



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:18 PM UTC

PDB ID : 4CNU / pdb_00004cnu
Title : CRYSTAL STRUCTURE OF WT HUMAN CRMP-4 from lattice translocation
Authors : Ponnusamy, R.; Lebedev, A.; Lohkamp, B.
Deposited on : 2014-01-24
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

<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

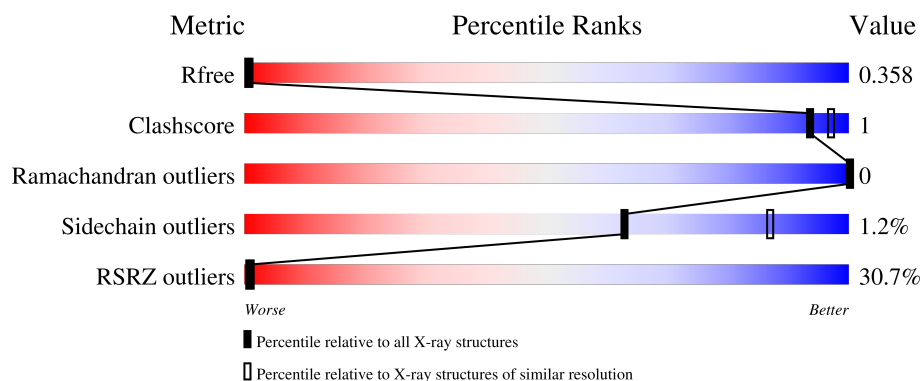
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (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 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	570	15% 82% 14%
1	B	570	38% 82% 14%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 7512 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 DIHYDROPYRIMIDINASE-LIKE 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	488	Total	C	N	O	S	0	0	0
			3756	2373	635	725	23			
1	B	488	Total	C	N	O	S	0	0	0
			3756	2373	635	725	23			

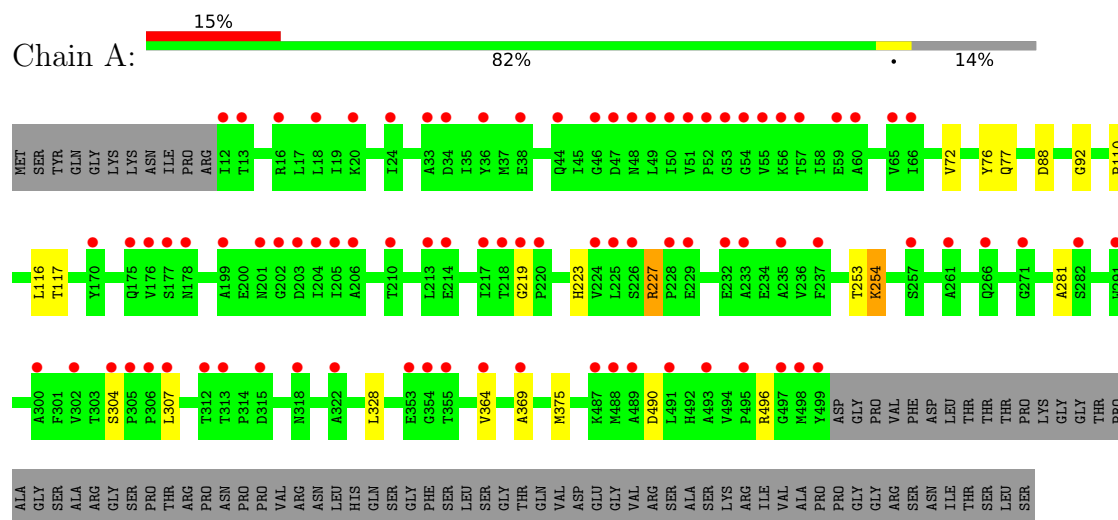
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	76	TYR	PHE	conflict	UNP Q14195
B	76	TYR	PHE	conflict	UNP Q14195

