



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2023 – 04:44 PM JST

PDB ID : 8H4G
Title : Blasnase-T13A/M57N
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Deposited on : 2022-10-10
Resolution : 1.81 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)
Xtrriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

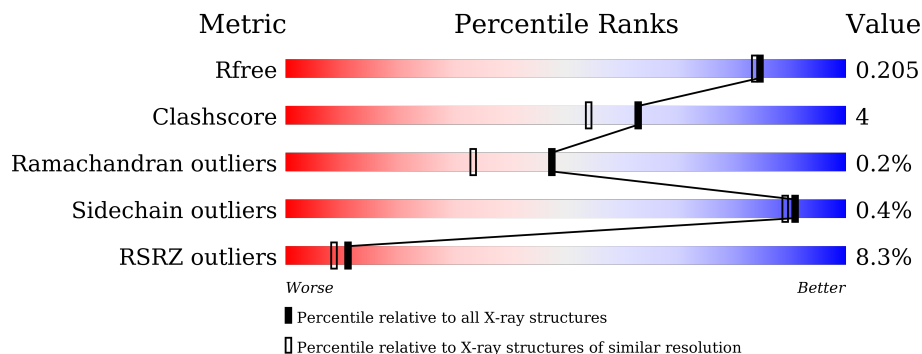
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.81 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	7484 (1.84-1.80)
Clashscore	141614	8401 (1.84-1.80)
Ramachandran outliers	138981	8290 (1.84-1.80)
Sidechain outliers	138945	8290 (1.84-1.80)
RSRZ outliers	127900	7371 (1.84-1.80)

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	A	329	
1	B	329	

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
3	FMT	A	406	-	-	X	-
3	FMT	A	409	-	-	-	X
3	FMT	B	406	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5587 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 L-asparaginase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	319	2487	1581	425	474	7	0	0	0
1	B	323	2506	1592	427	480	7	0	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	13	ALA	THR	engineered mutation	UNP A0A6I7U6Y2
A	57	ASN	MET	engineered mutation	UNP A0A6I7U6Y2
A	323	LEU	-	expression tag	UNP A0A6I7U6Y2
A	324	GLU	-	expression tag	UNP A0A6I7U6Y2
A	325	HIS	-	expression tag	UNP A0A6I7U6Y2
A	326	HIS	-	expression tag	UNP A0A6I7U6Y2
A	327	HIS	-	expression tag	UNP A0A6I7U6Y2
A	328	HIS	-	expression tag	UNP A0A6I7U6Y2
A	329	HIS	-	expression tag	UNP A0A6I7U6Y2
B	13	ALA	THR	engineered mutation	UNP A0A6I7U6Y2
B	57	ASN	MET	engineered mutation	UNP A0A6I7U6Y2
B	323	LEU	-	expression tag	UNP A0A6I7U6Y2
B	324	GLU	-	expression tag	UNP A0A6I7U6Y2
B	325	HIS	-	expression tag	UNP A0A6I7U6Y2
B	326	HIS	-	expression tag	UNP A0A6I7U6Y2
B	327	HIS	-	expression tag	UNP A0A6I7U6Y2
B	328	HIS	-	expression tag	UNP A0A6I7U6Y2
B	329	HIS	-	expression tag	UNP A0A6I7U6Y2

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

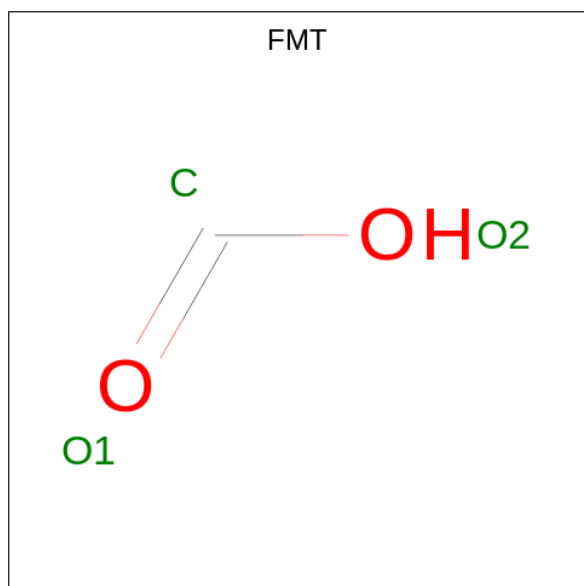
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mg	2	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
2	B	1	1	1	1	0

- Molecule 3 is FORMIC ACID (three-letter code: FMT) (formula: CH₂O₂).



