



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:09 AM UTC

PDB ID : 6AM5 / pdb_00006am5
Title : Crystal structure of DMF5 TCR bound to HLA-A2 presenting synthetic peptide SMLGIGIVPV
Authors : Riley, T.P.; Baker, B.M.
Deposited on : 2017-08-09
Resolution : 2.39 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

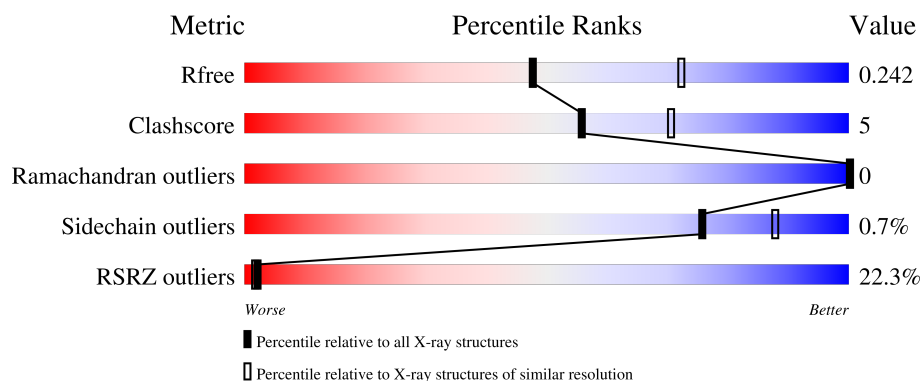
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.39 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	275	18% 88% 11%
2	B	100	6% 91% 9%
3	C	10	100%
4	D	189	34% 90% 10%
5	E	242	25% 85% 15%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6696 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 HLA class I histocompatibility antigen, A-2 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	275	Total	C	N	O	S	0	0	0
			2247	1403	409	426	9			

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	100	Total	C	N	O	S	0	0	0
			837	533	141	159	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	initiating methionine	UNP P61769

- Molecule 3 is a protein called SER-MET-LEU-GLY-ILE-GLY-ILE-VAL-PRO-VAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	10	Total	C	N	O	S	0	0	0
			68	45	10	12	1			

- Molecule 4 is a protein called DMF5 TCR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	189	Total	C	N	O	S	0	0	0
			1455	907	241	299	8			

- Molecule 5 is a protein called DMF5 TCR beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	242	Total	C	N	O	S	0	0	0
			1877	1181	330	358	8			

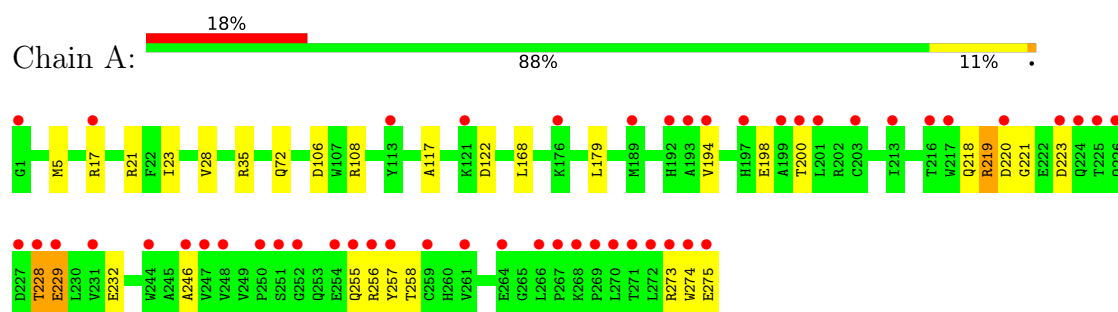
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	97	Total 97	O 97	0	0
6	B	41	Total 41	O 41	0	0
6	C	5	Total 5	O 5	0	0
6	D	29	Total 29	O 29	0	0
6	E	40	Total 40	O 40	0	0

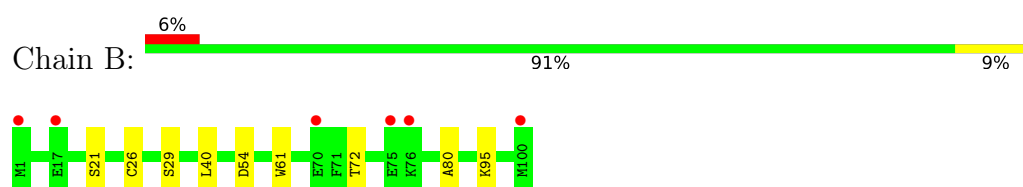
3 Residue-property plots [i](#)

