



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:41 PM UTC

PDB ID : 4PER / pdb_00004per
Title : Structure of Gallus gallus ribonuclease inhibitor complexed with Gallus gallus ribonuclease I
Authors : Bianchetti, C.M.; Lomax, J.E.; Raines, R.T.; Fox, B.G.
Deposited on : 2014-04-24
Resolution : 1.92 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

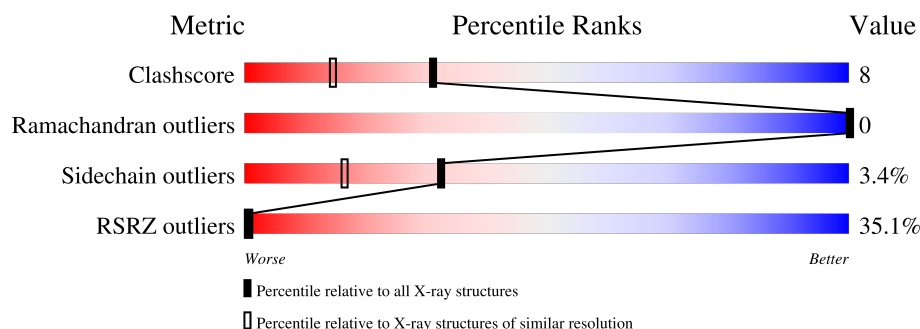
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.92 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))
Clashscore	190562	1209 (1.92-1.92)
Ramachandran outliers	187476	1195 (1.92-1.92)
Sidechain outliers	187428	1195 (1.92-1.92)
RSRZ outliers	180081	1188 (1.92-1.92)

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	460	30% 84% 15% .
2	B	113	55% 72% 22% . .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4636 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 Ribonuclease Inhibitor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	458	3533	2198	596	701	38	0	10	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	TYR	-	expression tag	UNP Q5ZIIY8
A	-2	PHE	-	expression tag	UNP Q5ZIIY8
A	-1	GLN	-	expression tag	UNP Q5ZIIY8
A	0	GLY	-	expression tag	UNP Q5ZIIY8
A	10	ILE	MET	conflict	UNP Q5ZIIY8

- Molecule 2 is a protein called Angiogenin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	109	870	538	171	154	7	0	0	0

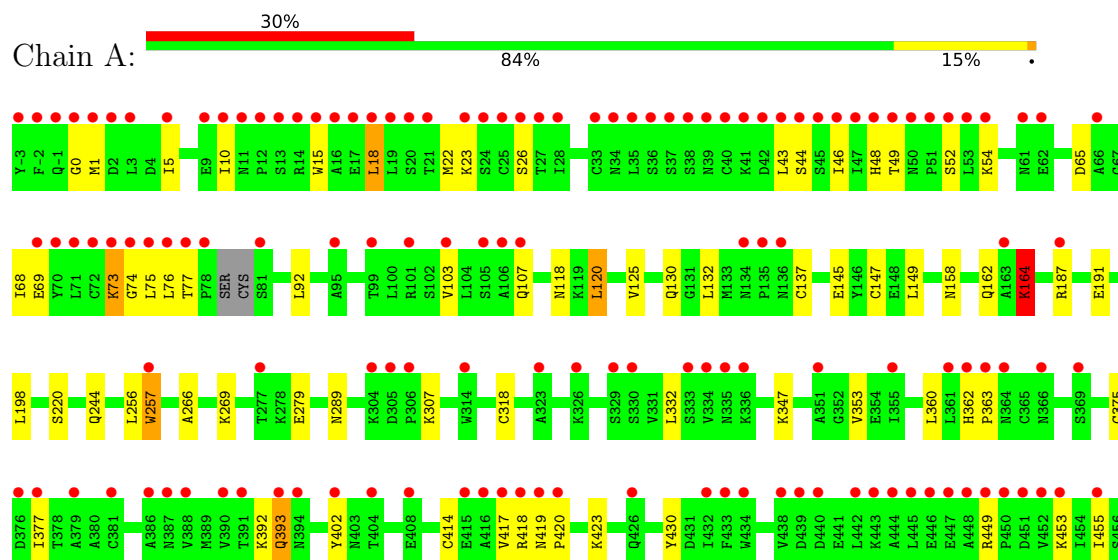
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	195	Total	O	0	0
			195	195		
3	B	38	Total	O	0	0
			38	38		

