



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 8, 2026 – 02:04 PM JST

PDB ID : 9VS6 / pdb_00009vs6
Title : Crystal structure of isoflavone 4'-O-methyltransferase from Glycyrrhiza glabra L.
Authors : Lin, W.
Deposited on : 2025-07-08
Resolution : 2.37 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

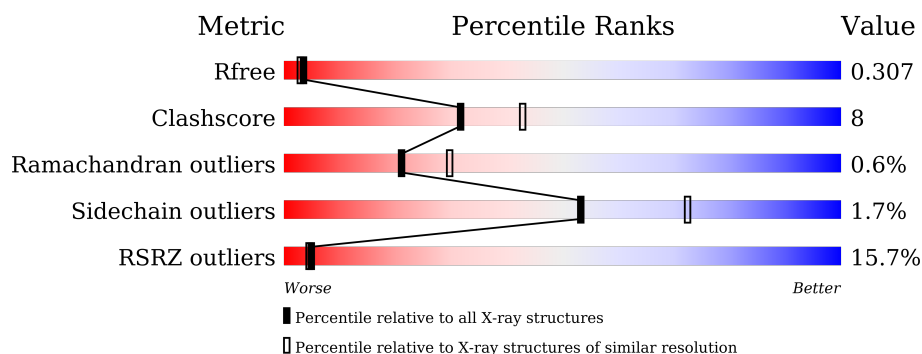
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.37 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}	180053	7164 (2.40-2.36)
Clashscore	190562	7722 (2.40-2.36)
Ramachandran outliers	187476	7626 (2.40-2.36)
Sidechain outliers	187428	7627 (2.40-2.36)
RSRZ outliers	180081	7170 (2.40-2.36)

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	366	<div> <div>14%</div> <div> <div></div> <div>77%</div> <div>18%</div> <div>• •</div> </div> </div>
1	B	366	<div> <div>15%</div> <div> <div></div> <div>75%</div> <div>17%</div> <div>• 7%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5520 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 Isoflavone 4'-O-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	351	Total	C	N	O	S	0	0	0
			2757	1772	451	521	13			
1	B	342	Total	C	N	O	S	0	0	0
			2692	1734	439	506	13			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ASP	ALA	conflict	UNP Q84KK6
A	11	SER	ILE	conflict	UNP Q84KK6
A	56	GLN	GLU	conflict	UNP Q84KK6
A	70	VAL	ILE	conflict	UNP Q84KK6
A	96	GLU	ASP	conflict	UNP Q84KK6
A	?	-	GLU	deletion	UNP Q84KK6
A	145	ASN	LYS	conflict	UNP Q84KK6
B	2	ASP	ALA	conflict	UNP Q84KK6
B	11	SER	ILE	conflict	UNP Q84KK6
B	56	GLN	GLU	conflict	UNP Q84KK6
B	70	VAL	ILE	conflict	UNP Q84KK6
B	96	GLU	ASP	conflict	UNP Q84KK6
B	?	-	GLU	deletion	UNP Q84KK6
B	145	ASN	LYS	conflict	UNP Q84KK6

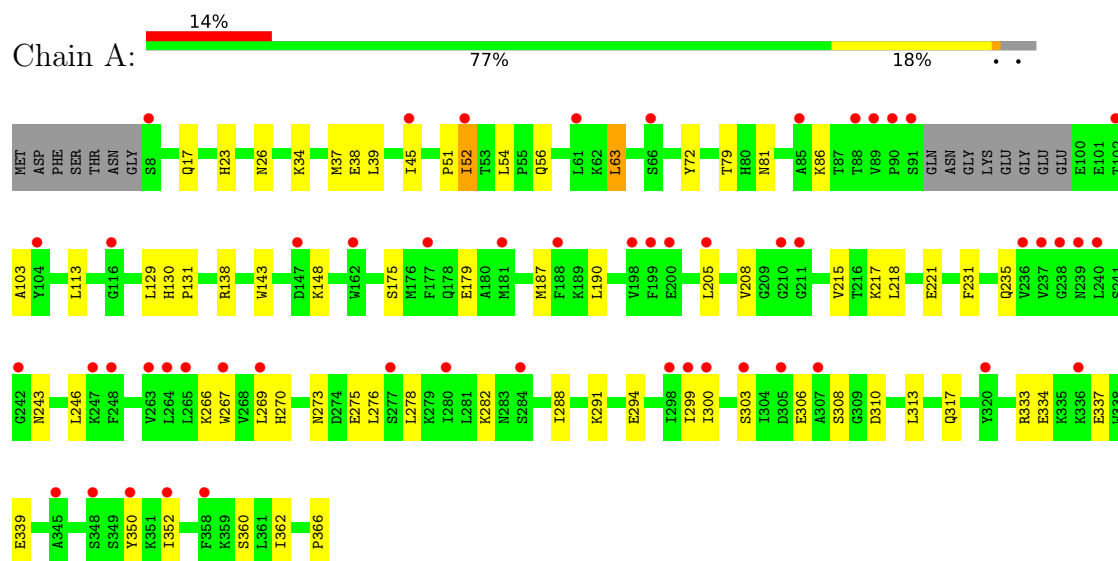
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	31	Total	O	0	0
			31	31		
2	B	40	Total	O	0	0
			40	40		

