



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2026 – 06:51 PM UTC

PDB ID : 7SR3 / pdb_00007sr3
Title : Single chain trimer HLA-A*02:01 (H98L, Y108C) with HPV.16 E7 peptide
YMLDLQPETTDL
Authors : Finton, K.A.K.; Rupert, P.B.
Deposited on : 2021-11-07
Resolution : 2.49 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

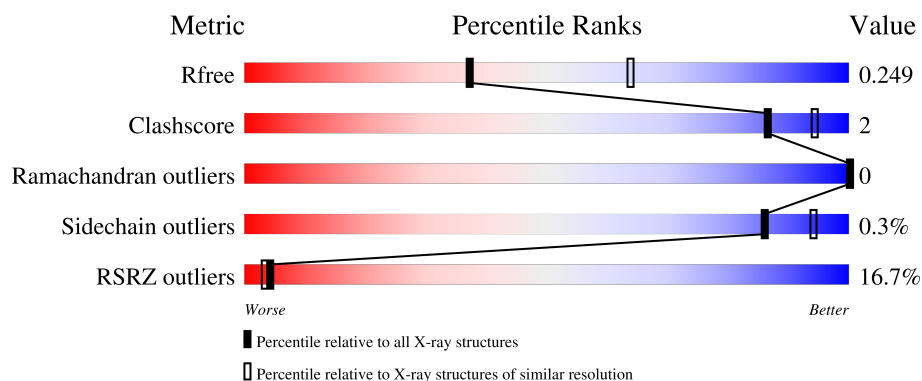
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.49 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	427	14% 79% 17%
1	C	427	17% 78% 18%
2	B	116	12% 92% •
2	D	116	9% 91% 7% •

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7255 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 Protein E7 peptide,Beta-2-microglobulin,MHC class I antigen chimera.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	356	Total	C	N	O	S	0	0	0
			2754	1743	482	517	12			
1	C	352	Total	C	N	O	S	0	0	0
			2714	1714	481	507	12			

There are 86 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	13	GLY	-	linker	UNP P03129
A	14	CYS	-	linker	UNP P03129
A	14A	GLY	-	linker	UNP P03129
A	14B	GLY	-	linker	UNP P03129
A	14C	SER	-	linker	UNP P03129
A	14D	GLY	-	linker	UNP P03129
A	14E	GLY	-	linker	UNP P03129
A	14F	GLY	-	linker	UNP P03129
A	14G	GLY	-	linker	UNP P03129
A	14H	SER	-	linker	UNP P03129
A	14I	GLY	-	linker	UNP P03129
A	14J	GLY	-	linker	UNP P03129
A	14K	GLY	-	linker	UNP P03129
A	14L	GLY	-	linker	UNP P03129
A	14M	SER	-	linker	UNP P03129
A	124	GLY	-	linker	UNP P16213
A	125	GLY	-	linker	UNP P16213
A	126	GLY	-	linker	UNP P16213
A	127	GLY	-	linker	UNP P16213
A	128	SER	-	linker	UNP P16213
A	129	GLY	-	linker	UNP P16213
A	130	GLY	-	linker	UNP P16213
A	131	GLY	-	linker	UNP P16213
A	132	GLY	-	linker	UNP P16213

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Chain	Residue	Modelled	Actual	Comment	Reference
A	133	SER	-	linker	UNP P16213
A	134	GLY	-	linker	UNP P16213
A	135	GLY	-	linker	UNP P16213
A	136	GLY	-	linker	UNP P16213
A	137	GLY	-	linker	UNP P16213
A	138	SER	-	linker	UNP P16213
A	139	GLY	-	linker	UNP P16213
A	140	GLY	-	linker	UNP P16213
A	141	GLY	-	linker	UNP P16213
A	142	GLY	-	linker	UNP P16213
A	143	SER	-	linker	UNP P16213
A	217	LEU	HIS	engineered mutation	UNP A0A678ZGP6
A	227	CYS	TYR	engineered mutation	UNP A0A678ZGP6
A	419	HIS	-	expression tag	UNP A0A678ZGP6
A	420	HIS	-	expression tag	UNP A0A678ZGP6
A	421	HIS	-	expression tag	UNP A0A678ZGP6
A	422	HIS	-	expression tag	UNP A0A678ZGP6
A	423	HIS	-	expression tag	UNP A0A678ZGP6
A	424	HIS	-	expression tag	UNP A0A678ZGP6
C	13	GLY	-	linker	UNP P03129
C	14	CYS	-	linker	UNP P03129
C	14A	GLY	-	linker	UNP P03129
C	14B	GLY	-	linker	UNP P03129
C	14C	SER	-	linker	UNP P03129
C	14D	GLY	-	linker	UNP P03129
C	14E	GLY	-	linker	UNP P03129
C	14F	GLY	-	linker	UNP P03129
C	14G	GLY	-	linker	UNP P03129
C	14H	SER	-	linker	UNP P03129
C	14I	GLY	-	linker	UNP P03129
C	14J	GLY	-	linker	UNP P03129
C	14K	GLY	-	linker	UNP P03129
C	14L	GLY	-	linker	UNP P03129
C	14M	SER	-	linker	UNP P03129
C	124	GLY	-	linker	UNP P16213
C	125	GLY	-	linker	UNP P16213
C	126	GLY	-	linker	UNP P16213
C	127	GLY	-	linker	UNP P16213
C	128	SER	-	linker	UNP P16213
C	129	GLY	-	linker	UNP P16213
C	130	GLY	-	linker	UNP P16213
C	131	GLY	-	linker	UNP P16213

