



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 06:23 pm GMT

PDB ID : 5J6D
Title : Discovery of acyl guanidine tryptophan hydroxylase-1 inhibitors
Authors : Stein, A.J.; Goldberg, D.R.; De Lombaert, S.
Deposited on : 2016-04-04
Resolution : 1.90 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

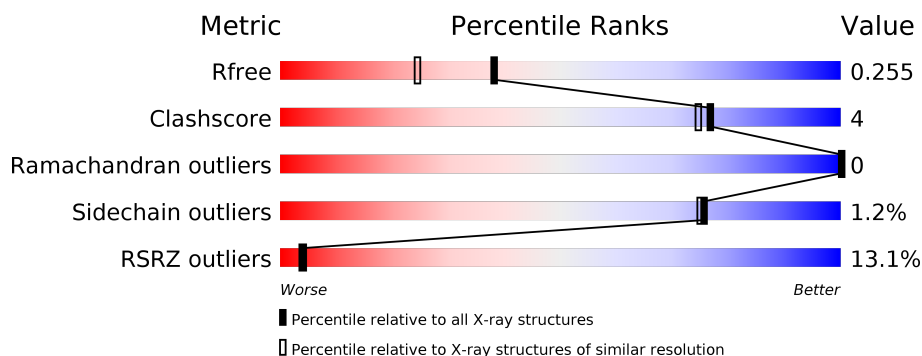
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	100719	5047 (1.90-1.90)
Clashscore	112137	5731 (1.90-1.90)
Ramachandran outliers	110173	5669 (1.90-1.90)
Sidechain outliers	110143	5670 (1.90-1.90)
RSRZ outliers	101464	5100 (1.90-1.90)

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	307	<div> <div>2%</div> <div>92%</div> <div>5%</div> </div>
1	B	307	<div> <div>21%</div> <div>71%</div> <div>8%</div> <div>19%</div> </div>

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	FE	A	501	-	-	-	X
4	GOL	A	503	-	-	-	X
4	GOL	B	503	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4335 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 Tryptophan 5-hydroxylase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	292	Total	C	N	O	S	0	1	0
			2317	1494	385	425	13			
1	B	248	Total	C	N	O	S	0	1	0
			1768	1136	293	326	13			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	403	HIS	-	expression tag	UNP P17752
A	404	HIS	-	expression tag	UNP P17752
A	405	HIS	-	expression tag	UNP P17752
A	406	HIS	-	expression tag	UNP P17752
A	407	HIS	-	expression tag	UNP P17752
A	408	HIS	-	expression tag	UNP P17752
B	403	HIS	-	expression tag	UNP P17752
B	404	HIS	-	expression tag	UNP P17752
B	405	HIS	-	expression tag	UNP P17752
B	406	HIS	-	expression tag	UNP P17752
B	407	HIS	-	expression tag	UNP P17752
B	408	HIS	-	expression tag	UNP P17752

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Fe	0	0
			1	1		
2	A	1	Total	Fe	0	0
			1	1		

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C₄H₁₂NO₃).



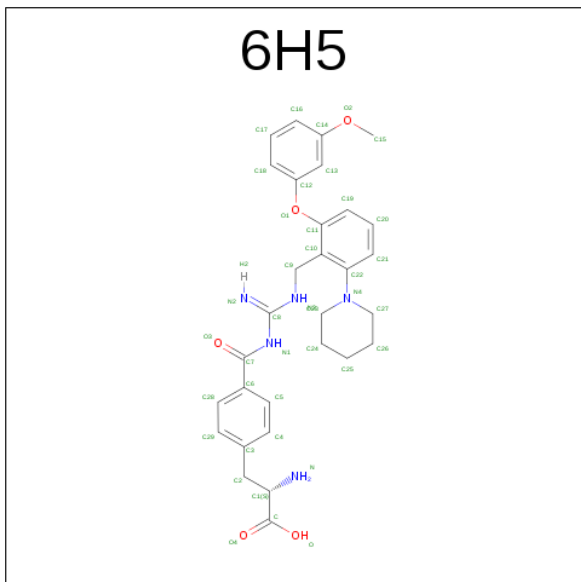
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			8	4	1	3		
3	B	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is 4-[(N-{[2-(3-methoxyphenoxy)-6-(piperidin-1-yl)phenyl]methyl}carbamimidoyl)carbamoyl]-L-phenylalanine (three-letter code: 6H5) (formula: C₃₀H₃₅N₅O₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			40	30	5	5		
5	B	1	Total	C	N	O	0	0
			40	30	5	5		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	123	Total	O	0	0
			123	123		
6	B	17	Total	O	0	0
			17	17		

