]	GLU	2.7
1	B	262	PHE	2.7
1	A	68	CYS	2.7
1	A	112	ILE	2.7
1	C	51	GLU	2.7
1	C	252	GLY	2.7
1	A	230	SER	2.6
1	C	205	ILE	2.6
1	B	166	ALA	2.6
1	C	218	LEU	2.6
1	C	126	TYR	2.6
1	A	205	ILE	2.6
1	C	100	ILE	2.6
1	C	227	PHE	2.6
1	C	41	LEU	2.6
1	A	62	ASN	2.6
1	A	46	ILE	2.6
1	A	267	ILE	2.6
1	A	89	ASP	2.5
1	B	165	GLY	2.5
1	C	69	ARG	2.5
1	C	52	TRP	2.5
1	C	64	TRP	2.5
1	A	50	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	88	SER	2.4
1	C	158	CYS	2.4
1	C	219	VAL	2.4
1	B	206	LEU	2.4
1	B	52	TRP	2.4
1	A	53	ILE	2.4
1	A	270	LEU	2.4
1	A	228	SER	2.4
1	B	80	ASP	2.4
1	B	43[A]	SER	2.4
1	B	158	CYS	2.4
1	C	137	TYR	2.3
1	A	99	LEU	2.3
1	C	131	ILE	2.3
1	A	215	TRP	2.3
1	C	260	VAL	2.3
1	A	41	LEU	2.3
1	C	239	ASP	2.3
1	A	166	ALA	2.3
1	B	178	VAL	2.3
1	A	232	GLU	2.3
1	A	110	PHE	2.3
1	C	134	THR	2.2
1	C	217	ALA	2.2
1	B	110	PHE	2.2
1	C	256	HIS	2.2
1	B	196	VAL	2.2
1	A	70	GLN	2.2
1	B	205	ILE	2.2
1	A	149	GLU	2.2
1	A	224	PHE	2.2
1	C	210	PHE	2.2
1	C	224	PHE	2.2
1	B	68	CYS	2.1
1	B	228	SER	2.1
1	B	197	ILE	2.1
1	C	53	ILE	2.1
1	C	215	TRP	2.1
1	A	122	SER	2.1
1	B	236	GLU	2.0
1	C	132[A]	GLU	2.0
1	A	260	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	43[A]	SER	2.0
1	B	40	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(Å ²)	Q<0.9
2	TRS	C	1	8/8	0.87	0.20	0.58	30,39,41,43	0
2	TRS	A	2	8/8	0.87	0.17	0.02	25,29,32,33	0
2	TRS	B	3	8/8	0.92	0.16	-0.11	26,32,34,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.