



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:55 AM GMT

PDB ID : 3K48
Title : Crystal structure of APRIL bound to a peptide
Authors : Hymowitz, S.G.
Deposited on : 2009-10-05
Resolution : 2.80 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

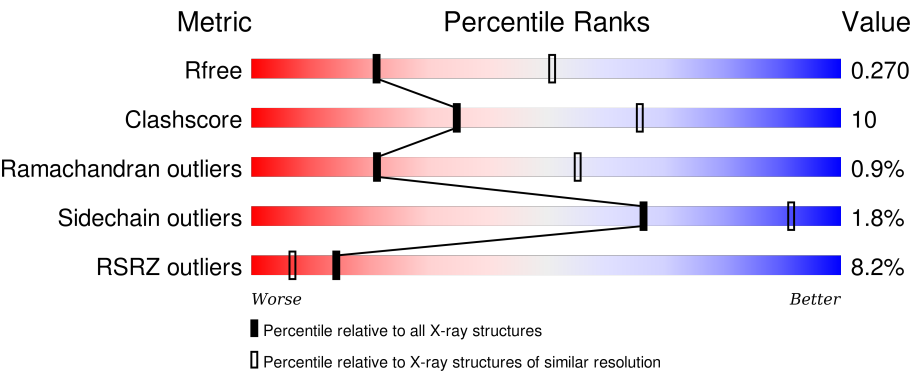
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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 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 <=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	140	<div><div>9%</div><div>79%</div><div>17%</div><div>...</div></div>
1	B	140	<div><div>9%</div><div>81%</div><div>16%</div><div>..</div></div>
1	D	140	<div><div>6%</div><div>83%</div><div>14%</div><div>..</div></div>
2	R	16	<div><div>19%</div><div>69%</div><div>25%</div><div>6%</div></div>
2	S	16	<div><div>69%</div><div>13%</div><div>19%</div></div>

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Mol	Chain	Length	Quality of chain
2	T	16	 A horizontal bar chart showing the quality of chain T. The bar is divided into three segments: a green segment representing 75%, a yellow segment representing 6%, and a grey segment representing 19%. The percentages are labeled below the bar.

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3613 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 Tumor necrosis factor ligand superfamily member 13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	137	Total	C	N	O	S	0	0	0
			1080	683	198	194	5			
1	B	137	Total	C	N	O	S	0	0	0
			1080	683	198	194	5			
1	D	137	Total	C	N	O	S	0	0	0
			1080	683	198	194	5			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	102	GLY	-	EXPRESSION TAG	UNP Q9D777
A	103	SER	-	EXPRESSION TAG	UNP Q9D777
B	102	GLY	-	EXPRESSION TAG	UNP Q9D777
B	103	SER	-	EXPRESSION TAG	UNP Q9D777
D	102	GLY	-	EXPRESSION TAG	UNP Q9D777
D	103	SER	-	EXPRESSION TAG	UNP Q9D777

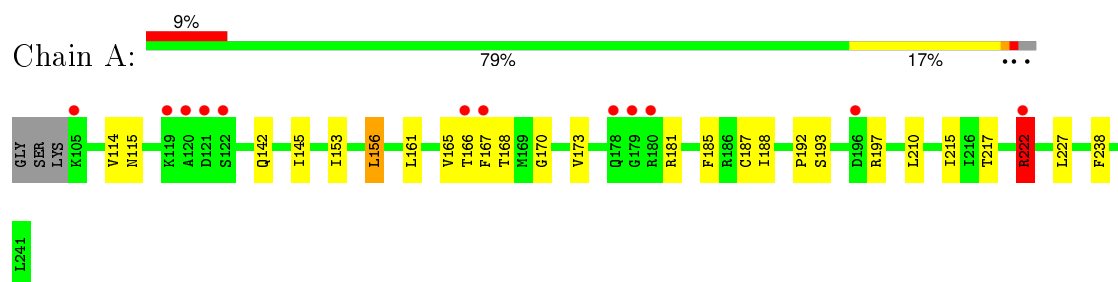
- Molecule 2 is a protein called peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	R	16	Total	C	N	O	S	0	0	0
			141	91	23	24	3			
2	S	13	Total	C	N	O	S	0	0	0
			116	77	18	18	3			
2	T	13	Total	C	N	O	S	0	0	0
			116	77	18	18	3			