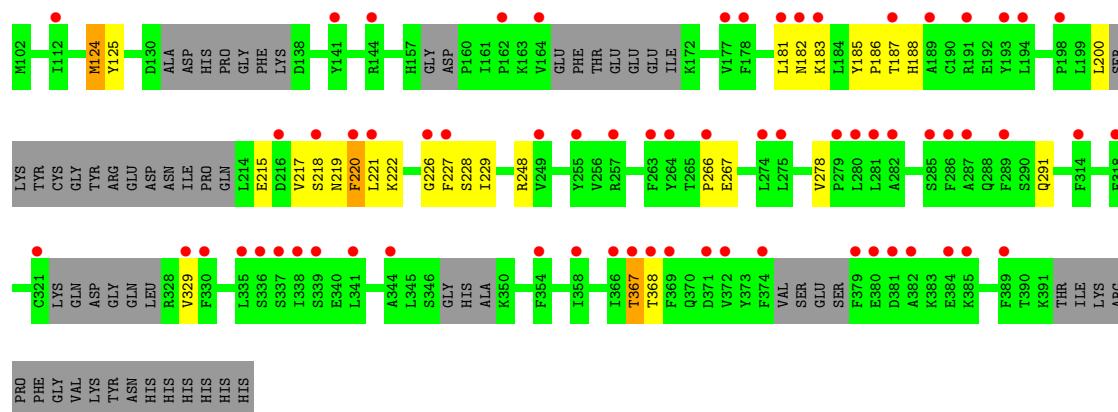
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Tryptophan 5-hydroxylase 1



• Molecule 1: Tryptophan 5-hydroxylase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.73Å 63.56Å 156.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.90 49.33 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-1.90) 99.9 (49.33-1.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.86 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.210 , 0.248 0.218 , 0.255	Depositor DCC
R_{free} test set	2245 reflections (5.01%)	DCC
Wilson B-factor (Å ²)	33.2	Xtriage
Anisotropy	0.075	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 58.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4335	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.74% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 6H5, GOL, TRS, FE

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	0.60	0/2384	0.71	3/3230 (0.1%)
1	B	0.54	0/1812	0.75	7/2472 (0.3%)
All	All	0.57	0/4196	0.73	10/5702 (0.2%)

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
1	B	0	1

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	124[A]	MET	CA-C-O	-8.26	102.75	120.10
1	B	124[B]	MET	CA-C-O	-8.26	102.75	120.10
1	B	124[A]	MET	CA-C-N	7.22	133.08	117.20
1	B	124[B]	MET	CA-C-N	7.22	133.08	117.20
1	A	328	ARG	NE-CZ-NH2	5.27	122.94	120.30
1	B	368	THR	N-CA-C	5.25	125.17	111.00
1	B	124[A]	MET	N-CA-C	5.16	124.94	111.00
1	B	124[B]	MET	N-CA-C	5.16	124.94	111.00
1	A	248	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	A	121	ARG	NE-CZ-NH2	5.01	122.81	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	367	THR	Peptide

