



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 24, 2025 – 05:10 pm BST

PDB ID : 5AFR / pdb\_00005afr  
Title : N-terminal fragment of dynein heavy chain  
Authors : Urnavicius, L.; Zhang, K.; Diamant, A.G.; Motz, C.; Schlager, M.A.; Yu, M.;  
Patel, N.A.; Robinson, C.V.; Carter, A.P.  
Deposited on : 2015-01-23  
Resolution : 5.00 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](mailto: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 Phenix2.0rc1  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.003 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.44

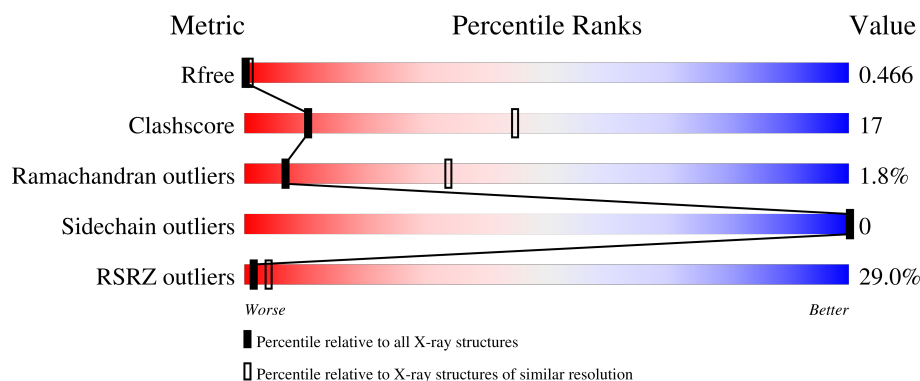
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 5.00 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))
$R_{free}$	164625	1015 (6.06-3.94)
Clashscore	180529	1031 (6.04-3.96)
Ramachandran outliers	177936	1102 (6.10-3.90)
Sidechain outliers	177891	1081 (6.10-3.90)
RSRZ outliers	164620	1011 (6.06-3.94)

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  $\geq 3$ , 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	557	<div> <div>18%</div> <div>52%</div> <div>7%</div> <div>40%</div> </div>
1	B	557	<div> <div>16%</div> <div>50%</div> <div>8%</div> <div>41%</div> </div>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3318 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.