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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 3 1 2	3	0
3	B	1	Total C O 3 1 2	0	0
3	B	1	Total C O 3 1 2	0	0

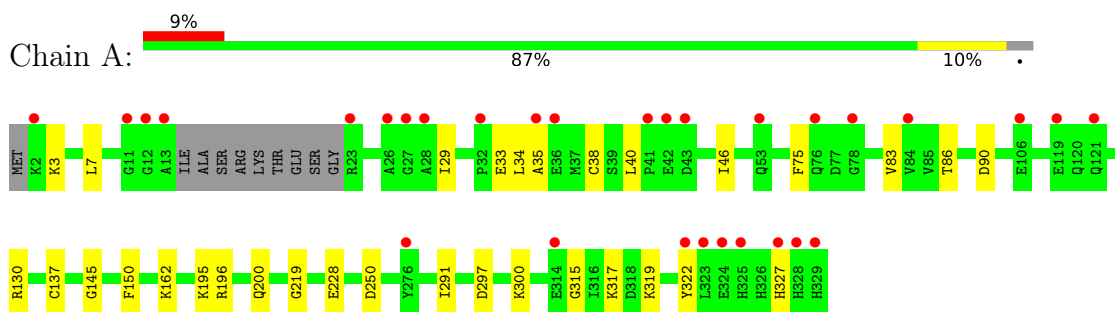
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	242	Total O 242 242	0	0
4	B	310	Total O 310 310	0	0

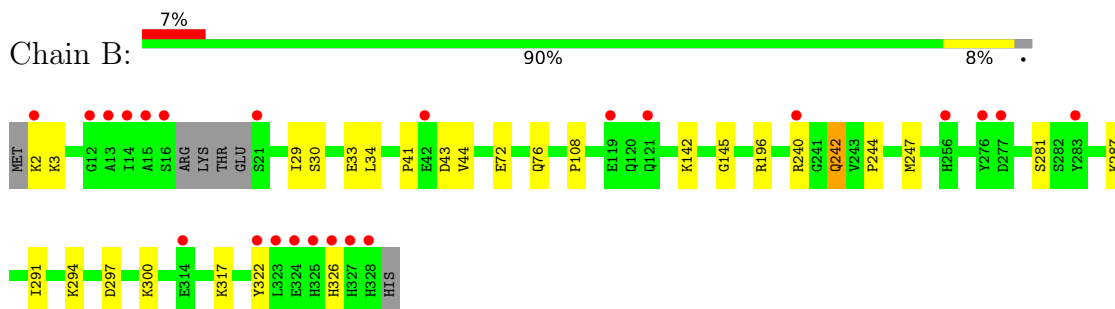
3 Residue-property plots [i](#)

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: L-asparaginase



- Molecule 1: L-asparaginase



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	92.31Å 92.31Å 233.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.95 – 1.81 19.95 – 1.81	Depositor EDS
% Data completeness (in resolution range)	99.9 (19.95-1.81) 100.0 (19.95-1.81)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.48 (at 1.81Å)	Xtrriage
Refinement program	PHENIX v1.16	Depositor
R, R_{free}	0.196 , 0.205 0.196 , 0.205	Depositor DCC
R_{free} test set	4703 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	32.4	Xtrriage
Anisotropy	0.287	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 38.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5587	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.09% 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: MG, FMT

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	2/2538 (0.1%)	0.66	0/3439
1	B	0.58	0/2556	0.65	0/3463
All	All	0.56	2/5094 (0.0%)	0.66	0/6902

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	228	GLU	CD-OE2	-5.25	1.19	1.25
1	A	228	GLU	CD-OE1	-5.07	1.20	1.25

There are no bond angle outliers.