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: HLA class I histocompatibility antigen, A-2 alpha chain



- Molecule 2: Beta-2-microglobulin

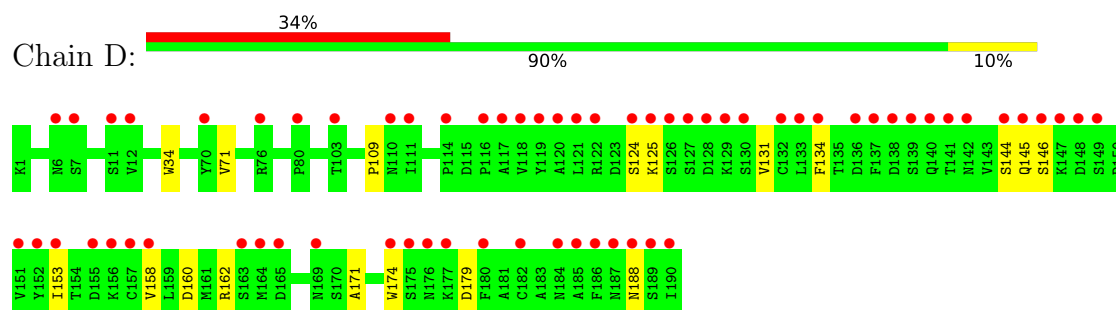


- Molecule 3: SER-MET-LEU-GLY-ILE-GLY-ILE-VAL-PRO-VAL

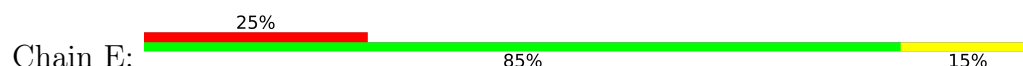


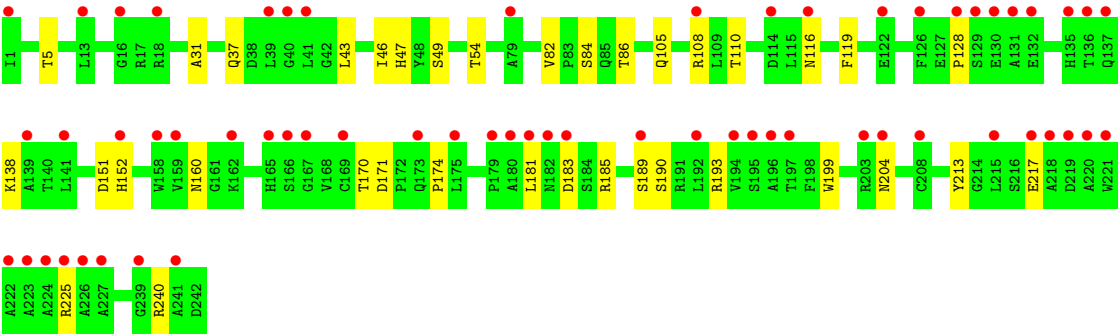
There are no outlier residues recorded for this chain.

- Molecule 4: DMF5 TCR alpha chain



- Molecule 5: DMF5 TCR beta chain





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	228.11Å 49.90Å 92.45Å 90.00° 95.72° 90.00°	Depositor
Resolution (Å)	38.75 – 2.39 38.75 – 2.39	Depositor EDS
% Data completeness (in resolution range)	93.6 (38.75-2.39) 93.2 (38.75-2.39)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.12 (at 2.39Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.201 , 0.244 0.200 , 0.242	Depositor DCC
R_{free} test set	2000 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	23.9	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 47.5	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	6696	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 4.93% 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](#)

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	0.22	0/2312	0.42	2/3137 (0.1%)
2	B	0.08	0/860	0.26	0/1162
3	C	0.08	0/68	0.29	0/90
4	D	0.11	0/1484	0.40	1/2007 (0.0%)
5	E	0.11	0/1926	0.28	0/2626
All	All	0.15	0/6650	0.36	3/9022 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	146	SER	N-CA-C	8.09	123.13	111.56
1	A	221	GLY	N-CA-C	5.87	120.66	113.79
1	A	228	THR	N-CA-C	5.04	117.47	109.50

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	2247	0	2096	23	0
2	B	837	0	803	7	0
3	C	68	0	80	0	0
4	D	1455	0	1376	15	0
5	E	1877	0	1797	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	97	0	0	1	0
6	B	41	0	0	0	0
6	C	5	0	0	0	0
6	D	29	0	0	0	0
6	E	40	0	0	0	0
All	All	6696	0	6152	59	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 5.