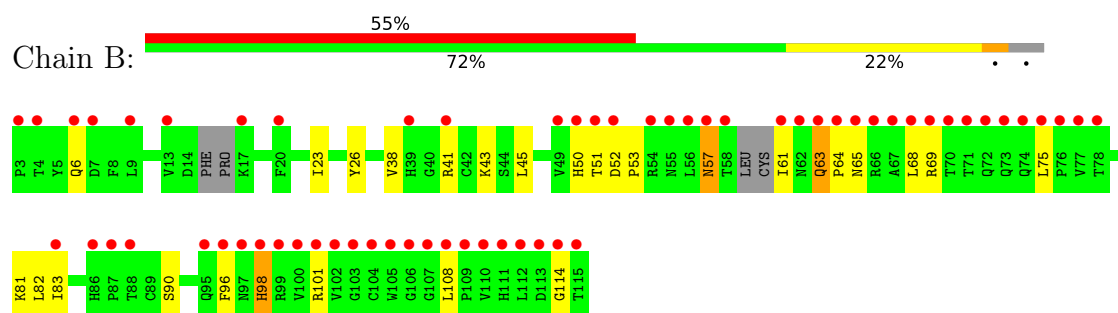
3 Residue-property plots [i](#)

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: Ribonuclease Inhibitor



• Molecule 2: Angiogenin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.66Å 84.54Å 121.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.81 – 1.92 39.81 – 1.92	Depositor EDS
% Data completeness (in resolution range)	97.5 (39.81-1.92) 96.9 (39.81-1.92)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 1.77Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.202 , 0.254 0.207 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	1.6	Xtriage
Anisotropy	2.584	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 57.5	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	0.90	EDS
Total number of atoms	4636	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.75% 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	0.53	0/3607	0.82	5/4886 (0.1%)
2	B	0.48	0/889	0.87	2/1205 (0.2%)
All	All	0.52	0/4496	0.83	7/6091 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	419	ASN	CA-C-N	5.64	125.26	119.56
1	A	419	ASN	C-N-CA	5.64	125.26	119.56
1	A	257	TRP	CA-CB-CG	-5.63	102.91	113.60
1	A	393	GLN	CA-CB-CG	5.61	125.31	114.10
1	A	164	LYS	N-CA-C	5.06	118.19	108.97
2	B	82	LEU	CA-C-N	-5.03	116.15	121.84
2	B	82	LEU	C-N-CA	-5.03	116.15	121.84

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	3533	0	3583	57	0
2	B	870	0	851	24	0
3	A	195	0	0	2	0
3	B	38	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4636	0	4434	72	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 8.