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	2487	0	2454	23	0
1	B	2506	0	2476	22	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0
3	A	21	0	7	4	0
3	B	18	0	6	3	0
4	A	242	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	310	0	0	2	0
All	All	5587	0	4943	43	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 (43) 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:300:LYS:HG3	3:A:406:FMT:H	1.50	0.92
1:B:300:LYS:HG3	3:B:406:FMT:H	1.61	0.82
1:A:327:HIS:HB3	4:A:508:HOH:O	1.89	0.73
1:A:300:LYS:CG	3:A:406:FMT:H	2.21	0.70
1:B:30:SER:OG	1:B:33:GLU:HG3	1.91	0.70
1:A:29:ILE:HG23	1:A:33:GLU:HG3	1.73	0.69
1:A:315:GLY:O	1:A:319:LYS:HG3	1.96	0.65
1:B:76:GLN:NE2	4:B:504:HOH:O	2.29	0.65
1:B:2:LYS:HE2	1:B:43:ASP:OD2	1.99	0.62
1:A:35:ALA:HA	1:A:40:LEU:HD12	1.81	0.62
1:B:29:ILE:HD12	1:B:34:LEU:HB2	1.81	0.61
1:A:38:CYS:O	1:A:130:ARG:HD3	2.02	0.60
1:B:41:PRO:HG2	1:B:44:VAL:HG23	1.84	0.60
1:B:300:LYS:CG	3:B:406:FMT:H	2.32	0.59
1:B:297:ASP:H	3:B:406:FMT:C	2.18	0.56
1:A:145:GLY:HA2	1:A:196:ARG:NH1	2.20	0.56
1:B:196:ARG:HG2	1:B:196:ARG:HH11	1.70	0.56
1:A:327:HIS:CB	4:A:508:HOH:O	2.50	0.56
1:A:297:ASP:H	3:A:406:FMT:C	2.20	0.54
1:A:300:LYS:HG3	3:A:406:FMT:C	2.32	0.54
1:B:242:GLN:HG3	1:B:281:SER:HA	1.91	0.51
1:A:7:LEU:HD22	1:A:34:LEU:HD21	1.93	0.50
1:A:291:ILE:HG12	1:A:317:LYS:HG3	1.94	0.49
1:A:195:LYS:HE3	4:A:529:HOH:O	2.13	0.48
1:B:287:LYS:HE3	4:B:756:HOH:O	2.12	0.48
1:A:34:LEU:HD23	1:A:46:ILE:HG21	1.94	0.48
1:A:322:TYR:O	4:A:501:HOH:O	2.20	0.46
1:B:294:LYS:HB2	1:B:326:HIS:CE1	2.51	0.46
1:A:3:LYS:HE3	1:A:137:CYS:HB3	1.97	0.46
1:B:2:LYS:HE3	1:B:3:LYS:HG2	1.98	0.45
1:B:244:PRO:HD2	1:B:247:MET:SD	2.56	0.45
1:A:75:PHE:CE1	1:A:83:VAL:HG23	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:41:PRO:HG2	1:B:44:VAL:CG2	2.46	0.44
1:A:219:GLY:HA3	1:A:250:ASP:OD2	2.18	0.43
1:B:29:ILE:CD1	1:B:34:LEU:HB2	2.49	0.43
1:B:291:ILE:HG12	1:B:317:LYS:HG3	2.01	0.42
1:A:90:ASP:OD2	1:B:242:GLN:NE2	2.39	0.42
1:B:72:GLU:O	1:B:76:GLN:HG2	2.21	0.41
1:B:145:GLY:HA2	1:B:196:ARG:NH1	2.36	0.41
1:A:7:LEU:HD11	1:A:86:THR:HG23	2.03	0.41
1:B:108:PRO:HD3	1:B:142:LYS:HG2	2.03	0.41
1:A:200:GLN:HE21	1:A:200:GLN:HB3	1.75	0.40
1:A:162:LYS:HZ1	1:B:240:ARG:HH11	1.69	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	315/329 (96%)	309 (98%)	6 (2%)	0	100	100
1	B	319/329 (97%)	312 (98%)	6 (2%)	1 (0%)	41	27
All	All	634/658 (96%)	621 (98%)	12 (2%)	1 (0%)	47	33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	322	TYR