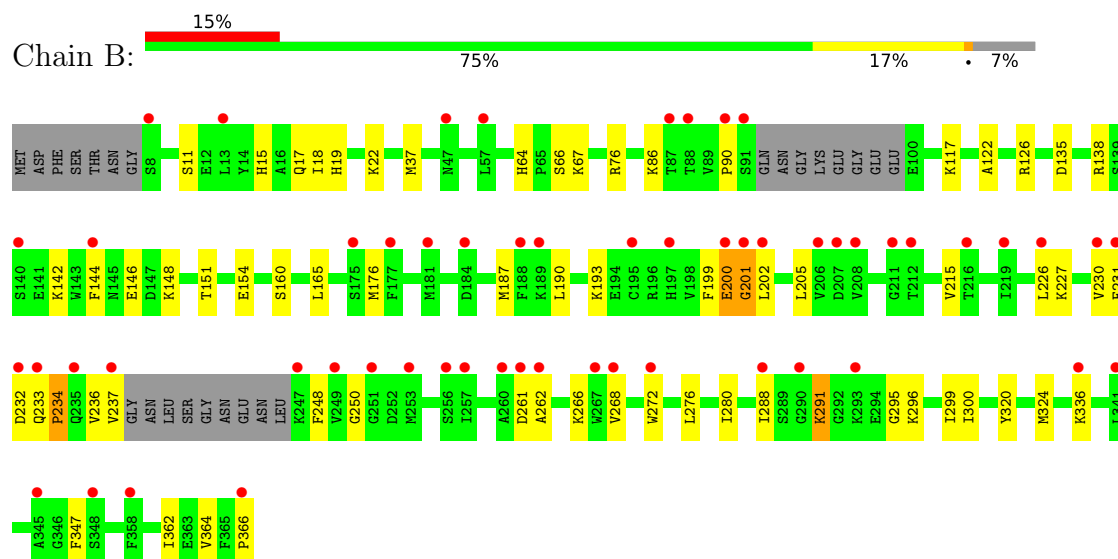
3 Residue-property plots [i](#)

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: Isoflavone 4'-O-methyltransferase



• Molecule 1: Isoflavone 4'-O-methyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	135.46Å 43.68Å 119.53Å 90.00° 96.48° 90.00°	Depositor
Resolution (Å)	42.23 – 2.37 42.23 – 2.37	Depositor EDS
% Data completeness (in resolution range)	97.9 (42.23-2.37) 97.9 (42.23-2.37)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 2.37Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.257 , 0.306 0.256 , 0.307	Depositor DCC
R_{free} test set	1389 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	47.2	Xtriage
Anisotropy	0.244	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 27.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5520	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.94% 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

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	0.12	0/2819	0.27	0/3803
1	B	0.17	0/2752	0.33	0/3710
All	All	0.15	0/5571	0.30	0/7513

There are no bond length outliers.

There are no bond angle outliers.

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	2757	0	2755	42	0
1	B	2692	0	2691	55	0
2	A	31	0	0	5	0
2	B	40	0	0	2	0
All	All	5520	0	5446	88	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 8.

