



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 01:49 AM UTC

PDB ID : 6EOO / pdb_00006eoo
Title : DPP8 - Apo, space group 20
Authors : Ross, B.R.; Huber, R.
Deposited on : 2017-10-10
Resolution : 2.50 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

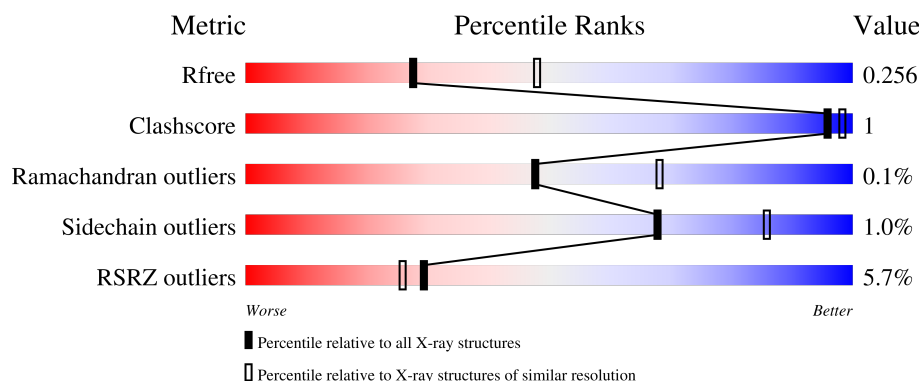
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	898	5% 88% 9%
1	B	898	4% 88% 9%
1	C	898	6% 88% 9%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 20373 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 Dipeptidyl peptidase 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	820	Total	C	N	O	S	0	1	0
			6674	4292	1117	1239	26			
1	B	819	Total	C	N	O	S	0	1	0
			6663	4283	1116	1238	26			
1	C	820	Total	C	N	O	S	0	1	0
			6670	4288	1117	1239	26			

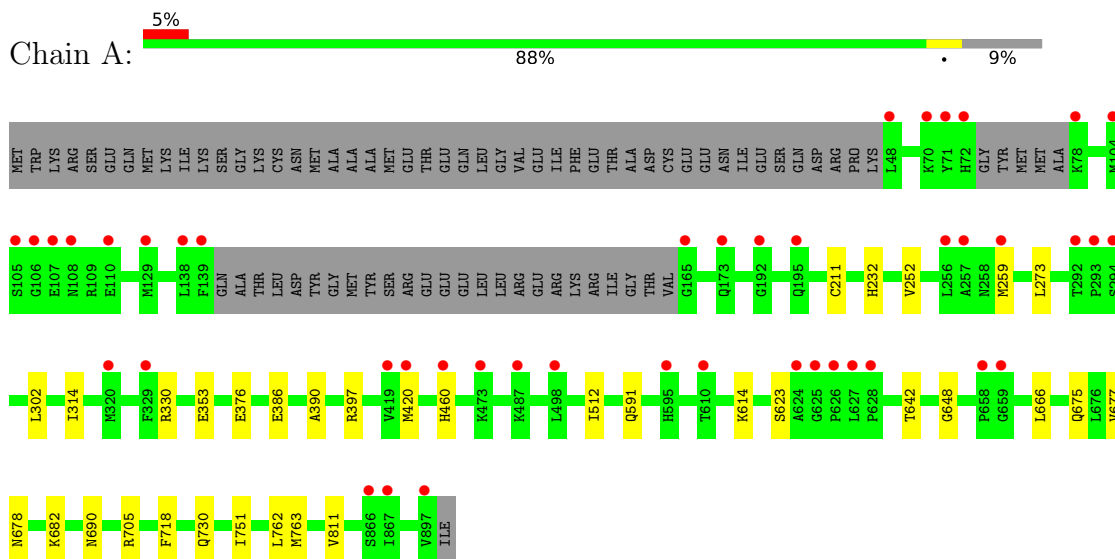
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	132	Total	O	0	0
			132	132		
2	B	131	Total	O	0	0
			131	131		
2	C	103	Total	O	0	0
			103	103		