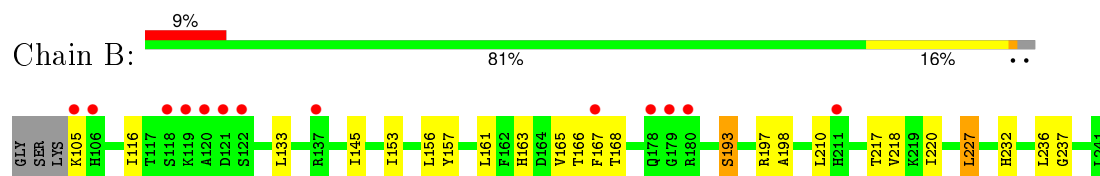
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

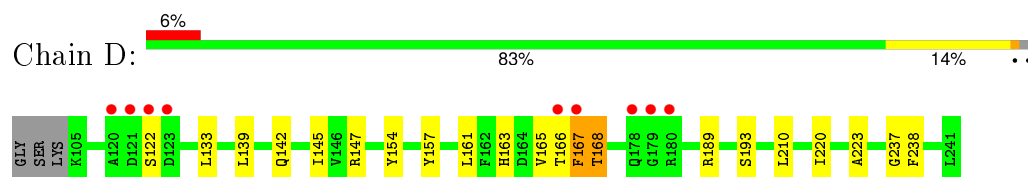
- Molecule 1: Tumor necrosis factor ligand superfamily member 13



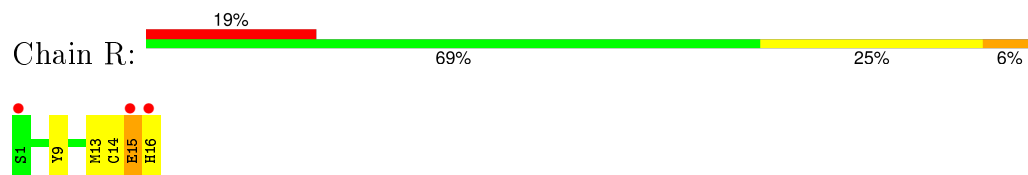
- Molecule 1: Tumor necrosis factor ligand superfamily member 13



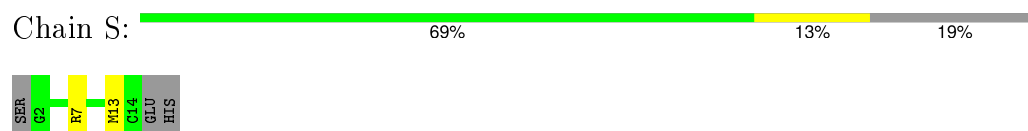
- Molecule 1: Tumor necrosis factor ligand superfamily member 13



- Molecule 2: peptide



- Molecule 2: peptide



- Molecule 2: peptide

Chain T:  75% 6% 19%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	100.81 Å 84.77 Å 55.56 Å 90.00° 99.45° 90.00°	Depositor
Resolution (Å)	30.00 – 2.80 29.19 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.6 (30.00-2.80) 99.6 (29.19-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 2.80 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.205 , 0.267 0.209 , 0.270	Depositor DCC
R_{free} test set	1143 reflections (11.14%)	DCC
Wilson B-factor (Å ²)	35.9	Xtriage
Anisotropy	0.072	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 11400 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3613	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.88% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.48	0/1104	0.68	1/1495 (0.1%)
1	B	0.48	0/1104	0.63	0/1495
1	D	0.49	0/1104	0.64	0/1495
2	R	0.60	0/149	0.81	0/203
2	S	0.62	0/123	0.62	0/168
2	T	0.56	0/123	0.63	0/168
All	All	0.50	0/3707	0.65	1/5024 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	222	ARG	NE-CZ-NH1	5.49	123.05	120.30

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	1080	0	1080	31	0
1	B	1080	0	1080	25	0
1	D	1080	0	1080	19	0
2	R	141	0	113	6	0
2	S	116	0	92	3	0
2	T	116	0	92	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	3613	0	3537	71	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 10.