All (88) 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:64:HIS:HD2	1:B:66:SER:H	1.11	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:234:PRO:HA	1:B:250:GLY:HA3	1.46	0.96
1:B:233:GLN:HB2	1:B:236:VAL:HG21	1.61	0.80
1:B:233:GLN:HB2	1:B:236:VAL:CG2	2.10	0.80
1:B:64:HIS:CD2	1:B:66:SER:H	2.02	0.77
1:B:126:ARG:HB3	1:B:176:MET:HE2	1.70	0.73
1:B:336:LYS:HD2	1:B:336:LYS:H	1.57	0.69
1:A:45:ILE:HA	1:A:52:ILE:HD11	1.74	0.69
1:B:187:MET:HE3	1:B:190:LEU:HD12	1.80	0.63
2:A:403:HOH:O	1:B:193:LYS:NZ	2.34	0.59
1:A:54:LEU:HD11	1:A:72:TYR:HB2	1.83	0.58
1:A:266:LYS:HA	1:A:300:ILE:HB	1.84	0.58
1:A:63:LEU:HD21	1:B:144:PHE:HE1	1.69	0.57
1:B:295:GLY:N	2:B:403:HOH:O	2.34	0.56
1:A:269:LEU:O	1:A:333:ARG:NH1	2.38	0.54
1:B:151:THR:OG1	1:B:154:GLU:HG3	2.08	0.54
1:B:262:ALA:HA	1:B:288:ILE:HD11	1.88	0.54
1:A:37:MET:HE1	1:A:113:LEU:HD13	1.88	0.54
1:B:232:ASP:O	1:B:250:GLY:HA2	2.07	0.54
1:B:205:LEU:HB3	1:B:226:LEU:HD21	1.91	0.53
1:B:266:LYS:HA	1:B:300:ILE:HB	1.91	0.53
1:B:299:ILE:HB	1:B:362:ILE:HB	1.90	0.53
1:B:202:LEU:HD11	1:B:296:LYS:HD3	1.90	0.52
1:A:278:LEU:HG	1:A:282:LYS:HD3	1.92	0.52
1:A:208:VAL:HG13	1:A:231:PHE:HD2	1.75	0.52
1:A:175:SER:O	1:A:179:GLU:HG3	2.11	0.51
1:A:81:ASN:O	1:B:19:HIS:NE2	2.42	0.51
1:B:347:PHE:CG	1:B:364:VAL:HG12	2.46	0.51
1:A:17:GLN:CD	1:B:187:MET:HG2	2.35	0.51
1:B:234:PRO:CA	1:B:250:GLY:HA3	2.32	0.51
1:A:215:VAL:HA	1:A:218:LEU:HD22	1.92	0.51
1:A:267:TRP:HZ3	1:A:270:HIS:CD2	2.29	0.50
1:B:146:GLU:HG3	1:B:148:LYS:H	1.76	0.50
1:A:34:LYS:O	1:A:38:GLU:HG3	2.10	0.50
1:B:336:LYS:HD2	1:B:336:LYS:N	2.25	0.50
1:A:138:ARG:NE	1:B:135:ASP:OD1	2.45	0.50
1:A:310:ASP:HB3	1:A:313:LEU:HB3	1.94	0.49
1:A:339:GLU:HG2	1:A:350:TYR:CE2	2.47	0.49
1:A:273:ASN:OD1	1:A:275:GLU:HG2	2.12	0.49
1:A:360:SER:OG	2:A:401:HOH:O	2.20	0.48
1:B:261:ASP:HA	1:B:291:LYS:HD3	1.95	0.48
1:A:334:GLU:HG3	1:A:337:GLU:OE2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:HIS:HA	1:A:26:ASN:HD22	1.79	0.48
1:B:11:SER:O	1:B:15:HIS:ND1	2.44	0.47
1:A:243:ASN:H	1:A:246:LEU:HB3	1.79	0.47