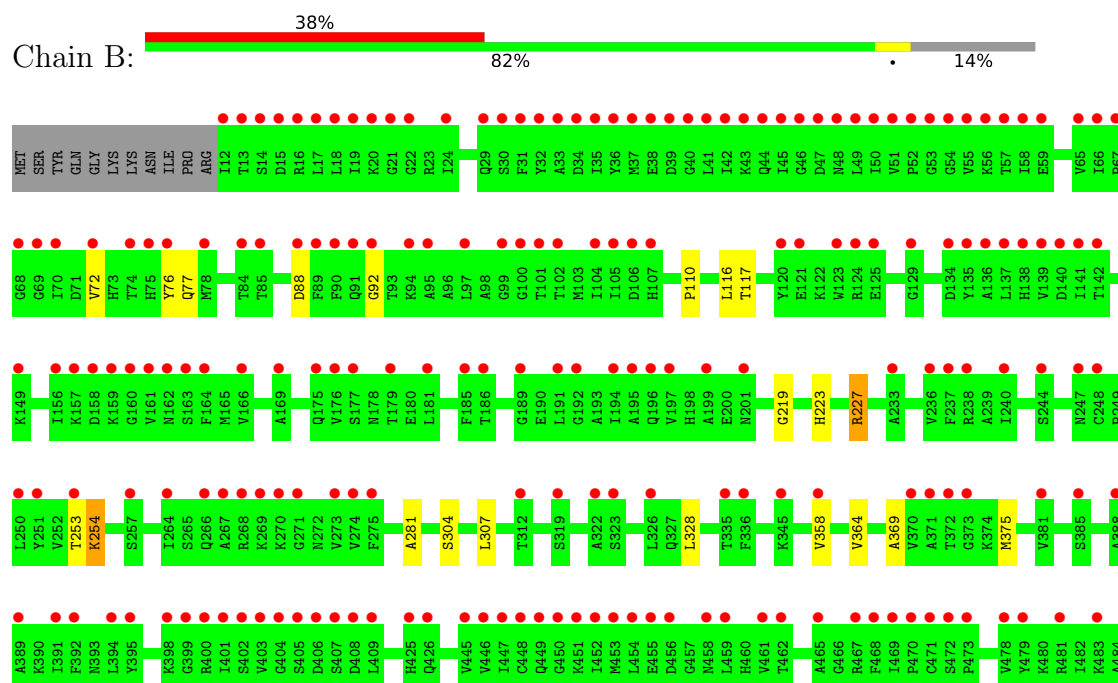
3 Residue-property plots [i](#)

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: DIHYDROPYRIMIDINASE-LIKE 3



• Molecule 1: DIHYDROPYRIMIDINASE-LIKE 3



VAL	ASP	GLU	GLY	VAL	ARG	SER	ALA	ALA	ASP	ASP	ASP	LEU	THR	THR	THR	THR	LYS	GLY	GLY	THR	PRO	PRO	GLY	THR	ALA	GLY	SER	GLY	ALA	ARG	GLY	SER	SER	PRO	PRO	PRO	VAL	ARG	ASN	LEU	HIS	GLN	SER	GLY	PHE	SER	SER	SER	GLY	THR					
R485	R486	R487	M488	M489	D490	L491	H492	A493	V494	R495	G497	M498	V499	ASP	GLY	PRO	VAL	PHE	SER	ASN	LEU	THR	THR	THR	LYS	GLY	GLY	THR	PRO	ALA	GLY	SER	GLY	ALA	ARG	GLY	SER	SER	PRO	PRO	PRO	VAL	ARG	ASN	LEU	HIS	GLN	SER	GLY	PHE	SER	SER	SER	GLY	THR

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	96.24Å 108.22Å 118.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.43 – 2.80 39.43 – 2.80	Depositor EDS
% Data completeness (in resolution range)	93.0 (39.43-2.80) 93.0 (39.43-2.80)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.74 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.255 , 0.295 0.322 , 0.358	Depositor DCC
R_{free} test set	1465 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	41.5	Xtriage
Anisotropy	0.570	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 20.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	7512	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 68.08 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.6339e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.45	0/3835	0.71	2/5201 (0.0%)
1	B	0.45	0/3835	0.71	2/5201 (0.0%)
All	All	0.45	0/7670	0.71	4/10402 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	219	GLY	CA-C-N	5.80	125.93	119.32
1	B	219	GLY	C-N-CA	5.80	125.93	119.32
1	A	219	GLY	CA-C-N	5.72	125.84	119.32
1	A	219	GLY	C-N-CA	5.72	125.84	119.32