All (72) 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)
2:B:53:PRO:O	2:B:57:ASN:ND2	2.06	0.87
2:B:57:ASN:HD22	2:B:57:ASN:H	1.27	0.82
1:A:455:ILE:HD12	2:B:41:ARG:HH11	1.46	0.79
1:A:75:LEU:HD12	1:A:103:VAL:HG22	1.67	0.77
2:B:57:ASN:HD22	2:B:57:ASN:N	1.82	0.76
2:B:38:VAL:HG23	2:B:41:ARG:HH21	1.53	0.74
1:A:23:LYS:NZ	1:A:49:THR:OG1	2.26	0.68
1:A:257:TRP:CZ3	2:B:83:ILE:O	2.49	0.66
1:A:5:ILE:HD11	1:A:18:LEU:HD21	1.79	0.65
1:A:75:LEU:HD11	1:A:103:VAL:HG13	1.78	0.65
1:A:402:TYR:OH	2:B:45:LEU:O	2.15	0.64
2:B:101:ARG:HB3	2:B:114:GLY:HA3	1.81	0.62
1:A:10:ILE:HG21	1:A:15:TRP:HE3	1.64	0.62
2:B:96:PHE:HB3	2:B:98:HIS:ND1	2.15	0.61
1:A:48:HIS:CD2	1:A:77:THR:HG22	2.35	0.61
1:A:256:LEU:C	1:A:257:TRP:HD1	2.10	0.59
1:A:402:TYR:OH	2:B:43:LYS:HE2	2.02	0.58
1:A:75:LEU:HD13	1:A:75:LEU:O	2.03	0.58
1:A:257:TRP:HZ3	2:B:83:ILE:O	1.89	0.55
1:A:65:ASP:O	1:A:69:GLU:HG3	2.07	0.54
1:A:455:ILE:HD12	2:B:41:ARG:NH1	2.20	0.54
1:A:393:GLN:HE22	1:A:423:LYS:HE2	1.73	0.53
1:A:393:GLN:NE2	1:A:423:LYS:HG2	2.24	0.53
1:A:455:ILE:HG23	2:B:41:ARG:HH11	1.74	0.52
1:A:43:LEU:HA	1:A:46:ILE:HD12	1.92	0.52
1:A:75:LEU:O	1:A:107:GLN:NE2	2.44	0.51
1:A:393:GLN:NE2	1:A:423:LYS:HE2	2.27	0.50
1:A:158:ASN:O	1:A:162:GLN:HG2	2.11	0.50
1:A:75:LEU:CD1	1:A:103:VAL:HG13	2.41	0.50
1:A:417:VAL:O	1:A:449:ARG:HD3	2.12	0.50
1:A:18:LEU:O	1:A:22:MET:HG3	2.11	0.49
1:A:0:GLY:HA3	1:A:26:SER:HB2	1.94	0.49
1:A:256:LEU:C	1:A:257:TRP:CD1	2.90	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:GLN:OE1	3:A:593:HOH:O	2.20	0.48
2:B:63:GLN:HG2	2:B:69:ARG:HD2	1.95	0.48
2:B:26:TYR:OH	2:B:50:HIS:HE1	1.97	0.48
1:A:347:LYS:HE2	1:A:347:LYS:HB3	1.56	0.47
1:A:332:LEU:HD13	1:A:360:LEU:HD23	1.96	0.47
2:B:83:ILE:HG12	2:B:90:SER:O	2.14	0.47
1:A:257:TRP:CD1	1:A:257:TRP:N	2.80	0.47
1:A:187:ARG:NH1	1:A:191:GLU:OE2	2.47	0.47
1:A:73:LYS:O	1:A:76:LEU:HG	2.14	0.47
1:A:353:VAL:HG21	1:A:377:ILE:HG21	1.97	0.46
1:A:10:ILE:HG21	1:A:15:TRP:CE3	2.47	0.46
2:B:57:ASN:ND2	2:B:57:ASN:N	2.57	0.46
1:A:125:VAL:HG21	1:A:149:LEU:HD21	1.98	0.46
1:A:187:ARG:NH2	3:A:501:HOH:O	2.21	0.46
1:A:455:ILE:HG23	2:B:41:ARG:NH1	2.31	0.45
2:B:51:THR:HG21	2:B:75:LEU:HD13	1.98	0.45
1:A:266:ALA:O	1:A:269:LYS:HG3	2.17	0.45
1:A:137:CYS:SG	1:A:164:LYS:HE3	2.57	0.44
1:A:44:SER:O	1:A:74:GLY:HA3	2.17	0.43
1:A:132:LEU:O	1:A:164:LYS:HE2	2.18	0.43
1:A:414:CYS:O	1:A:418:ARG:HG3	2.18	0.43
1:A:392:LYS:HA	1:A:392:LYS:HD2	1.78	0.43
1:A:420:PRO:O	1:A:423:LYS:NZ	2.50	0.43
1:A:68:ILE:HD13	1:A:92:LEU:HD21	2.01	0.43
2:B:45:LEU:HD22	2:B:81:LYS:HE2	2.00	0.43
1:A:120:LEU:HD23	1:A:147:CYS:SG	2.59	0.42
1:A:198:LEU:C	1:A:198:LEU:HD23	2.44	0.42
1:A:362:HIS:O	1:A:392:LYS:NZ	2.52	0.42
2:B:63:GLN:HB3	2:B:64:PRO:HD2	2.01	0.42
2:B:108:LEU:HA	2:B:108:LEU:HD23	1.71	0.41
1:A:362:HIS:HA	1:A:363:PRO:HD3	1.90	0.41
1:A:289:ASN:O	1:A:318:CYS:HA	2.20	0.41
1:A:430:TYR:CG	2:B:43:LYS:HE3	2.55	0.41
1:A:52:SER:O	1:A:54:LYS:HG3	2.21	0.41
1:A:375[B]:CYS:SG	1:A:377:ILE:HG23	2.60	0.41
1:A:118:ASN:O	1:A:120:LEU:HD22	2.21	0.41
2:B:68:LEU:HD13	2:B:101:ARG:HH21	1.86	0.41
1:A:18:LEU:HA	1:A:18:LEU:HD12	1.66	0.40
1:A:279:GLU:HG3	1:A:307:LYS:HG2	2.02	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	464/460 (101%)	452 (97%)	12 (3%)	0	100	100
2	B	103/113 (91%)	97 (94%)	6 (6%)	0	100	100
All	All	567/573 (99%)	549 (97%)	18 (3%)	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	415/407 (102%)	405 (98%)	10 (2%)	43	28
2	B	99/103 (96%)	91 (92%)	8 (8%)	11	2
All	All	514/510 (101%)	496 (96%)	18 (4%)	32	16