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	2317	0	2236	3	0
1	B	1768	0	1518	25	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	8	0	9	0	0
3	B	8	0	10	0	0
4	A	6	0	8	0	0
4	B	6	0	8	0	0
5	A	40	0	0	0	0
5	B	40	0	0	0	0
6	A	123	0	0	0	0
6	B	17	0	0	0	0
All	All	4335	0	3789	28	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 (28) 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:B:124[B]:MET:HE3	1:B:124[B]:MET:HA	1.45	0.98
1:B:221:LEU:HD11	1:B:278:VAL:HG13	1.54	0.89
1:B:182:ASN:O	1:B:186:PRO:HD3	1.84	0.77
1:B:124[B]:MET:HA	1:B:124[B]:MET:CE	2.15	0.76
1:B:221:LEU:HD21	1:B:278:VAL:HG13	1.73	0.69
1:B:200:LEU:HD22	1:B:220:PHE:CE2	2.31	0.66
1:B:124[B]:MET:CA	1:B:124[B]:MET:CE	2.74	0.65
1:B:124[B]:MET:CA	1:B:124[B]:MET:HE3	2.25	0.57
1:B:217:VAL:O	1:B:221:LEU:HG	2.05	0.57
1:B:220:PHE:C	1:B:220:PHE:CD1	2.80	0.54
1:B:200:LEU:HD22	1:B:220:PHE:HE2	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:221:LEU:HD21	1:B:278:VAL:CG1	2.40	0.50
1:B:221:LEU:HD11	1:B:278:VAL:CG1	2.33	0.49
1:B:221:LEU:CD1	1:B:278:VAL:HG13	2.34	0.47
1:A:272:HIS:HA	1:A:336:SER:CB	2.45	0.47
1:B:218:SER:HB2	1:B:229:ILE:HB	1.96	0.46
1:B:266:PRO:HB2	1:B:367:THR:HG22	1.98	0.45
1:B:183:LYS:O	1:B:186:PRO:HD2	2.18	0.44
1:B:125:TYR:OH	1:B:267:GLU:OE2	2.30	0.43
1:B:215:GLU:OE2	1:B:219:ASN:ND2	2.51	0.43
1:B:181:LEU:O	1:B:185:TYR:N	2.51	0.43
1:B:222:LYS:O	1:B:226:GLY:HA2	2.19	0.43
1:B:200:LEU:HD22	1:B:220:PHE:CZ	2.54	0.43
1:A:380:GLU:OE1	1:A:383:LYS:NZ	2.45	0.43
1:B:248:ARG:NE	1:B:291:GLN:OE1	2.44	0.41
1:B:217:VAL:HG11	1:B:278:VAL:HG21	2.03	0.41
1:A:122:VAL:HG21	1:A:233:ALA:HB3	2.02	0.41
1:B:188:HIS:O	1:B:329:VAL:HG12	2.20	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	291/307 (95%)	288 (99%)	3 (1%)	0	100	100
1	B	233/307 (76%)	226 (97%)	7 (3%)	0	100	100
All	All	524/614 (85%)	514 (98%)	10 (2%)	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	248/273 (91%)	247 (100%)	1 (0%)	93	93
1	B	160/273 (59%)	156 (98%)	4 (2%)	53	45
All	All	408/546 (75%)	403 (99%)	5 (1%)	75	75

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	227	PHE
1	B	187	THR
1	B	220	PHE
1	B	227	PHE
1	B	228	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	117	HIS

5.3.3 RNA [i](#)

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 carbohydrates in this entry.

5.6 Ligand geometry

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 for Mogul analysis.

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	$\# Z > 2$
3	TRS	A	502	2	7,7,7	0.41	0	9,9,9	0.45	0
4	GOL	A	503	-	5,5,5	0.25	0	5,5,5	0.34	0
5	6H5	A	504	-	38,43,43	0.83	1 (2%)	50,58,58	1.41	3 (6%)
3	TRS	B	502	2	7,7,7	0.54	0	9,9,9	0.82	0
4	GOL	B	503	-	5,5,5	0.56	0	5,5,5	0.57	0
5	6H5	B	504	-	38,43,43	0.82	1 (2%)	50,58,58	1.72	7 (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
3	TRS	A	502	2	-	0/9/9/9	0/0/0/0
4	GOL	A	503	-	-	0/4/4/4	0/0/0/0
5	6H5	A	504	-	-	0/27/39/39	0/4/4/4
3	TRS	B	502	2	-	0/9/9/9	0/0/0/0
4	GOL	B	503	-	-	0/4/4/4	0/0/0/0
5	6H5	B	504	-	-	0/27/39/39	0/4/4/4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	504	6H5	C8-N1	-3.50	1.28	1.36
5	B	504	6H5	C8-N1	-3.26	1.29	1.36