All (71) 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:145:ILE:HG22	1:A:217:THR:HG22	1.48	0.96
1:A:197:ARG:HD2	1:D:167:PHE:HA	1.50	0.93
1:D:161:LEU:HD21	2:T:13:MET:CE	2.13	0.79
1:D:161:LEU:HD21	2:T:13:MET:HE2	1.66	0.77
1:D:165:VAL:HG22	1:D:193:SER:HA	1.65	0.76
1:B:116:ILE:CD1	1:B:227:LEU:HD11	2.19	0.73
1:B:116:ILE:HD12	1:B:227:LEU:CD1	2.19	0.72
1:D:166:THR:O	1:D:166:THR:HG23	1.91	0.71
1:A:197:ARG:CD	1:D:167:PHE:HA	2.20	0.70
1:A:161:LEU:HD21	2:R:13:MET:CE	2.21	0.70
1:B:116:ILE:HD12	1:B:227:LEU:HD11	1.73	0.70
1:B:161:LEU:HD21	2:S:13:MET:HE2	1.74	0.69
1:A:222:ARG:HG3	1:A:222:ARG:HH11	1.56	0.68
1:B:161:LEU:HD21	2:S:13:MET:CE	2.25	0.67
1:D:154:TYR:CD1	1:D:210:LEU:HD12	2.30	0.66
1:B:166:THR:O	1:B:166:THR:HG23	1.96	0.66
1:A:145:ILE:HB	1:A:215:ILE:HG23	1.79	0.64
2:R:15:GLU:O	2:R:16:HIS:CB	2.46	0.63
1:A:161:LEU:HD21	2:R:13:MET:HE2	1.81	0.62
1:A:156:LEU:HD11	1:A:238:PHE:CE2	2.36	0.61
1:D:166:THR:O	1:D:168:THR:N	2.34	0.61
1:D:157:TYR:CZ	1:D:237:GLY:HA3	2.39	0.58
1:A:166:THR:O	1:A:166:THR:HG23	2.05	0.56
1:A:142:GLN:HB3	1:A:145:ILE:HD12	1.88	0.56
1:A:153:ILE:HD12	1:B:133:LEU:HD21	1.89	0.55
1:D:163:HIS:CG	1:D:163:HIS:O	2.59	0.55
1:D:166:THR:O	1:D:166:THR:CG2	2.55	0.54
1:A:145:ILE:CG2	1:A:217:THR:HG22	2.32	0.54
1:A:145:ILE:O	1:A:145:ILE:HD12	2.08	0.53
1:B:116:ILE:HD12	1:B:227:LEU:HD12	1.90	0.53
1:A:222:ARG:CG	1:A:222:ARG:HH11	2.21	0.52
1:B:166:THR:O	1:B:168:THR:N	2.43	0.52
1:A:161:LEU:HD21	2:R:13:MET:HE3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:157:TYR:CZ	1:B:237:GLY:HA3	2.47	0.49
1:B:218:VAL:HG21	1:B:236:LEU:HD13	1.95	0.48
1:D:220:ILE:N	1:D:220:ILE:HD12	2.28	0.48
1:A:188:ILE:HD12	1:A:188:ILE:N	2.29	0.48
1:B:163:HIS:CG	1:B:163:HIS:O	2.66	0.48
1:B:165:VAL:HG22	1:B:193:SER:HA	1.96	0.47
1:A:156:LEU:HD13	1:A:210:LEU:HD11	1.96	0.47
2:R:15:GLU:O	2:R:16:HIS:HB2	2.13	0.47
1:A:170:GLY:HA3	1:A:187:CYS:O	2.14	0.47
1:A:156:LEU:CD1	1:A:210:LEU:HD11	2.45	0.46
1:A:181:ARG:NE	2:S:7:ARG:HB3	2.31	0.46
1:B:163:HIS:HA	1:B:198:ALA:O	2.16	0.46
1:A:114:VAL:HG13	1:A:115:ASN:HB3	1.98	0.45
1:B:166:THR:O	1:B:166:THR:CG2	2.61	0.45
1:A:142:GLN:HB3	1:A:145:ILE:CD1	2.47	0.45
1:B:156:LEU:HD11	1:B:210:LEU:HD11	1.97	0.45
1:A:153:ILE:CD1	1:B:133:LEU:HD21	2.46	0.44
1:B:220:ILE:N	1:B:220:ILE:HD12	2.32	0.44
1:A:165:VAL:HG23	1:A:192:PRO:O	2.17	0.44
1:A:166:THR:O	1:A:168:THR:N	2.51	0.44
1:B:227:LEU:HD12	1:B:227:LEU:O	2.18	0.43
1:A:227:LEU:C	1:A:227:LEU:HD12	2.38	0.43
1:D:142:GLN:HE21	1:D:147:ARG:NH2	2.16	0.43
1:D:165:VAL:CG2	1:D:193:SER:HA	2.43	0.43
1:A:193:SER:HB3	1:B:197:ARG:HH12	1.83	0.43
1:D:163:HIS:CD2	1:D:163:HIS:O	2.72	0.43
2:R:9:TYR:CE1	2:R:14:CYS:SG	3.12	0.43
1:B:145:ILE:HG22	1:B:217:THR:HG22	2.00	0.43
1:D:139:LEU:HD13	1:D:238:PHE:CG	2.54	0.42
1:D:122:SER:O	1:D:223:ALA:HB2	2.20	0.42
1:A:222:ARG:CG	1:A:222:ARG:NH1	2.81	0.42
1:B:145:ILE:C	1:B:145:ILE:HD12	2.39	0.42
1:A:185:PHE:HA	1:B:232:HIS:HB2	2.00	0.42
1:A:156:LEU:HD23	1:A:173:VAL:HG11	2.02	0.41
1:B:116:ILE:CD1	1:B:227:LEU:CD1	2.87	0.41
1:B:153:ILE:HD12	1:D:133:LEU:HD21	2.03	0.40
1:D:145:ILE:C	1:D:145:ILE:HD12	2.42	0.40
1:A:165:VAL:CG2	1:A:193:SER:HA	2.50	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	135/140 (96%)	128 (95%)	6 (4%)	1 (1%)	26	62
1	B	135/140 (96%)	129 (96%)	5 (4%)	1 (1%)	26	62
1	D	135/140 (96%)	126 (93%)	8 (6%)	1 (1%)	26	62
2	R	14/16 (88%)	11 (79%)	2 (14%)	1 (7%)	1	3
2	S	11/16 (69%)	9 (82%)	2 (18%)	0	100	100
2	T	11/16 (69%)	9 (82%)	2 (18%)	0	100	100
All	All	441/468 (94%)	412 (93%)	25 (6%)	4 (1%)	21	55