1:B:237:VAL:HG13	1:B:248:PHE:HB3	1.96	0.47
1:B:272:TRP:HE3	1:B:276:LEU:HD13	1.79	0.46
1:A:299:ILE:HB	1:A:362:ILE:HB	1.98	0.46
1:A:317:GLN:NE2	2:A:401:HOH:O	2.49	0.45
1:B:200:GLU:O	1:B:202:LEU:N	2.38	0.45
1:A:79:THR:HG21	1:A:86:LYS:HG2	1.97	0.45
1:A:130:HIS:CD2	1:A:131:PRO:HD2	2.52	0.45
1:B:205:LEU:CB	1:B:226:LEU:HD21	2.45	0.45
1:B:276:LEU:O	1:B:280:ILE:HG13	2.17	0.45
1:B:37:MET:HE1	1:B:122:ALA:HB1	1.98	0.45
1:A:148:LYS:N	2:A:404:HOH:O	2.49	0.45
1:B:142:LYS:NZ	2:B:411:HOH:O	2.49	0.45
1:A:143:TRP:O	1:B:67:LYS:HE3	2.17	0.45
1:B:18:ILE:HG12	1:B:22:LYS:HE3	1.99	0.45
1:B:86:LYS:O	1:B:86:LYS:HG3	2.17	0.45
1:A:52:ILE:HG22	1:A:56:GLN:HB2	1.99	0.45
1:B:154:GLU:HG2	1:B:160:SER:HA	1.98	0.45
1:B:165:LEU:HD23	1:B:165:LEU:HA	1.83	0.45
1:A:306:GLU:OE2	1:B:76:ARG:HD2	2.17	0.44
1:B:117:LYS:HD2	1:B:117:LYS:HA	1.75	0.44
1:B:231:PHE:O	1:B:231:PHE:CG	2.70	0.44
1:B:227:LYS:HD2	1:B:227:LYS:HA	1.70	0.44
1:A:288:ILE:HD12	1:A:366:PRO:HG3	2.00	0.44
1:A:291:LYS:HB3	1:A:294:GLU:HB2	2.00	0.44
1:B:199:PHE:HA	1:B:202:LEU:HD12	2.00	0.44
1:B:295:GLY:O	1:B:366:PRO:HD2	2.18	0.44
1:A:51:PRO:HB2	1:A:103:ALA:HB1	2.00	0.44
1:A:17:GLN:NE2	1:B:187:MET:HG2	2.33	0.44
1:B:233:GLN:O	1:B:236:VAL:HB	2.18	0.43
1:A:63:LEU:HD11	1:B:144:PHE:HD1	1.83	0.43
1:A:352:ILE:HD13	1:A:362:ILE:HG12	2.00	0.43
1:A:34:LYS:HG3	1:A:129:LEU:HB3	2.01	0.43
1:A:339:GLU:OE1	1:A:350:TYR:OH	2.32	0.42
1:B:200:GLU:HB3	1:B:201:GLY:H	1.75	0.42
1:B:135:ASP:O	1:B:138:ARG:HG2	2.19	0.42
1:A:187:MET:HG3	1:B:17:GLN:NE2	2.34	0.42
1:A:275:GLU:HG3	1:A:276:LEU:HD22	2.01	0.41
2:A:404:HOH:O	1:B:67:LYS:HE2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:234:PRO:C	1:B:236:VAL:N	2.78	0.41
1:B:320:TYR:O	1:B:324:MET:HG2	2.21	0.41
1:A:235:GLN:H	1:A:235:GLN:HG2	1.68	0.41
1:B:268:VAL:O	1:B:272:TRP:HD1	2.03	0.40
1:A:217:LYS:O	1:A:221:GLU:HG3	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	347/366 (95%)	334 (96%)	13 (4%)	0	100	100
1	B	336/366 (92%)	324 (96%)	8 (2%)	4 (1%)	10	14
All	All	683/732 (93%)	658 (96%)	21 (3%)	4 (1%)	21	30