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	504	6H5	C21-C22-N4	-5.22	114.08	122.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	504	6H5	C21-C22-N4	-4.74	114.84	122.28
5	B	504	6H5	O3-C7-C6	-2.21	117.02	120.94
5	A	504	6H5	C11-O1-C12	2.21	123.75	117.97
5	B	504	6H5	C9-C10-C22	2.37	124.00	121.63
5	B	504	6H5	C11-O1-C12	3.05	125.93	117.97
5	B	504	6H5	C6-C7-N1	3.44	121.57	116.25
5	B	504	6H5	C15-O2-C14	4.51	127.37	117.50
5	A	504	6H5	C23-N4-C27	6.20	124.71	111.57
5	B	504	6H5	C23-N4-C27	6.50	125.35	111.57

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	292/307 (95%)	0.26	5 (1%) 70 73	22, 33, 54, 82	0
1	B	248/307 (80%)	1.40	66 (26%) 1 1	32, 71, 96, 108	0
All	All	540/614 (87%)	0.79	71 (13%) 4 4	22, 44, 88, 108	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	181	LEU	9.0
1	B	354	PHE	7.6
1	B	220	PHE	6.4
1	B	274	LEU	6.1
1	B	358	ILE	5.3
1	B	227	PHE	5.0
1	B	329	VAL	4.9
1	B	289	PHE	4.8
1	B	338	ILE	4.7
1	B	379	PHE	4.6
1	B	389	PHE	4.5
1	B	286	PHE	4.2
1	B	279	PRO	4.2
1	B	367	THR	4.2
1	B	221	LEU	4.2
1	B	314	PHE	4.1
1	B	321	CYS	3.9
1	B	280	LEU	3.8
1	B	193	TYR	3.6
1	B	264	TYR	3.6
1	B	112	ILE	3.5
1	B	285	SER	3.5
1	B	255	TYR	3.5
1	B	162	PRO	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	384	GLU	3.4
1	B	369	PHE	3.3
1	B	366	ILE	3.3
1	B	372	VAL	3.2
1	B	381	ASP	3.2
1	B	266	PRO	3.1
1	B	275	LEU	3.0
1	B	371	ASP	3.0
1	B	281	LEU	2.9
1	B	249	VAL	2.9
1	B	344	ALA	2.8
1	B	336	SER	2.8
1	B	337	SER	2.8
1	B	282	ALA	2.7
1	B	318	PHE	2.7
1	B	177	VAL	2.7
1	B	178	PHE	2.7
1	B	182	ASN	2.7
1	B	189	ALA	2.6
1	B	257	ARG	2.6
1	A	130	ASP	2.6
1	A	102	MET	2.6
1	B	218	SER	2.6
1	B	380	GLU	2.5
1	B	335	LEU	2.4
1	B	368	THR	2.4
1	B	341	LEU	2.4
1	B	287	ALA	2.4
1	B	382	ALA	2.4
1	B	216	ASP	2.3
1	B	191	ARG	2.3
1	B	385	LYS	2.3
1	B	226	GLY	2.3
1	B	141	TYR	2.3
1	A	133	HIS	2.2
1	B	263	PHE	2.2
1	B	187	THR	2.2
1	B	374	PHE	2.2
1	B	194	LEU	2.1
1	B	144	ARG	2.1
1	B	339	SER	2.1
1	B	330	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	199	LEU	2.1
1	B	198	PRO	2.1
1	A	137	LYS	2.0
1	B	183	LYS	2.0
1	B	164	VAL	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	FE	A	501	1/1	1.00	0.18	5.32	23,23,23,23	0
4	GOL	A	503	6/6	0.79	0.24	4.99	39,47,51,52	0
4	GOL	B	503	6/6	0.92	0.18	3.46	40,43,46,47	0
3	TRS	A	502	8/8	0.95	0.14	1.84	24,24,26,26	0
3	TRS	B	502	8/8	0.93	0.14	-0.24	46,48,50,55	0
5	6H5	A	504	40/40	0.95	0.11	-0.27	25,31,37,49	0
5	6H5	B	504	40/40	0.87	0.14	-0.59	43,49,62,64	0
2	FE	B	501	1/1	0.97	0.12	-3.16	48,48,48,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.