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	167	PHE
1	D	167	PHE
1	A	167	PHE
2	R	15	GLU

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	119/122 (98%)	117 (98%)	2 (2%)	68	92
1	B	119/122 (98%)	116 (98%)	3 (2%)	55	86
1	D	119/122 (98%)	117 (98%)	2 (2%)	68	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	R	15/15 (100%)	15 (100%)	0	100	100
2	S	12/15 (80%)	12 (100%)	0	100	100
2	T	12/15 (80%)	12 (100%)	0	100	100
All	All	396/411 (96%)	389 (98%)	7 (2%)	66	91

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	156	LEU
1	A	222	ARG
1	B	105	LYS
1	B	193	SER
1	B	227	LEU
1	D	168	THR
1	D	189	ARG

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

Mol	Chain	Res	Type
1	B	142	GLN
1	B	163	HIS
1	B	178	GLN
1	D	142	GLN
1	D	178	GLN

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 carbohydrates 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	137/140 (97%)	0.10	12 (8%) 12 6	6, 16, 34, 43	0
1	B	137/140 (97%)	0.05	13 (9%) 10 5	5, 16, 34, 43	0
1	D	137/140 (97%)	0.00	9 (6%) 22 13	6, 16, 34, 43	0
2	R	16/16 (100%)	0.63	3 (18%) 2 1	22, 24, 36, 39	0
2	S	13/16 (81%)	0.08	0 100 100	22, 23, 29, 30	0
2	T	13/16 (81%)	0.04	0 100 100	22, 23, 28, 30	0
All	All	453/468 (96%)	0.07	37 (8%) 14 7	5, 17, 34, 43	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	179	GLY	6.6
1	A	179	GLY	4.2
1	B	118	SER	4.1
2	R	16	HIS	4.1
1	A	178	GLN	3.9
1	D	121	ASP	3.9
1	A	120	ALA	3.8
1	D	178	GLN	3.8
2	R	1	SER	3.7
1	B	121	ASP	3.5
1	A	105	LYS	3.5
1	B	105	LYS	3.4
1	A	166	THR	3.4
1	A	121	ASP	3.2
1	B	120	ALA	3.2
1	B	167	PHE	3.2
1	B	179	GLY	3.1
1	B	122	SER	3.1
1	B	178	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	122	SER	2.8
1	D	120	ALA	2.7
1	A	180	ARG	2.7
1	D	180	ARG	2.7
1	B	106	HIS	2.5
1	B	180	ARG	2.4
1	D	123	ASP	2.4
1	A	196	ASP	2.4
1	B	119	LYS	2.4
1	A	167	PHE	2.4
1	D	167	PHE	2.4
1	A	119	LYS	2.3
1	B	137	ARG	2.3
1	D	122	SER	2.2
2	R	15	GLU	2.2
1	B	211	HIS	2.1
1	D	166	THR	2.1
1	A	222	ARG	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.