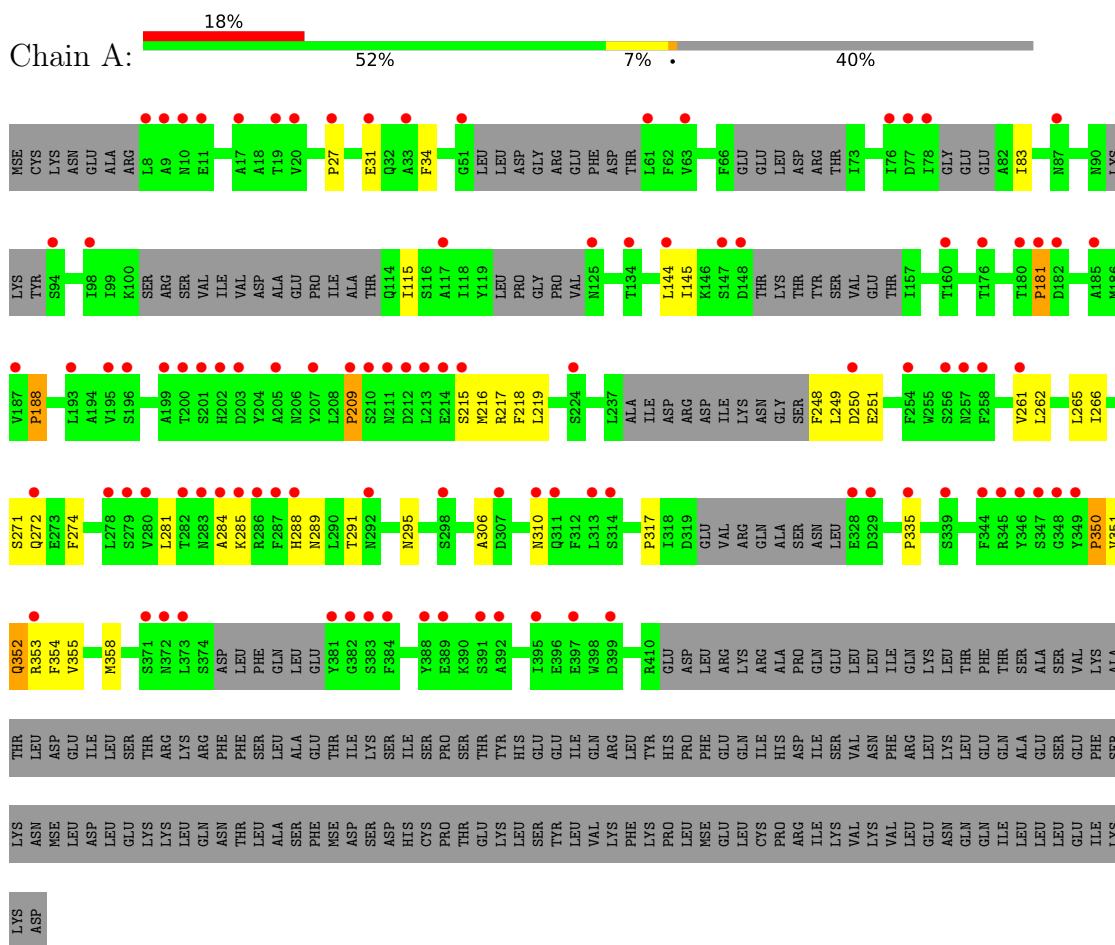
- Molecule 1 is a protein called DYNEIN HEAVY CHAIN, CYTOPLASMIC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	332	Total	C	N	O	Se	0	0	0
			1664	995	332	332	5			
1	B	330	Total	C	N	O	Se	0	0	0
			1654	989	330	330	5			

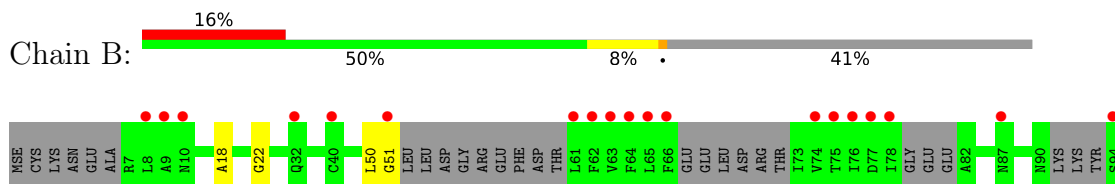
### 3 Residue-property plots

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: DYNEIN HEAVY CHAIN, CYTOPLASMIC



#### • Molecule 1: DYNEIN HEAVY CHAIN, CYTOPLASMIC





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	71.90Å 148.86Å 179.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	114.62 – 5.00 114.62 – 5.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (114.62-5.00) 99.7 (114.62-5.00)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	9.79 (at 5.10Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, $R_{free}$	0.393 , 0.437 0.406 , 0.466	Depositor DCC
$R_{free}$ test set	414 reflections (4.69%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	230.0	Xtriage
Anisotropy	0.566	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.44 , 999.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.79	EDS
Total number of atoms	3318	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	201.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.86	0/1648	1.16	8/2269 (0.4%)
1	B	0.90	0/1638	1.25	12/2255 (0.5%)
All	All	0.88	0/3286	1.21	20/4524 (0.4%)