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	200	GLU
1	B	234	PRO
1	B	201	GLY
1	B	90	PRO

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	305/317 (96%)	298 (98%)	7 (2%)	44	64
1	B	297/317 (94%)	294 (99%)	3 (1%)	68	82
All	All	602/634 (95%)	592 (98%)	10 (2%)	53	72

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	LEU
1	A	52	ILE
1	A	63	LEU
1	A	190	LEU
1	A	205	LEU
1	A	303	SER
1	A	308	SER
1	B	215	VAL
1	B	230	VAL
1	B	291	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	ASN
1	A	47	ASN
1	A	270	HIS
1	B	64	HIS
1	B	220	HIS

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 oligosaccharides 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, 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	351/366 (95%)	1.19	53 (15%) 5 5	32, 58, 73, 94	0
1	B	342/366 (93%)	1.09	56 (16%) 4 4	31, 47, 72, 85	0
All	All	693/732 (94%)	1.14	109 (15%) 5 4	31, 52, 73, 94	0

All (109) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	210	GLY	4.7
1	A	239	ASN	4.4
1	A	188	PHE	4.3
1	A	199	PHE	4.1
1	B	257	ILE	4.0
1	B	195	CYS	3.8
1	B	268	VAL	3.8
1	B	267	TRP	3.8
1	A	91	SER	3.7
1	A	305	ASP	3.7
1	B	177	PHE	3.6
1	A	90	PRO	3.5
1	B	249	VAL	3.5
1	A	205	LEU	3.5
1	B	237	VAL	3.5
1	A	303	SER	3.5
1	B	290	GLY	3.5
1	B	88	THR	3.4
1	B	188	PHE	3.3
1	B	211	GLY	3.3
1	B	144	PHE	3.3
1	A	147	ASP	3.2
1	A	240	LEU	3.2
1	A	88	THR	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	201	GLY	3.2
1	A	198	VAL	3.1
1	A	211	GLY	3.0
1	A	177	PHE	3.0
1	B	230	VAL	3.0
1	B	231	PHE	2.9
1	B	181	MET	2.9
1	B	184	ASP	2.9
1	B	251	GLY	2.9
1	A	267	TRP	2.9
1	B	235	GLN	2.8
1	B	207	ASP	2.7
1	B	212	THR	2.7
1	B	345	ALA	2.7
1	A	52	ILE	2.7
1	A	300	ILE	2.7
1	A	89	VAL	2.7
1	A	247	LYS	2.7
1	B	256	SER	2.7
1	B	197	HIS	2.6
1	B	200	GLU	2.6
1	A	358	PHE	2.6
1	A	263	VAL	2.6
1	A	242	GLY	2.6
1	A	200	GLU	2.6
1	B	226	LEU	2.6
1	B	260	ALA	2.6
1	A	181	MET	2.5
1	A	336	LYS	2.5
1	B	90	PRO	2.5
1	B	189	LYS	2.5
1	B	233	GLN	2.5
1	A	104	TYR	2.5
1	A	284	SER	2.4
1	B	208	VAL	2.4
1	B	253	MET	2.4
1	A	236	VAL	2.4
1	A	264	LEU	2.4
1	A	102	THR	2.4
1	B	348	SER	2.4
1	A	238	GLY	2.3
1	A	66	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	320	TYR	2.3
1	B	247	LYS	2.3
1	A	237	VAL	2.3
1	B	261	ASP	2.3
1	A	345	ALA	2.3
1	A	8	SER	2.3
1	A	280	ILE	2.3
1	B	91	SER	2.3
1	B	13	LEU	2.2
1	B	272	TRP	2.2
1	B	87	THR	2.2
1	B	216	THR	2.2
1	A	277	SER	2.2
1	A	265	LEU	2.2
1	B	341	LEU	2.2
1	B	47	ASN	2.2
1	B	232	ASP	2.2
1	B	336	LYS	2.2
1	A	307	ALA	2.2
1	B	175	SER	2.2
1	A	298	ILE	2.2
1	B	57	LEU	2.2
1	B	288	ILE	2.2
1	A	116	GLY	2.1
1	B	8	SER	2.1
1	A	162	TRP	2.1
1	B	358	PHE	2.1
1	B	262	ALA	2.1
1	A	61	LEU	2.1
1	A	269	LEU	2.1
1	B	219	ILE	2.1
1	B	206	VAL	2.1
1	B	366	PRO	2.1
1	A	348	SER	2.1
1	B	140	SER	2.1
1	B	293	LYS	2.1
1	B	202	LEU	2.1
1	A	45	ILE	2.1
1	A	85	ALA	2.0
1	A	350	TYR	2.0
1	A	248	PHE	2.0
1	A	299	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	352	ILE	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.