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Chain	Residue	Modelled	Actual	Comment	Reference
C	132	GLY	-	linker	UNP P16213
C	133	SER	-	linker	UNP P16213
C	134	GLY	-	linker	UNP P16213
C	135	GLY	-	linker	UNP P16213
C	136	GLY	-	linker	UNP P16213
C	137	GLY	-	linker	UNP P16213
C	138	SER	-	linker	UNP P16213
C	139	GLY	-	linker	UNP P16213
C	140	GLY	-	linker	UNP P16213
C	141	GLY	-	linker	UNP P16213
C	142	GLY	-	linker	UNP P16213
C	143	SER	-	linker	UNP P16213
C	217	LEU	HIS	engineered mutation	UNP A0A678ZGP6
C	227	CYS	TYR	engineered mutation	UNP A0A678ZGP6
C	419	HIS	-	expression tag	UNP A0A678ZGP6
C	420	HIS	-	expression tag	UNP A0A678ZGP6
C	421	HIS	-	expression tag	UNP A0A678ZGP6
C	422	HIS	-	expression tag	UNP A0A678ZGP6
C	423	HIS	-	expression tag	UNP A0A678ZGP6
C	424	HIS	-	expression tag	UNP A0A678ZGP6

- Molecule 2 is a protein called VHH.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	112	Total	C	N	O	S	0	0	0
			818	505	141	168	4			
2	D	113	Total	C	N	O	S	0	0	0
			834	514	143	173	4			

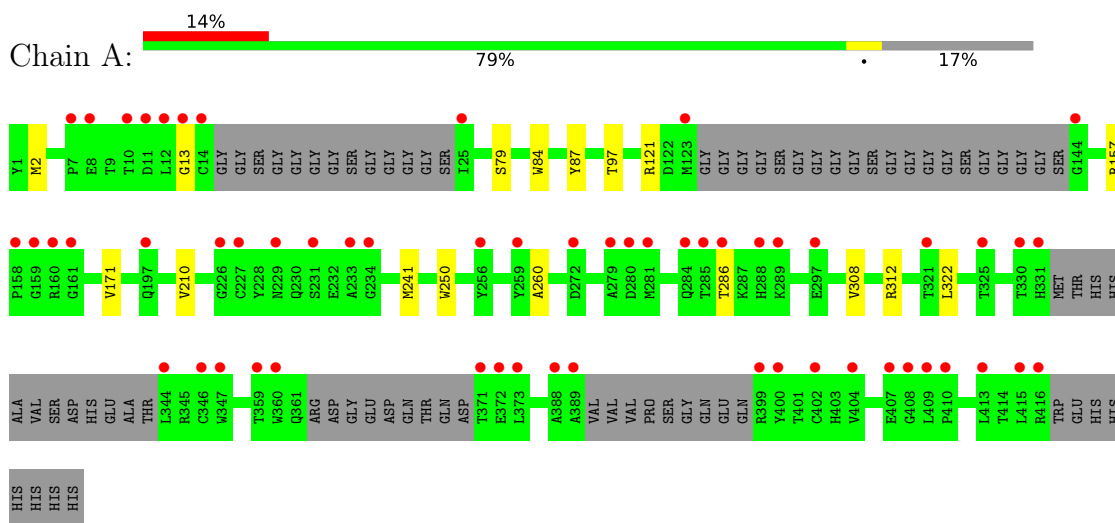
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	41	Total	O	0	0
			41	41		
3	B	24	Total	O	0	0
			24	24		
3	C	49	Total	O	0	0
			49	49		
3	D	21	Total	O	0	0
			21	21		