All (59) 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:228:THR:HG23	1:A:246:ALA:O	1.80	0.80
2:B:80:ALA:HB2	2:B:95:LYS:HD2	1.70	0.74
4:D:134:PHE:HB2	4:D:171:ALA:HB3	1.70	0.73
1:A:219:ARG:NH1	1:A:256:ARG:HD3	2.05	0.72
5:E:116:ASN:O	5:E:225:ARG:NH1	2.30	0.65
5:E:151:ASP:HB2	5:E:174:PRO:HG2	1.83	0.61
5:E:170:THR:HG23	5:E:190:SER:HB2	1.83	0.61
5:E:37:GLN:HB2	5:E:43:LEU:HD23	1.83	0.60
1:A:194:VAL:HG22	1:A:200:THR:HG23	1.84	0.59
1:A:35:ARG:HD3	2:B:54:ASP:OD2	2.03	0.58
4:D:124:SER:O	4:D:125:LYS:HB2	2.04	0.58
1:A:218:GLN:HG2	1:A:223:ASP:HA	1.87	0.56
1:A:122:ASP:OD1	2:B:61:TRP:NE1	2.36	0.56
4:D:34:TRP:HE1	4:D:71:VAL:HG22	1.73	0.54
1:A:72:GLN:HG2	5:E:54:THR:HG21	1.90	0.54
1:A:5:MET:HB2	1:A:168:LEU:HD13	1.91	0.52
5:E:138:LYS:HB3	5:E:193:ARG:HE	1.75	0.51
1:A:228:THR:HG22	1:A:229:GLU:N	2.25	0.51
4:D:160:ASP:OD2	4:D:162:ARG:HG2	2.10	0.51
5:E:171:ASP:OD2	5:E:189:SER:HB3	2.11	0.51
5:E:86:THR:HG23	5:E:110:THR:HA	1.96	0.48
1:A:194:VAL:CG2	1:A:200:THR:HG23	2.45	0.47
2:B:21:SER:HA	2:B:72:THR:HG22	1.96	0.47
1:A:232:GLU:OE1	2:B:29:SER:OG	2.29	0.46
1:A:28:VAL:HG11	1:A:179:LEU:HD13	1.98	0.46
5:E:5:THR:HG23	5:E:105:GLN:HE22	1.81	0.46
4:D:145:GLN:CB	4:D:153:ILE:HB	2.46	0.46
4:D:144:SER:H	4:D:188:ASN:ND2	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:128:PRO:HD2	5:E:199:TRP:CZ2	2.51	0.46
1:A:228:THR:CG2	1:A:229:GLU:N	2.78	0.45
4:D:109:PRO:HG3	4:D:158:VAL:HG11	1.99	0.45
4:D:131:VAL:HG12	4:D:174:TRP:HB3	1.98	0.45
1:A:106:ASP:OD2	1:A:108:ARG:NH1	2.50	0.45
4:D:145:GLN:HB3	4:D:153:ILE:HB	1.98	0.45
5:E:82:VAL:HG12	5:E:84:SER:H	1.82	0.45
1:A:194:VAL:HG22	1:A:200:THR:CG2	2.45	0.45
1:A:258:THR:HG22	1:A:273:ARG:HG3	1.99	0.45
1:A:17:ARG:NH1	6:A:309:HOH:O	2.50	0.44
1:A:274:TRP:CD1	1:A:275:GLU:HG3	2.53	0.44
4:D:144:SER:H	4:D:188:ASN:HD21	1.65	0.44
5:E:31:ALA:HA	5:E:49:SER:O	2.18	0.44
4:D:145:GLN:HA	4:D:153:ILE:HD12	2.00	0.43
4:D:134:PHE:O	4:D:171:ALA:N	2.51	0.43
4:D:124:SER:O	4:D:125:LYS:CB	2.67	0.43
5:E:160:ASN:ND2	5:E:204:ASN:OD1	2.52	0.43
4:D:179:ASP:N	4:D:179:ASP:OD1	2.51	0.43
5:E:46:ILE:HG22	5:E:47:HIS:CD2	2.54	0.43
1:A:117:ALA:HB2	2:B:61:TRP:CE2	2.55	0.42
4:D:144:SER:N	4:D:188:ASN:OD1	2.52	0.42
5:E:119:PHE:CE1	5:E:185:ARG:NH1	2.87	0.42
5:E:152:HIS:HB3	5:E:213:TYR:HB2	2.01	0.42
2:B:26:CYS:HB2	2:B:40:LEU:HD21	2.02	0.42
1:A:21:ARG:CZ	1:A:23:ILE:HD11	2.50	0.42
5:E:181:LEU:HB3	5:E:183:ASP:OD1	2.20	0.41
1:A:219:ARG:HH11	1:A:256:ARG:HD3	1.81	0.41
1:A:219:ARG:O	1:A:220:ASP:C	2.62	0.41
5:E:217:GLU:N	5:E:217:GLU:OE1	2.54	0.41
5:E:108:ARG:HD2	5:E:152:HIS:CD2	2.56	0.41
1:A:219:ARG:HG3	1:A:257:TYR:CE2	2.56	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	273/275 (99%)	261 (96%)	12 (4%)	0	100	100
2	B	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
3	C	8/10 (80%)	8 (100%)	0	0	100	100
4	D	187/189 (99%)	175 (94%)	12 (6%)	0	100	100
5	E	240/242 (99%)	230 (96%)	10 (4%)	0	100	100
All	All	806/816 (99%)	771 (96%)	35 (4%)	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	231/231 (100%)	227 (98%)	4 (2%)	53	74
2	B	95/95 (100%)	95 (100%)	0	100	100
3	C	8/8 (100%)	8 (100%)	0	100	100
4	D	164/165 (99%)	164 (100%)	0	100	100
5	E	198/198 (100%)	197 (100%)	1 (0%)	81	91
All	All	696/697 (100%)	691 (99%)	5 (1%)	76	88