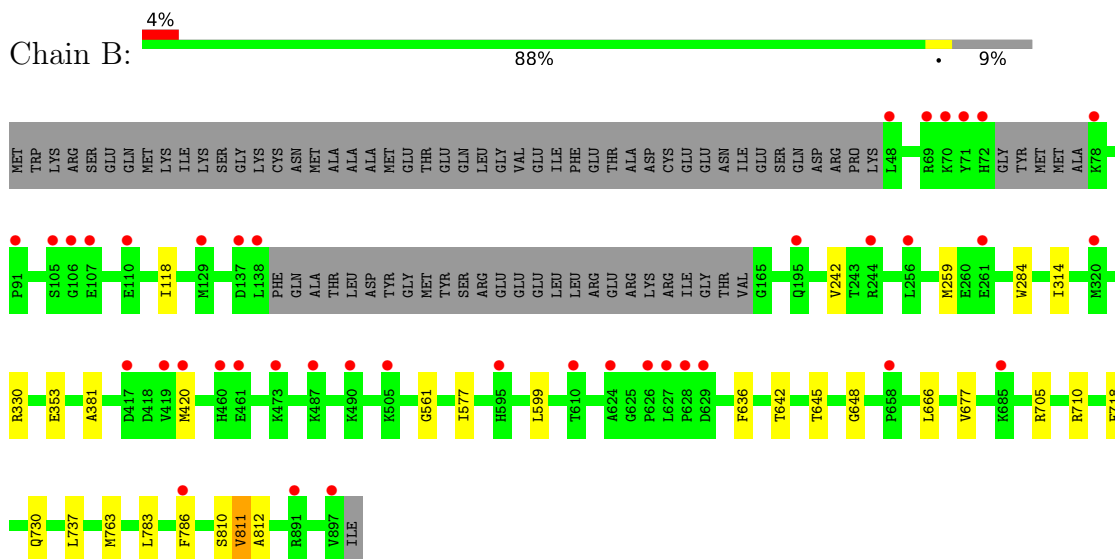
3 Residue-property plots [i](#)

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.

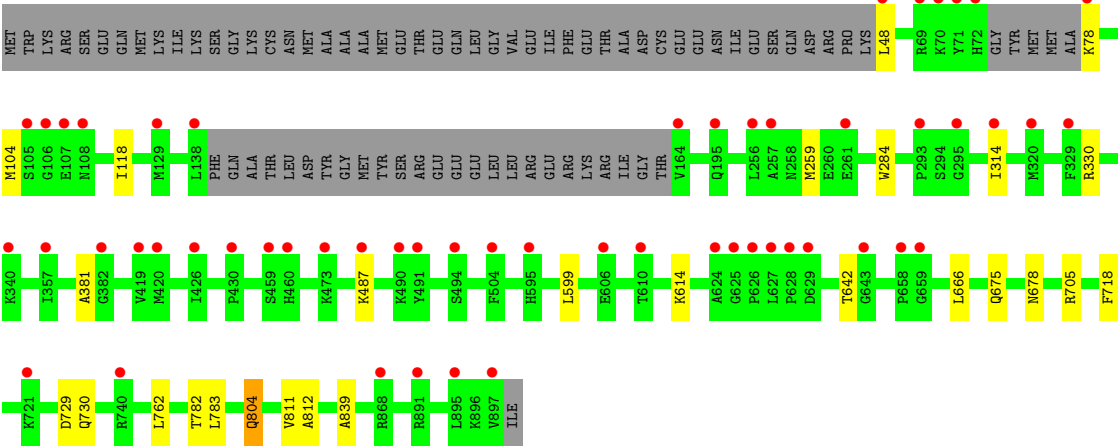
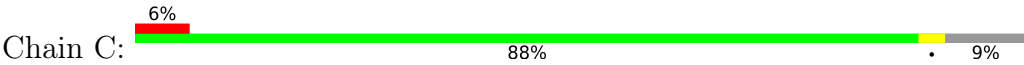
- Molecule 1: Dipeptidyl peptidase 8



- Molecule 1: Dipeptidyl peptidase 8



- Molecule 1: Dipeptidyl peptidase 8



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	162.84Å 247.06Å 260.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.65 – 2.50 44.65 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.9 (44.65-2.50) 99.9 (44.65-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.19 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.229 , 0.254 0.232 , 0.256	Depositor DCC
R_{free} test set	9013 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	60.9	Xtriage
Anisotropy	0.434	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 26.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	20373	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.26% 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	0.51	0/6862	0.71	0/9311
1	B	0.51	0/6850	0.72	0/9295
1	C	0.51	0/6857	0.72	0/9305
All	All	0.51	0/20569	0.72	0/27911

There are no bond length outliers.

