



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:36 AM UTC

PDB ID : 5AFR / pdb_00005afr
Title : N-terminal fragment of dynein heavy chain
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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

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
Mogul : 2022.3.0, CSD as543be (2022)
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

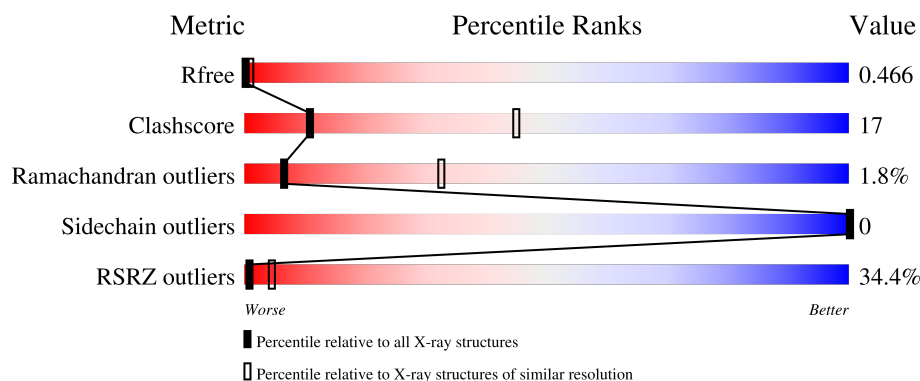
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	180053	1009 (6.02-3.98)
Clashscore	190562	1040 (6.00-4.00)
Ramachandran outliers	187476	1015 (6.06-3.92)
Sidechain outliers	187428	1136 (6.10-3.90)
RSRZ outliers	180081	1004 (6.02-3.98)

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	557	20% 52% 7% 40%
1	B	557	20% 50% 8% 41%

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			

- 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, α , β , γ	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
$\langle I/\sigma(I) \rangle$ ¹	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 (4.70%)	wwPDB-VP
Wilson B-factor (Å ²)	230.0	Xtriage
Anisotropy	0.566	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 999.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	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 ²)	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.*

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	0.86	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

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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

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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%)	12	47
All	All	618/1114 (56%)	585 (95%)	22 (4%)	11 (2%)	6	32

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

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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, 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	327/557 (58%)	1.77	112 (34%)  	33, 179, 457, 500	0
1	B	325/557 (58%)	1.67	112 (34%)  	21, 186, 417, 500	0
All	All	652/1114 (58%)	1.72	224 (34%)  	21, 184, 438, 500	0

All (224) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	148	ASP	15.5
1	A	212	ASP	11.8
1	A	211	ASN	10.0
1	A	283	ASN	8.8
1	A	346	TYR	8.7
1	B	382	GLY	8.4
1	B	94	SER	8.2
1	A	347	SER	7.7
1	B	342	LYS	7.4
1	A	213	LEU	7.3
1	A	210	SER	7.2
1	B	77	ASP	7.0
1	A	214	GLU	6.6
1	A	285	LYS	6.5
1	A	310	ASN	6.1
1	B	200	THR	5.7
1	A	345	ARG	5.6
1	B	391	SER	5.5
1	B	75	THR	5.5
1	B	272	GLN	5.5
1	B	395	ILE	5.5
1	A	257	ASN	5.5
1	B	392	ALA	5.4
1	A	78	ILE	5.4