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	188	PRO	N-CA-CB	15.74	111.73	102.92
1	B	181	PRO	N-CA-CB	9.66	111.86	103.36
1	B	350	PRO	N-CA-CB	9.00	111.32	103.31
1	A	27	PRO	N-CA-CB	7.93	110.37	103.31
1	B	270	GLN	N-CA-C	7.52	119.66	110.41
1	A	209	PRO	N-CA-CB	7.47	111.09	103.25
1	A	335	PRO	N-CA-CB	7.39	111.46	103.33
1	B	335	PRO	N-CA-CB	7.13	111.17	103.33
1	A	188	PRO	N-CA-CB	6.83	110.42	103.25
1	B	311	GLN	N-CA-C	-6.24	100.67	109.96
1	A	350	PRO	N-CA-CB	6.10	109.65	103.25
1	B	275	GLN	N-CA-C	-6.05	104.68	111.28
1	A	181	PRO	N-CA-CB	6.04	109.59	103.25
1	B	209	PRO	N-CA-CB	5.84	109.38	103.25
1	B	184	LEU	N-CA-C	5.70	122.95	110.80
1	B	317	PRO	N-CA-CB	5.67	109.20	103.25
1	B	232	VAL	N-CA-C	5.64	116.29	110.82
1	B	185	ALA	N-CA-C	5.49	117.18	108.79
1	A	215	SER	N-CA-C	5.26	117.58	110.06
1	A	285	LYS	N-CA-C	5.05	117.45	111.33

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	1664	0	752	38	0
1	B	1654	0	748	42	0
All	All	3318	0	1500	80	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 17.

All (80) 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:214:GLU:O	1:B:216:MSE:HA	1.07	1.19
1:B:18:ALA:O	1:B:22:GLY:N	1.81	1.12
1:B:214:GLU:O	1:B:216:MSE:CA	2.03	1.06
1:A:31:GLU:O	1:A:34:PHE:N	1.88	1.05
1:B:215:SER:CB	1:B:219:LEU:H	1.75	0.99
1:B:370:LEU:O	1:B:374:SER:N	1.96	0.97
1:A:271:SER:O	1:A:274:PHE:N	1.97	0.96
1:B:214:GLU:C	1:B:216:MSE:HA	1.93	0.94
1:A:281:LEU:O	1:A:284:ALA:CA	2.16	0.93
1:A:281:LEU:O	1:A:284:ALA:HB3	1.70	0.92
1:B:306:ALA:O	1:B:310:ASN:N	2.03	0.91
1:A:281:LEU:O	1:A:284:ALA:N	2.07	0.86
1:B:281:LEU:O	1:B:286:ARG:CB	2.26	0.84
1:A:281:LEU:O	1:A:284:ALA:CB	2.26	0.83
1:B:292:ASN:O	1:B:296:GLU:N	2.10	0.83
1:A:248:PHE:O	1:A:251:GLU:N	2.13	0.81
1:B:215:SER:CB	1:B:219:LEU:N	2.47	0.77
1:B:215:SER:CB	1:B:219:LEU:CB	2.63	0.77
1:B:215:SER:CB	1:B:216:MSE:O	2.34	0.76
1:A:216:MSE:O	1:A:219:LEU:N	2.18	0.75
1:B:18:ALA:O	1:B:22:GLY:CA	2.34	0.75
1:B:307:ASP:O	1:B:311:GLN:N	2.15	0.75
1:A:271:SER:O	1:A:274:PHE:CA	2.35	0.74
1:B:281:LEU:C	1:B:286:ARG:CB	2.64	0.71
1:A:31:GLU:O	1:A:34:PHE:CA	2.39	0.70