There are no bond angle outliers.

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	6674	0	6485	14	0
1	B	6663	0	6476	15	0
1	C	6670	0	6485	14	0
2	A	132	0	0	0	0
2	B	131	0	0	0	0
2	C	103	0	0	0	0
All	All	20373	0	19446	43	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 1.

All (43) 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:C:642:THR:HG21	1:C:705:ARG:NH1	2.11	0.65
1:B:642:THR:HG21	1:B:705:ARG:NH1	2.11	0.64
1:A:642:THR:HG21	1:A:705:ARG:NH1	2.14	0.62
1:B:783:LEU:HD13	1:B:812:ALA:HB3	1.88	0.53
1:A:666:LEU:HD21	1:A:730:GLN:HE21	1.75	0.51
1:C:783:LEU:HD13	1:C:812:ALA:HB3	1.92	0.51
1:C:675:GLN:HE21	1:C:678:ASN:HD22	1.58	0.50
1:A:675:GLN:HE21	1:A:678:ASN:HD22	1.59	0.50
1:C:78:LYS:HD2	1:C:104:MET:HE3	1.93	0.50
1:A:666:LEU:HD23	1:A:751:ILE:HD12	1.94	0.49
1:A:648:GLY:HA2	1:A:677:VAL:HG21	1.94	0.49
1:C:259:MET:HE1	1:C:330:ARG:HG2	1.94	0.48
1:B:118:ILE:HD12	1:B:599:LEU:HD22	1.96	0.48
1:C:762:LEU:HD13	1:C:811:VAL:HG21	1.94	0.48
1:B:763:MET:SD	1:B:811:VAL:HG12	2.54	0.48
1:A:259:MET:HE2	1:A:330:ARG:HG2	1.96	0.48
1:C:118:ILE:HD12	1:C:599:LEU:HD22	1.95	0.47
1:B:648:GLY:HA2	1:B:677:VAL:HG21	1.95	0.47
1:A:591:GLN:HE22	1:A:682:LYS:HG2	1.81	0.46
1:C:118:ILE:HD12	1:C:599:LEU:CD2	2.45	0.46
1:B:284:TRP:CZ2	1:B:381:ALA:HB3	2.51	0.46
1:B:259:MET:HE2	1:B:330:ARG:HG2	1.97	0.45
1:C:666:LEU:HD21	1:C:730:GLN:HE21	1.82	0.45
1:B:577:ILE:HD12	1:B:577:ILE:N	2.32	0.45
1:B:666:LEU:HD21	1:B:730:GLN:HE21	1.83	0.44
1:B:118:ILE:HD12	1:B:599:LEU:CD2	2.48	0.43
1:C:782:THR:HA	1:C:811:VAL:HG22	2.01	0.43
1:B:636:PHE:CZ	1:B:737:LEU:HD11	2.53	0.43
1:C:284:TRP:CZ2	1:C:381:ALA:HB3	2.54	0.42
1:A:302:LEU:HD22	1:A:390:ALA:HB1	2.00	0.42
1:A:763:MET:SD	1:A:811:VAL:HG12	2.60	0.42
1:C:705:ARG:NH1	1:C:729:ASP:OD1	2.53	0.42
1:A:211:CYS:HB3	1:A:232:HIS:CE1	2.55	0.42
1:A:376:GLU:HG3	1:A:397:ARG:HB2	2.01	0.41
1:A:591:GLN:HE22	1:A:682:LYS:CG	2.33	0.41
1:B:645:THR:O	1:B:710:ARG:NH1	2.50	0.41
1:B:783:LEU:HD12	1:B:810:SER:HB3	2.02	0.41
1:C:804:GLN:HE21	1:C:804:GLN:HA	1.85	0.41
1:A:420:MET:HE2	1:A:420:MET:HA	2.02	0.41
1:B:420:MET:HA	1:B:420:MET:HE2	2.03	0.41
1:A:762:LEU:HD13	1:A:811:VAL:HG21	2.03	0.40
1:B:783:LEU:HD23	1:B:786:PHE:CE1	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:675:GLN:NE2	1:C:678:ASN:HD22	2.20	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	815/898 (91%)	795 (98%)	20 (2%)	0	100	100
1	B	814/898 (91%)	790 (97%)	23 (3%)	1 (0%)	48	68
1	C	815/898 (91%)	789 (97%)	25 (3%)	1 (0%)	48	68
All	All	2444/2694 (91%)	2374 (97%)	68 (3%)	2 (0%)	48	68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	839	ALA
1	B	561	GLY