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Mol	Chain	Res	Type	RSRZ
1	B	76	ILE	5.4
1	B	387	LEU	5.4
1	B	78	ILE	5.3
1	A	372	ASN	5.3
1	B	9	ALA	5.2
1	A	349	TYR	5.2
1	A	348	GLY	5.2
1	A	344	PHE	5.1
1	B	362	SER	4.9
1	A	397	GLU	4.9
1	A	215	SER	4.8
1	B	292	ASN	4.8
1	A	87	ASN	4.7
1	B	61	LEU	4.7
1	B	329	ASP	4.7
1	A	20	VAL	4.6
1	A	388	TYR	4.6
1	B	203	ASP	4.6
1	A	292	ASN	4.6
1	B	388	TYR	4.6
1	A	202	HIS	4.6
1	A	329	ASP	4.6
1	A	258	PHE	4.5
1	A	392	ALA	4.5
1	A	147	SER	4.4
1	A	311	GLN	4.4
1	A	287	PHE	4.4
1	A	381	TYR	4.4
1	A	353	ARG	4.4
1	A	261	VAL	4.4
1	A	328	GLU	4.4
1	B	162	ARG	4.2
1	A	182	ASP	4.2
1	B	407	LEU	4.2
1	A	193	LEU	4.2
1	A	76	ILE	4.1
1	B	160	THR	4.1
1	B	119	TYR	4.1
1	A	383	SER	4.1
1	B	95	THR	4.1
1	B	212	ASP	4.1
1	B	384	PHE	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	114	GLN	4.0
1	A	284	ALA	4.0
1	A	399	ASP	4.0
1	B	296	GLU	3.9
1	B	410	ARG	3.9
1	A	125	ASN	3.9
1	B	125	ASN	3.9
1	B	289	ASN	3.9
1	B	40	CYS	3.8
1	B	218	PHE	3.8
1	A	254	PHE	3.8
1	A	339	SER	3.8
1	A	195	VAL	3.8
1	B	165	ASP	3.8
1	A	10	ASN	3.7
1	A	382	GLY	3.7
1	B	367	ASP	3.7
1	B	147	SER	3.7
1	A	180	THR	3.7
1	B	381	TYR	3.6
1	A	286	ARG	3.6
1	A	61	LEU	3.6
1	B	385	LEU	3.6
1	B	298	SER	3.6
1	A	373	LEU	3.6
1	A	185	ALA	3.5
1	B	10	ASN	3.5
1	B	295	ASN	3.5
1	A	196	SER	3.5
1	B	64	PHE	3.5
1	B	66	PHE	3.5
1	B	406	ASN	3.5
1	A	8	LEU	3.5
1	A	160	THR	3.4
1	A	176	THR	3.4
1	B	274	PHE	3.4
1	B	328	GLU	3.4
1	B	374	SER	3.4
1	A	288	HIS	3.4
1	B	176	THR	3.4
1	B	63	VAL	3.4
1	B	287	PHE	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	250	ASP	3.3
1	B	249	LEU	3.3
1	A	17	ALA	3.3
1	B	127	GLY	3.3
1	B	343	LYS	3.3
1	A	205	ALA	3.3
1	B	8	LEU	3.3
1	B	341	LEU	3.3
1	B	408	LEU	3.3
1	B	297	GLY	3.3
1	A	187	VAL	3.3
1	A	391	SER	3.3
1	B	87	ASN	3.2
1	A	201	SER	3.1
1	B	51	GLY	3.1
1	A	250	ASP	3.1
1	A	181	PRO	3.1
1	A	280	VAL	3.1
1	B	353	ARG	3.1
1	B	339	SER	3.1
1	A	9	ALA	3.1
1	A	335	PRO	3.0
1	A	389	GLU	3.0
1	A	314	SER	3.0
1	B	65	LEU	3.0
1	A	207	TYR	2.9
1	B	409	ILE	2.9
1	A	209	PRO	2.9
1	B	228	LYS	2.9
1	B	336	VAL	2.9
1	B	288	HIS	2.9
1	A	199	ALA	2.8
1	B	340	SER	2.8
1	B	211	ASN	2.8
1	A	256	SER	2.8
1	A	384	PHE	2.8
1	B	312	PHE	2.8
1	A	63	VAL	2.8
1	B	270	GLN	2.8
1	B	293	LEU	2.8
1	A	77	ASP	2.8
1	A	19	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	117	ALA	2.7
1	B	251	GLU	2.7
1	A	94	SER	2.7
1	A	298	SER	2.7
1	A	31	GLU	2.7
1	A	279	SER	2.6
1	B	62	PHE	2.6
1	B	135	HIS	2.6
1	A	282	THR	2.6
1	A	27	PRO	2.6
1	B	209	PRO	2.6
1	A	51	GLY	2.6
1	A	33	ALA	2.6
1	B	166	ASP	2.6
1	A	272	GLN	2.6
1	B	172	GLN	2.6
1	A	224	SER	2.6
1	B	372	ASN	2.6
1	A	134	THR	2.6
1	B	32	GLN	2.5
1	B	214	GLU	2.5
1	B	248	PHE	2.5
1	B	290	LEU	2.5
1	A	11	GLU	2.5
1	A	98	ILE	2.5
1	A	200	THR	2.5
1	B	300	SER	2.5
1	B	196	SER	2.5
1	A	203	ASP	2.5
1	A	307	ASP	2.5
1	B	74	VAL	2.5
1	B	205	ALA	2.5
1	B	319	ASP	2.4
1	A	278	LEU	2.4
1	A	313	LEU	2.4
1	A	395	ILE	2.4
1	B	305	LEU	2.4
1	B	7	ARG	2.4
1	A	144	LEU	2.4
1	B	363	GLN	2.3
1	B	21	THR	2.3
1	B	311	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	204	TYR	2.3
1	A	371	SER	2.3
1	A	170	GLN	2.2
1	B	389	GLU	2.2
1	A	297	GLY	2.2
1	B	317	PRO	2.2
1	A	135	HIS	2.2
1	A	21	THR	2.2
1	A	374	SER	2.2
1	A	255	TRP	2.2
1	B	35	ILE	2.2
1	A	119	TYR	2.2
1	B	398	TRP	2.2
1	B	213	LEU	2.2
1	B	254	PHE	2.1
1	B	269	THR	2.1
1	A	396	GLU	2.1
1	B	364	GLU	2.1
1	B	30	ASN	2.1
1	B	134	THR	2.1
1	A	96	LEU	2.1
1	A	169	LYS	2.1
1	B	180	THR	2.1
1	B	236	THR	2.1
1	B	291	THR	2.1
1	B	190	ILE	2.1
1	B	217	ARG	2.1
1	B	204	TYR	2.1
1	A	116	SER	2.1
1	B	271	SER	2.0
1	A	226	ALA	2.0
1	B	335	PRO	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.