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:271:SER:O	1:A:274:PHE:HA	1.92	0.69
1:B:215:SER:CB	1:B:216:MSE:C	2.66	0.69
1:B:281:LEU:O	1:B:284:ALA:O	2.12	0.68
1:B:291:THR:O	1:B:294:LEU:N	2.27	0.66
1:A:31:GLU:CB	1:A:34:PHE:CB	2.73	0.66
1:B:268:GLN:O	1:B:273:GLU:CB	2.45	0.65
1:B:144:LEU:O	1:B:145:ILE:C	2.40	0.64
1:B:144:LEU:O	1:B:146:LYS:N	2.31	0.64
1:B:203:ASP:O	1:B:206:ASN:N	2.31	0.63
1:A:271:SER:C	1:A:274:PHE:H	2.06	0.63
1:A:262:LEU:O	1:A:266:ILE:N	2.33	0.61
1:A:281:LEU:O	1:A:284:ALA:C	2.42	0.61
1:A:281:LEU:C	1:A:284:ALA:HB3	2.26	0.60
1:A:31:GLU:O	1:A:34:PHE:CB	2.50	0.60
1:B:291:THR:O	1:B:295:ASN:N	2.29	0.60
1:A:281:LEU:C	1:A:284:ALA:H	2.10	0.59
1:B:203:ASP:O	1:B:206:ASN:CA	2.51	0.59
1:A:351:VAL:C	1:A:353:ARG:N	2.58	0.59
1:A:351:VAL:O	1:A:352:GLN:C	2.45	0.58
1:A:291:THR:O	1:A:295:ASN:N	2.24	0.58
1:A:281:LEU:O	1:A:284:ALA:O	2.22	0.58
1:A:306:ALA:O	1:A:310:ASN:N	2.27	0.57
1:A:351:VAL:O	1:A:353:ARG:N	2.38	0.57
1:B:50:LEU:O	1:B:51:GLY:O	2.22	0.57
1:A:281:LEU:HA	1:A:284:ALA:HB3	1.86	0.56
1:A:281:LEU:CA	1:A:284:ALA:HB3	2.36	0.56
1:A:248:PHE:O	1:A:249:LEU:C	2.48	0.55
1:B:18:ALA:O	1:B:22:GLY:HA3	2.04	0.55
1:B:279:SER:O	1:B:283:ASN:N	2.41	0.54
1:A:216:MSE:O	1:A:217:ARG:C	2.52	0.53
1:A:288:HIS:O	1:A:289:ASN:C	2.53	0.52
1:B:291:THR:O	1:B:292:ASN:C	2.53	0.52
1:B:144:LEU:C	1:B:146:LYS:N	2.68	0.50
1:B:144:LEU:O	1:B:147:SER:N	2.43	0.48
1:A:281:LEU:HA	1:A:284:ALA:CB	2.44	0.48
1:B:281:LEU:O	1:B:286:ARG:CA	2.62	0.48
1:A:144:LEU:O	1:A:145:ILE:C	2.57	0.47
1:B:215:SER:CB	1:B:216:MSE:CA	2.92	0.47
1:B:290:LEU:O	1:B:293:LEU:N	2.38	0.47
1:B:291:THR:C	1:B:293:LEU:N	2.70	0.46
1:A:352:GLN:O	1:A:355:VAL:N	2.49	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:351:VAL:C	1:A:353:ARG:H	2.24	0.46
1:B:350:PRO:CB	1:B:353:ARG:CB	2.95	0.45
1:A:354:PHE:O	1:A:358:MSE:HG2	2.17	0.45
1:B:270:GLN:O	1:B:273:GLU:CB	2.65	0.44
1:A:272:GLN:C	1:A:274:PHE:N	2.73	0.44
1:B:308:LYS:O	1:B:311:GLN:O	2.35	0.43
1:B:354:PHE:O	1:B:358:MSE:HG2	2.19	0.42
1:A:261:VAL:O	1:A:265:LEU:N	2.48	0.41
1:B:390:LYS:O	1:B:394:MSE:HG3	2.20	0.41
1:A:248:PHE:C	1:A:250:ASP:N	2.76	0.41
1:B:292:ASN:O	1:B:296:GLU:CB	2.68	0.41
1:B:214:GLU:C	1:B:216:MSE:CA	2.78	0.41
1:A:216:MSE:C	1:A:218:PHE:N	2.79	0.40
1:B:215:SER:CB	1:B:219:LEU:CA	3.00	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	310/557 (56%)	291 (94%)	11 (4%)	8 (3%)	4	25
1	B	308/557 (55%)	294 (96%)	11 (4%)	3 (1%)	13	49
All	All	618/1114 (56%)	585 (95%)	22 (4%)	11 (2%)	7	34