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

Mol	Chain	Res	Type
1	A	198	GLU
1	A	219	ARG
1	A	229	GLU
1	A	255	GLN
5	E	240	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	180	GLN
4	D	63	GLN
4	D	176	ASN

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	275/275 (100%)	0.67	50 (18%) 3 3	12, 37, 117, 166	0
2	B	100/100 (100%)	0.16	6 (6%) 27 24	18, 30, 69, 86	0
3	C	10/10 (100%)	-0.46	0 100 100	15, 17, 23, 28	0
4	D	189/189 (100%)	1.47	65 (34%) 1 1	16, 55, 130, 145	0
5	E	242/242 (100%)	1.18	61 (25%) 1 1	13, 57, 103, 130	0
All	All	816/816 (100%)	0.93	182 (22%) 2 2	12, 44, 114, 166	0

All (182) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	E	41	LEU	7.0
5	E	39	LEU	6.2
4	D	126	SER	5.7
1	A	194	VAL	5.4
4	D	134	PHE	5.3
4	D	140	GLN	5.2
5	E	218	ALA	4.7
5	E	224	ALA	4.7
4	D	6	ASN	4.6
4	D	176	ASN	4.6
4	D	180	PHE	4.6
4	D	157	CYS	4.4
1	A	193	ALA	4.3
4	D	151	VAL	4.3
4	D	137	PHE	4.2
5	E	175	LEU	4.2
4	D	153	ILE	4.1
5	E	197	THR	4.0
4	D	136	ASP	3.9
4	D	189	SER	3.9