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	3756	0	3700	10	0
1	B	3756	0	3700	11	0
All	All	7512	0	7400	21	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 (21) 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:76:TYR:CE1	1:B:92:GLY:HA3	2.43	0.53
1:A:76:TYR:CE1	1:A:92:GLY:HA3	2.43	0.53
1:A:223:HIS:O	1:A:227:ARG:HG3	2.11	0.51
1:A:253:THR:C	1:A:254:LYS:HG2	2.36	0.49
1:B:223:HIS:O	1:B:227:ARG:HG3	2.13	0.49
1:B:77:GLN:OE1	1:B:88:ASP:HB2	2.14	0.48
1:A:77:GLN:OE1	1:A:88:ASP:HB2	2.14	0.47
1:B:253:THR:C	1:B:254:LYS:HG2	2.39	0.47
1:B:110:PRO:HG3	1:B:116:LEU:HG	1.99	0.45
1:A:110:PRO:HG3	1:A:116:LEU:HG	1.99	0.45
1:B:281:ALA:HB1	1:B:307:LEU:HD11	1.98	0.45
1:A:281:ALA:HB1	1:A:307:LEU:HD11	1.99	0.44
1:A:72:VAL:HG11	1:A:328:LEU:HD12	2.02	0.42
1:B:369:ALA:CB	1:B:375:MET:HE3	2.50	0.42
1:A:369:ALA:CB	1:A:375:MET:HE3	2.50	0.42
1:B:72:VAL:HG11	1:B:328:LEU:HD12	2.02	0.41
1:A:490:ASP:O	1:A:490:ASP:CG	2.63	0.41
1:B:490:ASP:O	1:B:490:ASP:CG	2.63	0.41
1:A:254:LYS:CE	1:A:304:SER:O	2.68	0.41
1:B:76:TYR:OH	1:B:358:VAL:HG21	2.20	0.41
1:B:254:LYS:CE	1:B:304:SER:O	2.69	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	486/570 (85%)	461 (95%)	25 (5%)	0	100	100
1	B	486/570 (85%)	463 (95%)	23 (5%)	0	100	100
All	All	972/1140 (85%)	924 (95%)	48 (5%)	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	404/471 (86%)	399 (99%)	5 (1%)	63	87
1	B	404/471 (86%)	399 (99%)	5 (1%)	63	87
All	All	808/942 (86%)	798 (99%)	10 (1%)	63	87

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	117	THR
1	A	227	ARG
1	A	254	LYS
1	A	364	VAL
1	A	496	ARG
1	B	117	THR
1	B	227	ARG
1	B	254	LYS
1	B	364	VAL
1	B	496	ARG

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

Mol	Chain	Res	Type
1	A	29	GLN
1	A	196	GLN
1	A	460	HIS
1	B	29	GLN
1	B	460	HIS

5.3.3 RNA ⓘ

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	488/570 (85%)	0.98	86 (17%) 4 3	26, 42, 66, 108	0
1	B	488/570 (85%)	1.92	214 (43%) 0 0	25, 46, 75, 99	0
All	All	976/1140 (85%)	1.45	300 (30%) 1 1	25, 44, 72, 108	0

All (300) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	55	VAL	9.2
1	B	489	ALA	8.8
1	B	12	ILE	8.1
1	A	51	VAL	7.8
1	B	51	VAL	7.2
1	B	13	THR	6.8
1	B	492	HIS	6.4
1	A	12	ILE	6.1
1	B	50	ILE	6.1
1	A	49	LEU	6.0
1	A	50	ILE	5.7
1	B	452	ILE	5.7
1	B	488	MET	5.7
1	B	491	LEU	5.7
1	B	58	ILE	5.6
1	A	52	PRO	5.5
1	B	49	LEU	5.4
1	A	499	TYR	5.4
1	B	18	LEU	5.3
1	B	53	GLY	5.1
1	A	318	ASN	5.1
1	B	35	ILE	5.1
1	B	499	TYR	5.0
1	B	40	GLY	4.9

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Mol	Chain	Res	Type	RSRZ
1	B	52	PRO	4.9
1	B	39	ASP	4.9
1	B	44	GLN	4.8
1	B	57	THR	4.8
1	B	19	ILE	4.7
1	B	17	LEU	4.7
1	B	15	ASP	4.7
1	B	407	SER	4.7
1	B	54	GLY	4.6
1	B	92	GLY	4.5
1	B	14	SER	4.5
1	B	158	ASP	4.5
1	B	446	VAL	4.5
1	B	34	ASP	4.5
1	B	402	SER	4.5
1	B	373	GLY	4.4
1	A	175	GLN	4.4
1	B	16	ARG	4.3
1	B	247	ASN	4.3
1	B	37	MET	4.3
1	B	462	THR	4.2
1	B	461	VAL	4.2
1	B	36	TYR	4.2
1	B	43	LYS	4.2
1	B	398	LYS	4.2
1	A	54	GLY	4.2
1	A	55	VAL	4.2
1	A	48	ASN	4.1
1	B	487	LYS	4.0
1	B	22	GLY	4.0
1	B	56	LYS	4.0
1	A	205	ILE	3.9
1	B	409	LEU	3.9
1	B	192	GLY	3.9
1	B	456	ASP	3.9
1	A	364	VAL	3.9
1	A	204	ILE	3.9
1	A	489	ALA	3.9
1	B	490	ASP	3.9
1	B	176	VAL	3.9
1	B	20	LYS	3.8
1	B	45	ILE	3.8