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	729/795 (92%)	718 (98%)	11 (2%)	57	80
1	B	728/795 (92%)	723 (99%)	5 (1%)	76	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	729/795 (92%)	723 (99%)	6 (1%)	73	88
All	All	2186/2385 (92%)	2164 (99%)	22 (1%)	68	86

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	252	VAL
1	A	273	LEU
1	A	314	ILE
1	A	353	GLU
1	A	386	GLU
1	A	460	HIS
1	A	512	ILE
1	A	614	LYS
1	A	623	SER
1	A	690	ASN
1	A	718	PHE
1	B	242	VAL
1	B	314	ILE
1	B	353	GLU
1	B	718	PHE
1	B	811	VAL
1	C	48	LEU
1	C	314	ILE
1	C	487	LYS
1	C	614	LYS
1	C	718	PHE
1	C	804	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (51) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	123	ASN
1	A	181	GLN
1	A	195	GLN
1	A	199	GLN
1	A	232	HIS
1	A	254	ASN
1	A	274	GLN
1	A	338	ASN
1	A	403	GLN

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Mol	Chain	Res	Type
1	A	550	HIS
1	A	573	HIS
1	A	579	GLN
1	A	591	GLN
1	A	675	GLN
1	A	704	ASN
1	A	730	GLN
1	A	801	GLN
1	A	829	HIS
1	A	858	GLN
1	A	862	GLN
1	B	123	ASN
1	B	274	GLN
1	B	403	GLN
1	B	573	HIS
1	B	675	GLN
1	B	704	ASN
1	B	730	GLN
1	B	801	GLN
1	B	829	HIS
1	B	875	HIS
1	B	882	HIS
1	C	111	ASN
1	C	123	ASN
1	C	173	GLN
1	C	188	HIS
1	C	200	GLN
1	C	274	GLN
1	C	403	GLN
1	C	458	GLN
1	C	573	HIS
1	C	579	GLN
1	C	591	GLN
1	C	654	HIS
1	C	675	GLN
1	C	704	ASN
1	C	730	GLN
1	C	804	GLN
1	C	814	GLN
1	C	829	HIS
1	C	882	HIS
1	C	885	GLN

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	820/898 (91%)	0.42	44 (5%)	31	27	28, 58, 93, 133	1 (0%)
1	B	819/898 (91%)	0.50	40 (4%)	35	31	24, 60, 95, 142	1 (0%)
1	C	820/898 (91%)	0.63	55 (6%)	24	21	28, 62, 98, 146	1 (0%)
All	All	2459/2694 (91%)	0.52	139 (5%)	29	26	24, 60, 96, 146	3 (0%)