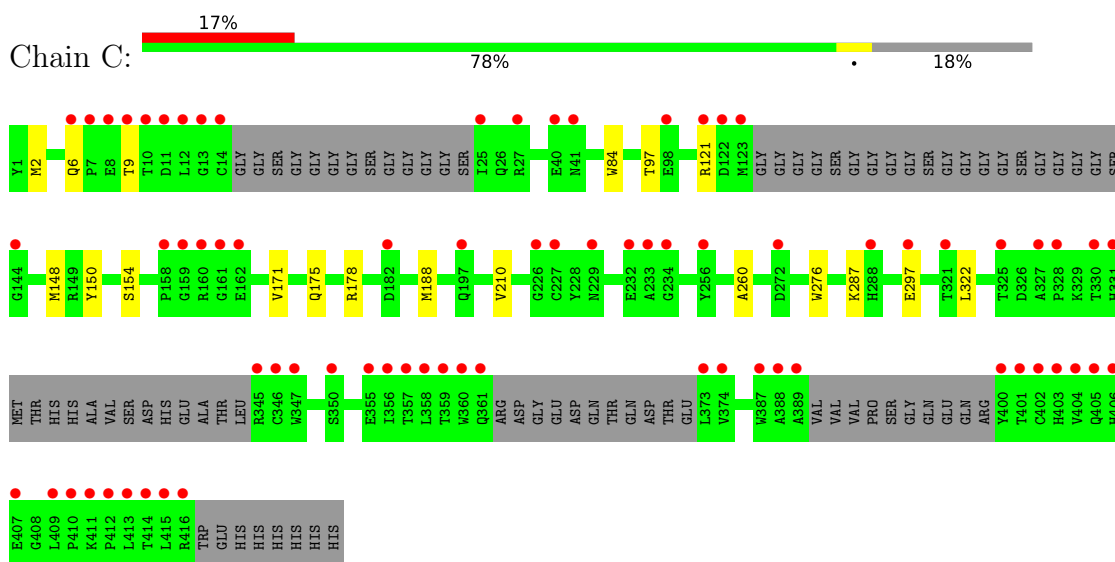
3 Residue-property plots

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: Protein E7 peptide,Beta-2-microglobulin,MHC class I antigen chimera

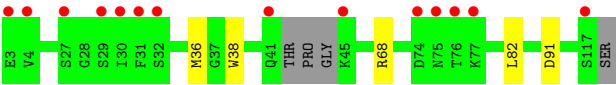


- Molecule 1: Protein E7 peptide,Beta-2-microglobulin,MHC class I antigen chimera

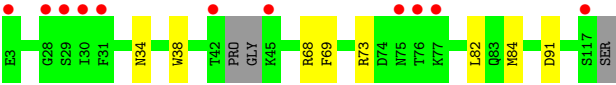
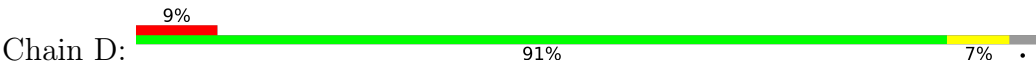


- Molecule 2: VHH





● Molecule 2: VHH



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	118.09Å 118.09Å 262.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.99 – 2.49 48.99 – 2.49	Depositor EDS
% Data completeness (in resolution range)	99.6 (48.99-2.49) 99.7 (48.99-2.49)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.89 (at 2.48Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.225 , 0.248 0.227 , 0.249	Depositor DCC
R_{free} test set	3217 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	38.8	Xtriage
Anisotropy	0.202	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 35.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7255	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 20.15 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 9.2646e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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](#)

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	0.10	0/2831	0.28	0/3861
1	C	0.10	0/2788	0.27	0/3797
2	B	0.09	0/831	0.28	0/1127
2	D	0.09	0/847	0.29	0/1148
All	All	0.10	0/7297	0.28	0/9933

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 [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	2754	0	2453	10	0
1	C	2714	0	2418	11	0
2	B	818	0	746	3	0
2	D	834	0	771	4	0
3	A	41	0	0	0	0
3	B	24	0	0	0	0
3	C	49	0	0	1	0
3	D	21	0	0	0	0
All	All	7255	0	6388	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 2.