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	18	LEU
1	A	73	LYS
1	A	120	LEU
1	A	130	GLN
1	A	145	GLU
1	A	164	LYS
1	A	220[A]	SER

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Mol	Chain	Res	Type
1	A	220[B]	SER
1	A	453	LYS
2	B	6	GLN
2	B	23	ILE
2	B	52	ASP
2	B	57	ASN
2	B	61	ILE
2	B	63	GLN
2	B	65	ASN
2	B	98	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	HIS
1	A	184	GLN
1	A	393	GLN
2	B	57	ASN
2	B	86	HIS
2	B	94	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	458/460 (99%)	1.50	137 (29%)	1 1	5, 27, 50, 64	10 (2%)
2	B	109/113 (96%)	2.84	62 (56%)	0 0	20, 36, 69, 76	0
All	All	567/573 (98%)	1.76	199 (35%)	1 0	5, 29, 58, 76	10 (1%)

All (199) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	78	PRO	9.4
2	B	65	ASN	9.1
1	A	76	LEU	8.8
1	A	13	SER	7.7
1	A	77	THR	7.7
2	B	61	ILE	7.6
1	A	18	LEU	7.6
1	A	48	HIS	6.5
1	A	38	SER	6.5
2	B	99	ARG	6.3
1	A	11	ASN	6.3
2	B	71	THR	6.3
2	B	115	THR	6.3
1	A	75	LEU	6.2
2	B	67	ALA	6.1
2	B	98	HIS	6.1
2	B	54	ARG	6.0
1	A	402	TYR	6.0
1	A	19	LEU	5.9
2	B	58	THR	5.9
1	A	12	PRO	5.9
2	B	114	GLY	5.8
1	A	333	SER	5.8
1	A	135	PRO	5.8

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Mol	Chain	Res	Type	RSRZ
1	A	10	ILE	5.8
2	B	62	ASN	5.8
2	B	68	LEU	5.6
1	A	-3	TYR	5.6
1	A	257	TRP	5.6
1	A	17	GLU	5.6
1	A	39	ASN	5.5
1	A	420	PRO	5.4
1	A	40	CYS	5.3
2	B	75	LEU	5.2
2	B	57	ASN	5.2
2	B	104	CYS	5.2
1	A	2	ASP	5.1
2	B	100	VAL	5.0
2	B	108	LEU	5.0
2	B	96	PHE	5.0
2	B	69	ARG	5.0
2	B	77	VAL	5.0
2	B	63	GLN	4.9
2	B	74	GLN	4.9
1	A	-1	GLN	4.9
1	A	364	ASN	4.9
2	B	72	GLN	4.8
1	A	330	SER	4.8
1	A	44	SER	4.8
1	A	52	SER	4.8
1	A	74	GLY	4.7
1	A	37	SER	4.7
2	B	64	PRO	4.6
2	B	4	THR	4.6
1	A	14	ARG	4.6
1	A	363	PRO	4.6
1	A	16	ALA	4.6
2	B	70	THR	4.6
2	B	102	VAL	4.6
1	A	23	LYS	4.5
1	A	393	GLN	4.5
1	A	9	GLU	4.5
1	A	45	SER	4.5
2	B	107	GLY	4.4
1	A	66	ALA	4.4
2	B	3	PRO	4.3