All (139) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	138	LEU	7.2
1	B	138	LEU	7.0
1	C	897	VAL	6.7
1	A	139	PHE	6.1
1	C	164	VAL	5.7
1	C	419	VAL	5.7
1	B	71	TYR	5.4
1	B	419	VAL	5.3
1	A	628	PRO	5.2
1	A	71	TYR	5.1
1	B	897	VAL	5.1
1	C	48	LEU	4.9
1	A	48	LEU	4.8
1	A	419	VAL	4.8
1	C	71	TYR	4.7
1	B	626	PRO	4.7
1	A	106	GLY	4.6
1	C	72	HIS	4.6
1	A	72	HIS	4.5
1	C	627	LEU	4.4
1	A	70	LYS	4.3
1	B	72	HIS	4.2
1	A	626	PRO	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	105	SER	3.9
1	C	129	MET	3.8
1	A	329[A]	PHE	3.8
1	A	627	LEU	3.8
1	C	628	PRO	3.7
1	B	461	GLU	3.6
1	A	108	ASN	3.6
1	C	420	MET	3.6
1	B	129	MET	3.5
1	B	420	MET	3.5
1	A	256	LEU	3.5
1	C	487	LYS	3.4
1	B	628	PRO	3.3
1	B	107	GLU	3.3
1	C	625	GLY	3.3
1	A	420	MET	3.3
1	A	320	MET	3.3
1	A	195	GLN	3.2
1	A	460	HIS	3.2
1	A	897	VAL	3.2
1	B	48	LEU	3.1
1	C	595	HIS	3.1
1	A	595	HIS	3.1
1	C	626	PRO	3.1
1	A	192	GLY	3.1
1	B	473	LYS	3.0
1	C	105	SER	3.0
1	A	624	ALA	3.0
1	C	659	GLY	3.0
1	B	487	LYS	3.0
1	C	106	GLY	2.9
1	A	110	GLU	2.9
1	A	257	ALA	2.9
1	C	610	THR	2.9
1	A	867	ILE	2.8
1	A	104	MET	2.8
1	B	490	LYS	2.8
1	C	494	SER	2.8
1	A	625	GLY	2.8
1	B	137	ASP	2.8
1	C	430	PRO	2.7
1	C	473	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	78	LYS	2.7
1	C	314	ILE	2.7
1	C	868	ARG	2.7
1	B	106	GLY	2.6
1	B	78	LYS	2.6
1	C	490	LYS	2.6
1	B	627	LEU	2.6
1	A	107	GLU	2.6
1	B	624	ALA	2.6
1	C	624	ALA	2.6
1	B	685	LYS	2.6
1	C	78	LYS	2.6
1	A	129	MET	2.5
1	A	498	LEU	2.5
1	B	70	LYS	2.5
1	C	256	LEU	2.5
1	B	244	ARG	2.5
1	B	110	GLU	2.4
1	C	382	GLY	2.4
1	C	70	LYS	2.4
1	B	195	GLN	2.4
1	C	460	HIS	2.4
1	B	91	PRO	2.4
1	A	292	THR	2.4
1	A	487	LYS	2.4
1	B	658	PRO	2.4
1	B	891	ARG	2.4
1	C	629	ASP	2.4
1	C	195	GLN	2.3
1	C	658	PRO	2.3
1	C	459	SER	2.3
1	A	138	LEU	2.3
1	C	426	ILE	2.3
1	C	491	TYR	2.3
1	B	256	LEU	2.3
1	B	786	PHE	2.3
1	C	107	GLU	2.3
1	A	659	GLY	2.3
1	A	866	SER	2.3
1	B	595	HIS	2.3
1	C	357	ILE	2.3
1	C	895	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	294	SER	2.2
1	B	629	ASP	2.2
1	B	261	GLU	2.2
1	C	740	ARG	2.2
1	A	173	GLN	2.2
1	A	165	GLY	2.2
1	C	257	ALA	2.2
1	B	105	SER	2.2
1	C	606	GLU	2.2
1	C	721	LYS	2.2
1	B	460	HIS	2.1
1	A	259	MET	2.1
1	C	320	MET	2.1
1	A	610	THR	2.1
1	A	473	LYS	2.1
1	A	658	PRO	2.1
1	C	293	PRO	2.1
1	C	108	ASN	2.1
1	C	69	ARG	2.1
1	C	261	GLU	2.1
1	B	505	LYS	2.1
1	A	293	PRO	2.1
1	C	504	PHE	2.1
1	C	643	GLY	2.1
1	B	417	ASP	2.1
1	B	320	MET	2.1
1	B	69	ARG	2.0
1	C	295	GLY	2.0
1	C	340	LYS	2.0
1	C	329[A]	PHE	2.0
1	C	891	ARG	2.0
1	B	610	THR	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.