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:A:13:GLY:H	1:A:286:THR:HG22	1.51	0.75
1:C:2:MET:HE1	1:C:210:VAL:HB	1.77	0.66
2:B:68:ARG:NH2	2:B:91:ASP:OD2	2.27	0.63
1:C:175:GLN:NE2	3:C:501:HOH:O	2.33	0.62
2:D:68:ARG:NH2	2:D:91:ASP:OD2	2.29	0.61
1:A:97:THR:O	1:A:121:ARG:NH1	2.34	0.60
1:A:250:TRP:O	1:A:312:ARG:NH1	2.34	0.60
1:C:148:MET:HE3	1:C:150:TYR:HE2	1.73	0.54
1:A:2:MET:HE1	1:A:210:VAL:HB	1.91	0.53
1:C:178:ARG:C	1:C:188:MET:HE3	2.38	0.49
2:D:69:PHE:CE2	2:D:84:MET:HG2	2.49	0.48
1:C:276:TRP:HB2	1:C:287:LYS:HG3	1.97	0.46
1:C:97:THR:O	1:C:121:ARG:NH1	2.50	0.45
1:C:6:GLN:O	1:C:9:THR:OG1	2.35	0.45
1:C:297:GLU:N	1:C:297:GLU:CD	2.75	0.45
1:A:250:TRP:HB3	1:A:312:ARG:HD3	1.98	0.44
1:C:84:TRP:CE2	1:C:260:ALA:HB2	2.53	0.44
2:D:34:ASN:O	2:D:73:ARG:NH1	2.45	0.44
1:A:308:VAL:O	1:A:312:ARG:HG3	2.18	0.44
1:A:79:SER:HB3	1:A:87:TYR:CZ	2.54	0.42
1:C:171:VAL:HG11	1:C:322:LEU:HD13	2.00	0.42
2:D:38:TRP:CZ3	2:D:82:LEU:HB2	2.55	0.42
1:A:84:TRP:CE2	1:A:260:ALA:HB2	2.54	0.42
1:A:171:VAL:HG11	1:A:322:LEU:HD13	2.02	0.42
2:B:36:MET:HE2	2:B:36:MET:HB3	1.84	0.41
1:A:241:MET:HE3	1:A:241:MET:HB3	1.78	0.41
1:C:297:GLU:CD	1:C:297:GLU:H	2.29	0.41
2:B:38:TRP:CZ3	2:B:82:LEU:HB2	2.55	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	344/427 (81%)	336 (98%)	8 (2%)	0	100	100
1	C	340/427 (80%)	332 (98%)	8 (2%)	0	100	100
2	B	108/116 (93%)	106 (98%)	2 (2%)	0	100	100
2	D	109/116 (94%)	107 (98%)	2 (2%)	0	100	100
All	All	901/1086 (83%)	881 (98%)	20 (2%)	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	268/351 (76%)	267 (100%)	1 (0%)	84	93
1	C	261/351 (74%)	260 (100%)	1 (0%)	84	93
2	B	84/97 (87%)	84 (100%)	0	100	100
2	D	88/97 (91%)	88 (100%)	0	100	100
All	All	701/896 (78%)	699 (100%)	2 (0%)	86	94

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

Mol	Chain	Res	Type
1	A	157	ARG
1	C	154	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	HIS
1	A	175	GLN
1	A	197	GLN

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Mol	Chain	Res	Type
1	A	284	GLN
2	B	41	GLN
2	B	83	GLN
2	B	85	ASN
2	B	113	GLN
1	C	37	HIS
1	C	175	GLN
1	C	331	HIS
2	D	113	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	356/427 (83%)	0.78	58 (16%)	4 3	24, 40, 76, 106	0
1	C	352/427 (82%)	0.99	73 (20%)	2 2	24, 41, 90, 120	1 (0%)
2	B	112/116 (96%)	0.33	14 (12%)	8 6	22, 31, 66, 94	0
2	D	113/116 (97%)	0.35	11 (9%)	13 11	22, 32, 70, 89	0
All	All	933/1086 (85%)	0.75	156 (16%)	4 3	22, 38, 80, 120	1 (0%)

All (156) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	361	GLN	8.5
1	C	400	TYR	7.1
1	A	371	THR	7.1
1	C	122	ASP	6.8
2	D	3	GLU	6.6
2	D	75	ASN	6.6
1	C	360	TRP	6.5
1	A	25	ILE	6.1
1	A	14	CYS	6.1
1	C	414	THR	6.1
1	C	413	LEU	6.0
1	C	347	TRP	6.0
1	C	373	LEU	5.8
1	C	404	VAL	5.8
1	C	13	GLY	5.7
2	B	75	ASN	5.7
1	C	405	GLN	5.6
1	C	14	CYS	5.6
1	C	25	ILE	5.4
1	C	410	PRO	5.2
1	C	389	ALA	5.2