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	264/272 (97%)	263 (100%)	1 (0%)	91	89
1	B	266/272 (98%)	265 (100%)	1 (0%)	91	89
All	All	530/544 (97%)	528 (100%)	2 (0%)	91	89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	150	PHE
1	B	242	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	200	GLN
1	B	62	GLN
1	B	104	GLN
1	B	200	GLN
1	B	253	GLN
1	B	257	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 3 are monoatomic - leaving 13 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	FMT	A	407	-	2,2,2	0.27	0	1,1,1	0.08	0
3	FMT	B	406	-	2,2,2	0.13	0	1,1,1	0.03	0
3	FMT	A	405	-	2,2,2	0.14	0	1,1,1	0.18	0
3	FMT	B	403	-	2,2,2	0.72	0	1,1,1	0.25	0
3	FMT	A	403	2	2,2,2	0.21	0	1,1,1	0.06	0
3	FMT	B	407	-	2,2,2	0.15	0	1,1,1	0.12	0
3	FMT	A	408	-	2,2,2	0.22	0	1,1,1	0.14	0
3	FMT	A	409	-	2,2,2	0.26	0	1,1,1	0.17	0
3	FMT	B	404	-	2,2,2	0.19	0	1,1,1	0.02	0
3	FMT	B	405	-	2,2,2	0.13	0	1,1,1	0.15	0
3	FMT	A	406	-	2,2,2	0.13	0	1,1,1	0.03	0
3	FMT	A	404	-	2,2,2	0.72	0	1,1,1	0.25	0
3	FMT	B	402	-	2,2,2	0.09	0	1,1,1	0.19	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	406	FMT	3	0
3	A	406	FMT	4	0

5.7 Other polymers [i](#)

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, 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	319/329 (96%)	0.35	30 (9%) 8 6	24, 36, 66, 81	0
1	B	323/329 (98%)	0.19	23 (7%) 16 12	23, 33, 57, 80	0
All	All	642/658 (97%)	0.27	53 (8%) 11 8	23, 34, 61, 81	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	329	HIS	9.0
1	B	15	ALA	8.5
1	B	322	TYR	7.4
1	B	325	HIS	7.2
1	B	14	ILE	6.7
1	B	276	TYR	6.7
1	B	323	LEU	6.4
1	A	322	TYR	6.0
1	B	328	HIS	5.9
1	B	13	ALA	5.6
1	A	328	HIS	4.9
1	B	16	SER	4.9
1	A	119	GLU	4.8
1	A	43	ASP	4.6
1	A	42	GLU	4.6
1	A	13	ALA	4.5
1	B	21	SER	4.5
1	A	325	HIS	4.3
1	A	12	GLY	4.3
1	B	42	GLU	4.3
1	A	2	LYS	4.1
1	B	327	HIS	4.1
1	A	323	LEU	4.0
1	B	326	HIS	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	119	GLU	3.9
1	A	276	TYR	3.8
1	A	23	ARG	3.7
1	A	76	GLN	3.5
1	B	314	GLU	3.2
1	A	327	HIS	3.1
1	A	53	GLN	3.1
1	B	12	GLY	3.1
1	A	36	GLU	3.0
1	A	32	PRO	2.9
1	A	28	ALA	2.9
1	A	78	GLY	2.8
1	A	41	PRO	2.6
1	A	35	ALA	2.6
1	A	106	GLU	2.5
1	B	2	LYS	2.5
1	B	283	TYR	2.4
1	B	256	HIS	2.4
1	B	324	GLU	2.4
1	B	240	ARG	2.3
1	A	314	GLU	2.3
1	A	27	GLY	2.3
1	A	84	VAL	2.3
1	A	26	ALA	2.3
1	B	121	GLN	2.2
1	A	121	GLN	2.2
1	A	11	GLY	2.1
1	A	324	GLU	2.1
1	B	277	ASP	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](#)

LIGAND-RSR INFOmissingINFO

6.5 Other polymers [i](#)

There are no such residues in this entry.