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	83	ILE
1	A	181	PRO
1	A	317	PRO
1	B	317	PRO

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	209	PRO
1	A	350	PRO
1	A	352	GLN
1	B	209	PRO
1	A	115	ILE
1	A	188	PRO
1	B	180	THR

### 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	5/502 (1%)	5 (100%)	0	100	100
1	B	5/502 (1%)	5 (100%)	0	100	100
All	All	10/1004 (1%)	10 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	327/557 (58%)	1.50	99 (30%)  	33, 179, 457, 500	0
1	B	325/557 (58%)	1.42	90 (27%)  	21, 186, 417, 500	0
All	All	652/1114 (58%)	1.46	189 (28%)  	21, 184, 438, 500	0

All (189) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	148	ASP	13.9
1	A	212	ASP	10.5
1	A	211	ASN	9.3
1	A	283	ASN	8.2
1	A	346	TYR	8.0
1	B	382	GLY	7.6
1	B	94	SER	7.6
1	A	347	SER	7.0
1	A	213	LEU	6.7
1	A	210	SER	6.6
1	B	342	LYS	6.5
1	B	77	ASP	6.2
1	A	214	GLU	5.9
1	A	285	LYS	5.7
1	A	310	ASN	5.6
1	B	200	THR	5.1
1	B	391	SER	5.1
1	A	257	ASN	5.0
1	B	395	ILE	5.0
1	B	75	THR	4.9
1	A	78	ILE	4.9
1	B	76	ILE	4.9
1	B	387	LEU	4.9
1	B	272	GLN	4.9

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	372	ASN	4.9
1	A	345	ARG	4.9
1	B	392	ALA	4.8
1	B	78	ILE	4.8
1	A	344	PHE	4.7
1	A	349	TYR	4.7
1	A	348	GLY	4.6
1	B	9	ALA	4.6
1	B	362	SER	4.4
1	A	215	SER	4.4
1	B	292	ASN	4.4
1	A	397	GLU	4.3
1	A	87	ASN	4.3
1	B	61	LEU	4.2
1	A	292	ASN	4.2
1	A	388	TYR	4.2
1	B	388	TYR	4.2
1	A	20	VAL	4.1
1	A	258	PHE	4.1
1	A	202	HIS	4.1
1	A	287	PHE	4.1
1	B	329	ASP	4.1
1	B	203	ASP	4.1
1	A	147	SER	4.0
1	A	329	ASP	4.0
1	A	381	TYR	4.0
1	A	392	ALA	3.9
1	A	261	VAL	3.9
1	A	328	GLU	3.9
1	A	311	GLN	3.9
1	B	407	LEU	3.8
1	A	353	ARG	3.8
1	A	193	LEU	3.8
1	A	76	ILE	3.7
1	B	384	PHE	3.7
1	A	383	SER	3.7
1	B	119	TYR	3.7
1	A	182	ASP	3.7
1	B	162	ARG	3.6
1	B	160	THR	3.6
1	B	40	CYS	3.6
1	B	95	THR	3.6