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Mol	Chain	Res	Type	RSRZ
1	B	38	GLU	3.8
1	B	389	ALA	3.8
1	B	494	VAL	3.7
1	B	105	ILE	3.7
1	B	459	LEU	3.7
1	B	157	LYS	3.7
1	B	448	CYS	3.7
1	B	486	ARG	3.7
1	B	335	THR	3.7
1	B	72	VAL	3.7
1	B	196	GLN	3.7
1	B	426	GLN	3.7
1	B	467	ARG	3.7
1	B	399	GLY	3.6
1	B	162	ASN	3.6
1	B	267	ALA	3.6
1	B	90	PHE	3.6
1	B	273	VAL	3.6
1	A	57	THR	3.6
1	B	406	ASP	3.6
1	B	470	PRO	3.6
1	B	163	SER	3.5
1	B	455	GLU	3.5
1	B	141	ILE	3.5
1	B	408	ASP	3.5
1	B	189	GLY	3.5
1	A	300	ALA	3.5
1	A	322	ALA	3.5
1	B	177	SER	3.5
1	A	312	THR	3.5
1	B	195	ALA	3.5
1	B	401	ILE	3.4
1	B	139	VAL	3.4
1	B	372	THR	3.4
1	A	495	PRO	3.4
1	B	405	SER	3.4
1	B	138	HIS	3.4
1	B	275	PHE	3.4
1	B	450	GLY	3.4
1	A	232	GLU	3.4
1	A	210	THR	3.4
1	B	42	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	91	GLN	3.3
1	B	137	LEU	3.3
1	B	394	LEU	3.3
1	B	495	PRO	3.3
1	A	18	LEU	3.3
1	B	97	LEU	3.3
1	B	99	GLY	3.3
1	B	468	PHE	3.3
1	B	47	ASP	3.2
1	B	447	ILE	3.2
1	B	449	GLN	3.2
1	B	74	THR	3.2
1	B	24	ILE	3.2
1	B	469	ILE	3.2
1	B	199	ALA	3.2
1	B	479	TYR	3.2
1	B	175	GLN	3.2
1	A	213	LEU	3.2
1	B	451	LYS	3.2
1	B	66	ILE	3.2
1	B	67	PRO	3.2
1	B	41	LEU	3.1
1	B	445	VAL	3.1
1	B	102	THR	3.1
1	B	404	GLY	3.1
1	B	371	ALA	3.1
1	A	315	ASP	3.1
1	B	233	ALA	3.1
1	B	76	TYR	3.1
1	B	395	TYR	3.1
1	B	381	VAL	3.1
1	A	226	SER	3.1
1	B	48	ASN	3.1
1	B	493	ALA	3.0
1	B	472	SER	3.0
1	A	224	VAL	3.0
1	B	164	PHE	3.0
1	B	33	ALA	3.0
1	A	498	MET	3.0
1	B	185	PHE	3.0
1	B	32	TYR	3.0
1	B	88	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	201	ASN	3.0
1	B	471	CYS	3.0
1	A	491	LEU	3.0
1	B	21	GLY	3.0
1	B	191	LEU	2.9
1	B	473	PRO	2.9
1	B	160	GLY	2.9
1	A	44	GLN	2.9
1	A	60	ALA	2.9
1	B	70	ILE	2.9
1	A	53	GLY	2.9
1	A	16	ARG	2.9
1	B	124	ARG	2.9
1	B	483	LYS	2.9
1	A	13	THR	2.9
1	B	100	GLY	2.8
1	A	217	ILE	2.8
1	B	156	ILE	2.8
1	B	65	VAL	2.8
1	B	197	VAL	2.8
1	B	274	VAL	2.8
1	A	59	GLU	2.8
1	B	385	SER	2.8
1	A	488	MET	2.8
1	B	498	MET	2.8
1	B	478	VAL	2.8
1	B	136	ALA	2.8
1	B	94	LYS	2.8
1	A	266	GLN	2.7
1	B	95	ALA	2.7
1	A	34	ASP	2.7
1	B	140	ASP	2.7
1	B	125	GLU	2.7
1	B	194	ILE	2.7