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Mol	Chain	Res	Type	RSRZ
5	E	180	ALA	3.9
4	D	132	CYS	3.8
4	D	125	LYS	3.8
1	A	226	GLN	3.8
4	D	182	CYS	3.7
5	E	131	ALA	3.7
1	A	274	TRP	3.7
1	A	247	VAL	3.7
4	D	147	LYS	3.7
5	E	196	ALA	3.6
5	E	241	ALA	3.6
4	D	146	SER	3.6
4	D	120	ALA	3.6
1	A	227	ASP	3.5
4	D	185	ALA	3.5
4	D	169	ASN	3.5
5	E	194	VAL	3.5
4	D	130	SER	3.4
4	D	190	ILE	3.4
5	E	167	GLY	3.4
1	A	223	ASP	3.4
1	A	251	SER	3.3
5	E	130	GLU	3.3
1	A	257	TYR	3.3
4	D	139	SER	3.3
5	E	222	ALA	3.3
4	D	164	MET	3.3
4	D	186	PHE	3.3
4	D	80	PRO	3.2
4	D	124	SER	3.2
5	E	223	ALA	3.2
5	E	225	ARG	3.2
1	A	261	VAL	3.2
4	D	118	VAL	3.2
4	D	127	SER	3.1
1	A	199	ALA	3.1
5	E	132	GLU	3.1
5	E	226	ALA	3.1
4	D	103	THR	3.1
1	A	192	HIS	3.1
5	E	108	ARG	3.1
1	A	200	THR	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	225	THR	3.0
1	A	1	GLY	3.0
5	E	13	LEU	3.0
5	E	135	HIS	3.0
4	D	7	SER	3.0
1	A	220	ASP	3.0
5	E	122	GLU	3.0
4	D	142	ASN	2.9
5	E	192	LEU	2.9
4	D	119	TYR	2.9
4	D	149	SER	2.9
5	E	79	ALA	2.9
5	E	1	ILE	2.9
5	E	217	GLU	2.9
1	A	224	GLN	2.9
4	D	187	ASN	2.8
4	D	188	ASN	2.8
5	E	181	LEU	2.8
1	A	197	HIS	2.8
4	D	145	GLN	2.8
1	A	252	GLY	2.8
4	D	11	SER	2.7
5	E	221	TRP	2.7
1	A	259	CYS	2.7
1	A	201	LEU	2.7
1	A	255	GLN	2.7
5	E	195	SER	2.7
1	A	246	ALA	2.7
4	D	184	ASN	2.7
5	E	114	ASP	2.7
5	E	162	LYS	2.7
5	E	126	PHE	2.7
4	D	121	LEU	2.7
1	A	254	GLU	2.6
4	D	138	ASP	2.6
4	D	163	SER	2.6
4	D	76	ARG	2.6
5	E	136	THR	2.6
5	E	173	GLN	2.6
1	A	231	VAL	2.6
1	A	121	LYS	2.6
4	D	133	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
5	E	215	LEU	2.6
5	E	239	GLY	2.6
5	E	152	HIS	2.6
1	A	176	LYS	2.6
1	A	203	CYS	2.5
4	D	144	SER	2.5
5	E	139	ALA	2.5
1	A	17	ARG	2.5
5	E	158	TRP	2.5
1	A	272	LEU	2.5
4	D	156	LYS	2.5
1	A	113	TYR	2.4
5	E	227	ALA	2.4
2	B	70	GLU	2.4
5	E	40	GLY	2.4
1	A	271	THR	2.4
1	A	213	ILE	2.4
1	A	270	LEU	2.4
1	A	275	GLU	2.4
4	D	128	ASP	2.4
4	D	165	ASP	2.4
1	A	216	THR	2.4
1	A	228	THR	2.4
5	E	159	VAL	2.4
5	E	204	ASN	2.3
1	A	250	PRO	2.3
5	E	166	SER	2.3
1	A	248	VAL	2.3
5	E	203	ARG	2.3
4	D	148	ASP	2.3
5	E	179	PRO	2.3
5	E	169	CYS	2.3
4	D	177	LYS	2.3
5	E	183	ASP	2.3
4	D	117	ALA	2.3
4	D	175	SER	2.3
4	D	111	ILE	2.3
4	D	158	VAL	2.3
5	E	141	LEU	2.3
2	B	17	GLU	2.3
1	A	268	LYS	2.3
5	E	116	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	266	LEU	2.2
5	E	219	ASP	2.2
2	B	100	MET	2.2
4	D	129	LYS	2.2
4	D	141	THR	2.2
5	E	220	ALA	2.2
4	D	70	TYR	2.2
1	A	217	TRP	2.2
5	E	18	ARG	2.2
4	D	122	ARG	2.2
4	D	155	ASP	2.2
1	A	269	PRO	2.2
5	E	16	GLY	2.2
5	E	165	HIS	2.2
5	E	129	SER	2.2
5	E	189	SER	2.2
1	A	189	MET	2.1
1	A	267	PRO	2.1
2	B	1	MET	2.1
1	A	229	GLU	2.1
5	E	137	GLN	2.1
1	A	273	ARG	2.1
5	E	208	CYS	2.1
2	B	76	LYS	2.1
2	B	75	GLU	2.1
4	D	110	ASN	2.1
4	D	152	TYR	2.1
4	D	12	VAL	2.1
5	E	128	PRO	2.1
1	A	244	TRP	2.1
4	D	174	TRP	2.1
1	A	264	GLU	2.1
5	E	182	ASN	2.1
4	D	114	PRO	2.1
1	A	256	ARG	2.1
4	D	116	PRO	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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.