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Mol	Chain	Res	Type	RSRZ
1	A	41	LYS	4.3
1	A	-2	PHE	4.3
1	A	72	CYS	4.3
1	A	448	ALA	4.3
2	B	55	ASN	4.3
1	A	95	ALA	4.2
2	B	97	ASN	4.2
2	B	51	THR	4.2
1	A	70	TYR	4.2
1	A	106	ALA	4.1
2	B	52	ASP	4.1
1	A	73	LYS	4.1
1	A	445	LEU	4.1
1	A	47	ILE	4.1
1	A	103	VAL	4.0
1	A	26	SER	4.0
2	B	73	GLN	3.9
1	A	361	LEU	3.9
1	A	418	ARG	3.9
2	B	66	ARG	3.9
1	A	49	THR	3.9
1	A	390	VAL	3.9
1	A	0	GLY	3.9
2	B	106	GLY	3.9
1	A	42	ASP	3.9
1	A	43	LEU	3.8
1	A	15	TRP	3.8
1	A	305	ASP	3.8
1	A	81	SER	3.7
1	A	334	VAL	3.7
2	B	103	GLY	3.7
1	A	323	ALA	3.6
2	B	6	GLN	3.6
1	A	306	PRO	3.6
1	A	433	PHE	3.5
2	B	56	LEU	3.5
1	A	51	PRO	3.5
1	A	35	LEU	3.5
1	A	36	SER	3.5
2	B	112	LEU	3.4
1	A	20	SER	3.3
2	B	105	TRP	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	25	CYS	3.3
1	A	24	SER	3.3
1	A	34[A]	ASN	3.3
2	B	17	LYS	3.3
2	B	76	PRO	3.3
1	A	46	ILE	3.3
1	A	391	THR	3.3
2	B	110	VAL	3.2
1	A	449	ARG	3.2
2	B	101	ARG	3.2
1	A	326	LYS	3.1
1	A	450	PRO	3.1
2	B	88	THR	3.1
1	A	440	ASP	3.1
1	A	336	LYS	3.0
1	A	439	ASP	3.0
1	A	136	ASN	3.0
1	A	419	ASN	3.0
1	A	53	LEU	3.0
2	B	9	LEU	3.0
1	A	69	GLU	3.0
2	B	13	VAL	2.9
1	A	394	ASN	2.9
1	A	71	LEU	2.9
1	A	377	ILE	2.9
1	A	415	GLU	2.8
1	A	105	SER	2.8
1	A	329	SER	2.8
1	A	351	ALA	2.8
1	A	387	ASN	2.8
1	A	416	ALA	2.7
1	A	443	LYS	2.7
1	A	447	GLU	2.7
1	A	404	THR	2.7
1	A	134	ASN	2.7
1	A	304	LYS	2.7
1	A	335	ASN	2.7
1	A	417	VAL	2.6
2	B	50	HIS	2.6
2	B	95	GLN	2.6
1	A	99	THR	2.6
1	A	314	TRP	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	1	MET	2.6
1	A	444	ALA	2.6
1	A	62	GLU	2.5
1	A	3	LEU	2.5
2	B	7	ASP	2.5
1	A	455	ILE	2.5
1	A	362	HIS	2.5
1	A	27	THR	2.5
2	B	113	ASP	2.5
2	B	111	HIS	2.5
1	A	386	ALA	2.5
2	B	87	PRO	2.5
1	A	426	GLN	2.5
1	A	452	VAL	2.5
2	B	109	PRO	2.5
1	A	442	LEU	2.4
1	A	163	ALA	2.4
2	B	86	HIS	2.4
1	A	453	LYS	2.4
2	B	78	THR	2.4
2	B	83	ILE	2.4
1	A	388	VAL	2.4
1	A	369	SER	2.4
1	A	50	ASN	2.3
1	A	33	CYS	2.3
2	B	49	VAL	2.3
1	A	434	TRP	2.3
1	A	21	THR	2.3
1	A	376	ASP	2.3
1	A	451	ASP	2.3
1	A	61	ASN	2.3
1	A	366	ASN	2.3
1	A	355	ILE	2.2
2	B	20	PHE	2.2
1	A	381	CYS	2.2
1	A	187	ARG	2.2
1	A	107	GLN	2.2
1	A	277	THR	2.2
1	A	5	ILE	2.1
1	A	432	ILE	2.1
1	A	101	ARG	2.1
1	A	438	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	446	GLU	2.1
2	B	39	HIS	2.1
1	A	28	ILE	2.1
1	A	408	GLU	2.1
1	A	379	ALA	2.0
2	B	41	ARG	2.0
1	A	54	LYS	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.