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	125	ASN	3.6
1	B	125	ASN	3.6
1	B	212	ASP	3.5
1	B	218	PHE	3.5
1	A	284	ALA	3.5
1	B	289	ASN	3.5
1	B	114	GLN	3.5
1	A	254	PHE	3.5
1	B	296	GLU	3.5
1	A	399	ASP	3.5
1	A	339	SER	3.4
1	A	10	ASN	3.4
1	B	410	ARG	3.4
1	A	195	VAL	3.3
1	B	147	SER	3.3
1	A	382	GLY	3.3
1	B	298	SER	3.3
1	B	165	ASP	3.3
1	B	381	TYR	3.3
1	A	61	LEU	3.2
1	B	385	LEU	3.2
1	B	10	ASN	3.2
1	A	180	THR	3.2
1	A	373	LEU	3.2
1	B	367	ASP	3.2
1	B	64	PHE	3.2
1	B	66	PHE	3.2
1	B	295	ASN	3.2
1	B	406	ASN	3.2
1	A	196	SER	3.2
1	B	274	PHE	3.1
1	A	185	ALA	3.1
1	A	8	LEU	3.1
1	B	374	SER	3.1
1	A	286	ARG	3.1
1	B	287	PHE	3.1
1	B	328	GLU	3.0
1	A	160	THR	3.0
1	A	176	THR	3.0
1	A	288	HIS	3.0
1	B	176	THR	3.0
1	B	249	LEU	3.0

*Continued on next page...*

*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	63	VAL	3.0
1	A	391	SER	2.9
1	B	8	LEU	2.9
1	B	341	LEU	2.9
1	B	408	LEU	2.9
1	B	127	GLY	2.9
1	A	17	ALA	2.9
1	B	250	ASP	2.9
1	B	297	GLY	2.9
1	A	187	VAL	2.9
1	A	205	ALA	2.9
1	B	87	ASN	2.9
1	A	201	SER	2.8
1	B	343	LYS	2.8
1	B	339	SER	2.8
1	B	51	GLY	2.8
1	A	280	VAL	2.7
1	A	181	PRO	2.7
1	A	314	SER	2.7
1	A	9	ALA	2.7
1	A	250	ASP	2.7
1	B	65	LEU	2.7
1	A	389	GLU	2.6
1	A	335	PRO	2.6
1	B	353	ARG	2.6
1	A	207	TYR	2.6
1	B	409	ILE	2.6
1	B	340	SER	2.5
1	A	384	PHE	2.5
1	B	312	PHE	2.5
1	B	211	ASN	2.5
1	A	209	PRO	2.5
1	A	256	SER	2.5
1	B	336	VAL	2.5
1	B	288	HIS	2.5
1	A	199	ALA	2.5
1	B	293	LEU	2.4
1	B	228	LYS	2.4
1	A	63	VAL	2.4
1	A	94	SER	2.4
1	A	298	SER	2.4
1	B	62	PHE	2.4

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	270	GLN	2.4
1	A	19	THR	2.4
1	B	251	GLU	2.4
1	A	77	ASP	2.4
1	A	279	SER	2.4
1	A	117	ALA	2.3
1	A	31	GLU	2.3
1	A	224	SER	2.3
1	B	372	ASN	2.3
1	A	51	GLY	2.3
1	B	248	PHE	2.3
1	B	135	HIS	2.3
1	A	282	THR	2.3
1	A	27	PRO	2.3
1	B	209	PRO	2.3
1	A	33	ALA	2.3
1	A	272	GLN	2.2
1	B	172	GLN	2.2
1	B	290	LEU	2.2
1	B	166	ASP	2.2
1	B	300	SER	2.2
1	A	134	THR	2.2
1	A	98	ILE	2.2
1	B	214	GLU	2.2
1	B	196	SER	2.2
1	A	11	GLU	2.2
1	B	32	GLN	2.2
1	A	278	LEU	2.1
1	A	200	THR	2.1
1	A	395	ILE	2.1
1	B	74	VAL	2.1
1	A	313	LEU	2.1
1	B	205	ALA	2.1
1	B	305	LEU	2.1
1	A	203	ASP	2.1
1	A	307	ASP	2.1
1	A	144	LEU	2.1
1	B	319	ASP	2.1
1	A	371	SER	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.