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Mol	Chain	Res	Type	RSRZ
1	C	402	CYS	5.1
1	C	229	ASN	5.0
1	A	13	GLY	4.9
2	D	77	LYS	4.9
1	A	413	LEU	4.9
1	C	416	ARG	4.8
1	C	415	LEU	4.8
1	C	412	PRO	4.7
2	B	3	GLU	4.7
1	C	144	GLY	4.6
1	A	159	GLY	4.6
1	A	229	ASN	4.6
1	C	358	LEU	4.6
1	C	330	THR	4.5
1	A	7	PRO	4.5
1	C	346	CYS	4.4
2	B	30	ILE	4.3
1	C	123	MET	4.3
2	D	30	ILE	4.3
1	C	7	PRO	4.3
1	C	160	ARG	4.3
1	C	403	HIS	4.2
1	C	159	GLY	4.1
1	C	10	THR	4.1
1	A	144	GLY	4.0
1	C	409	LEU	4.0
2	B	76	THR	4.0
1	A	160	ARG	3.9
2	B	45	LYS	3.9
1	A	400	TYR	3.9
1	C	331	HIS	3.8
1	C	374	VAL	3.8
1	C	388	ALA	3.8
2	D	31	PHE	3.8
1	A	347	TRP	3.7
1	A	272	ASP	3.7
1	A	12	LEU	3.7
1	C	407	GLU	3.7
1	A	416	ARG	3.7
1	A	399	ARG	3.7
1	A	359	THR	3.6
1	A	279	ALA	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	288	HIS	3.6
1	C	359	THR	3.6
1	C	357	THR	3.5
1	C	197	GLN	3.5
1	A	281	MET	3.5
1	A	331	HIS	3.4
1	A	373	LEU	3.4
1	C	297	GLU	3.4
1	C	12	LEU	3.3
1	A	409	LEU	3.3
1	A	8	GLU	3.3
1	C	345	ARG	3.3
1	A	407	GLU	3.3
1	A	227	CYS	3.2
1	A	197	GLN	3.2
1	C	11	ASP	3.2
1	C	9	THR	3.2
1	C	234	GLY	3.2
2	B	41	GLN	3.1
1	C	387	TRP	3.1
1	C	41	ASN	3.1
1	C	233	ALA	3.0
1	A	389	ALA	3.0
2	B	32	SER	3.0
1	A	286	THR	2.9
2	D	29	SER	2.9
1	C	227	CYS	2.9
1	C	121	ARG	2.9
1	A	259	TYR	2.9
1	A	123	MET	2.9
1	C	161	GLY	2.9
1	C	356	ILE	2.9
1	A	10	THR	2.8
2	D	42	THR	2.8
2	D	28	GLY	2.8
1	C	350	SER	2.8
1	A	410	PRO	2.8
1	A	330	THR	2.8
1	A	346	CYS	2.7
1	A	344	LEU	2.7
1	C	182	ASP	2.7
1	A	11	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	360	TRP	2.7
1	C	232	GLU	2.7
2	B	29	SER	2.6
2	B	117	SER	2.6
1	A	226	GLY	2.6
1	A	284	GLN	2.6
1	A	158	PRO	2.6
1	A	415	LEU	2.6
2	B	27	SER	2.6
1	C	256	TYR	2.6
1	C	8	GLU	2.5
1	A	408	GLY	2.5
1	C	226	GLY	2.5
2	D	117	SER	2.5
2	B	74	ASP	2.5
1	A	289	LYS	2.5
1	C	6	GLN	2.4
1	A	325	THR	2.4
1	C	401	THR	2.4
1	C	288	HIS	2.4
1	A	404	VAL	2.4
1	C	325	THR	2.4
1	C	411	LYS	2.4
1	C	158	PRO	2.3
1	A	161	GLY	2.3
1	C	328	PRO	2.3
1	A	231	SER	2.3
2	B	31	PHE	2.3
1	A	285	THR	2.2
1	A	402	CYS	2.2
1	C	355	GLU	2.2
1	C	162	GLU	2.2
2	B	4	VAL	2.2
1	A	233	ALA	2.2
1	C	321	THR	2.2
1	A	280	ASP	2.2
1	A	372	GLU	2.1
1	C	272	ASP	2.1
2	B	77	LYS	2.1
1	A	321	THR	2.1
1	A	256	TYR	2.1
1	C	406	HIS	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	234	GLY	2.1
2	D	76	THR	2.1
1	C	40	GLU	2.1
1	C	27	ARG	2.1
1	C	98	GLU	2.1
2	D	45	LYS	2.1
1	C	327	ALA	2.0
1	A	297	GLU	2.0
1	A	388	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 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.