1	A	46	GLY	2.7
1	A	304	SER	2.7
1	A	235	ALA	2.7
1	B	169	ALA	2.7
1	B	391	ILE	2.7
1	A	219	GLY	2.7
1	A	203	ASP	2.7
1	B	266	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	177	SER	2.7
1	A	257	SER	2.7
1	B	244	SER	2.7
1	B	69	GLY	2.6
1	A	218	THR	2.6
1	A	20	LYS	2.6
1	B	134	ASP	2.6
1	B	30	SER	2.6
1	B	120	TYR	2.6
1	B	129	GLY	2.6
1	B	85	THR	2.6
1	B	159	LYS	2.6
1	B	29	GLN	2.6
1	A	307	LEU	2.6
1	B	166	VAL	2.6
1	B	186	THR	2.6
1	A	33	ALA	2.6
1	B	135	TYR	2.6
1	B	270	LYS	2.6
1	A	302	VAL	2.6
1	A	313	THR	2.6
1	B	161	VAL	2.6
1	A	38	GLU	2.6
1	B	322	ALA	2.6
1	B	107	HIS	2.5
1	B	454	LEU	2.5
1	A	66	ILE	2.5
1	B	78	MET	2.5
1	B	370	VAL	2.5
1	B	59	GLU	2.5
1	B	248	CYS	2.5
1	B	485	ARG	2.5
1	A	36	TYR	2.5
1	B	181	LEU	2.5
1	B	257	SER	2.5
1	A	199	ALA	2.5
1	A	225	LEU	2.4
1	B	89	PHE	2.4
1	B	253	THR	2.4
1	B	458	ASN	2.4
1	A	65	VAL	2.4
1	A	497	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	214	GLU	2.4
1	B	123	TRP	2.4
1	B	465	ALA	2.4
1	B	326	LEU	2.4
1	B	104	ILE	2.4
1	B	46	GLY	2.4
1	A	206	ALA	2.4
1	B	323	SER	2.4
1	A	56	LYS	2.3
1	B	271	GLY	2.3
1	A	47	ASP	2.3
1	B	142	THR	2.3
1	A	220	PRO	2.3
1	A	354	GLY	2.3
1	B	336	PHE	2.3
1	B	388	ALA	2.3
1	A	305	PRO	2.3
1	A	282	SER	2.3
1	B	236	VAL	2.3
1	B	68	GLY	2.3
1	B	250	LEU	2.3
1	A	291	TRP	2.3
1	B	75	HIS	2.2
1	B	481	ARG	2.2
1	B	101	THR	2.2
1	A	271	GLY	2.2
1	A	487	LYS	2.2
1	B	240	ILE	2.2
1	A	170	TYR	2.2
1	B	392	PHE	2.2
1	A	261	ALA	2.2
1	A	353	GLU	2.2
1	A	178	ASN	2.2
1	B	496	ARG	2.2
1	A	306	PRO	2.2
1	B	179	THR	2.2
1	B	453	MET	2.2
1	B	149	LYS	2.2
1	B	425	HIS	2.1
1	A	176	VAL	2.1
1	B	345	LYS	2.1
1	B	237	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	233	ALA	2.1
1	B	319	SER	2.1
1	B	403	VAL	2.1
1	A	369	ALA	2.1
1	B	238	ARG	2.1
1	A	237	PHE	2.1
1	A	355	THR	2.1
1	B	31	PHE	2.1
1	B	84	THR	2.1
1	B	251	TYR	2.1
1	B	358	VAL	2.1
1	A	228	PRO	2.1
1	A	201	ASN	2.1
1	B	106	ASP	2.1
1	A	24	ILE	2.1
1	B	264	ILE	2.1
1	A	229	GLU	2.1
1	B	269	LYS	2.0
1	B	400	ARG	2.0
1	A	493	ALA	2.0
1	B	268	ARG	2.0
1	A	202	GLY	2.0
1	B	312	THR	2.0
1	B	121	GLU	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.