



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:55 AM UTC

PDB ID : 2CDR / pdb_00002cdr
Title : Crystal structures of caspase-3 in complex with aza-peptide epoxide inhibitors.
Authors : Ganesan, R.; Jelakovic, S.; Campbell, A.J.; Li, Z.Z.; Asgian, J.L.; Powers, J.C.; Gruetter, M.G.
Deposited on : 2006-01-27
Resolution : 1.70 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

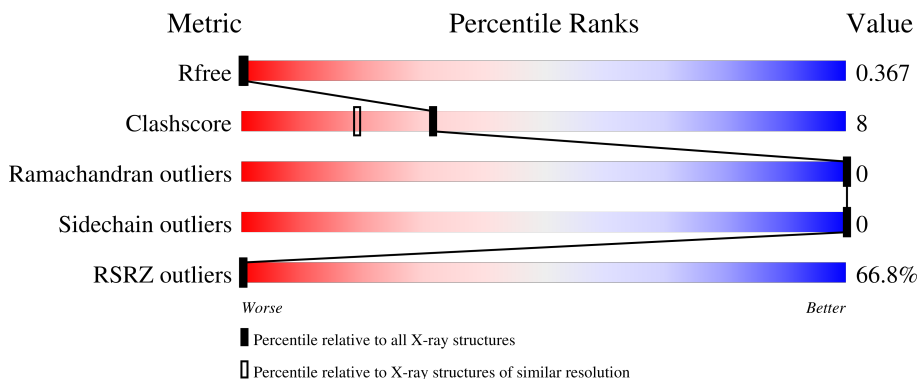
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	147	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">61%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 61%, orange 61%, yellow 84%, green 84%, grey 100%);"></div> <div style="text-align: right;">84% 16%</div> </div>
2	B	103	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">75%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 75%, orange 75%, yellow 76%, green 76%, grey 100%);"></div> <div style="text-align: right;">76% 24%</div> </div>
3	I	5	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">60%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 60%, orange 60%, yellow 80%, green 80%, grey 100%);"></div> <div style="text-align: right;">80% 20%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2429 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 CASPASE-3 SUBUNIT P17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	147	1161	716	208	228	9	0	0	0

- Molecule 2 is a protein called CASPASE-3 SUBUNIT P12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	103	843	547	135	154	7	0	0	0

- Molecule 3 is a protein called AZA-PEPTIDE EXPOXIDE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	I	5	62	42	6	14	0	0	0

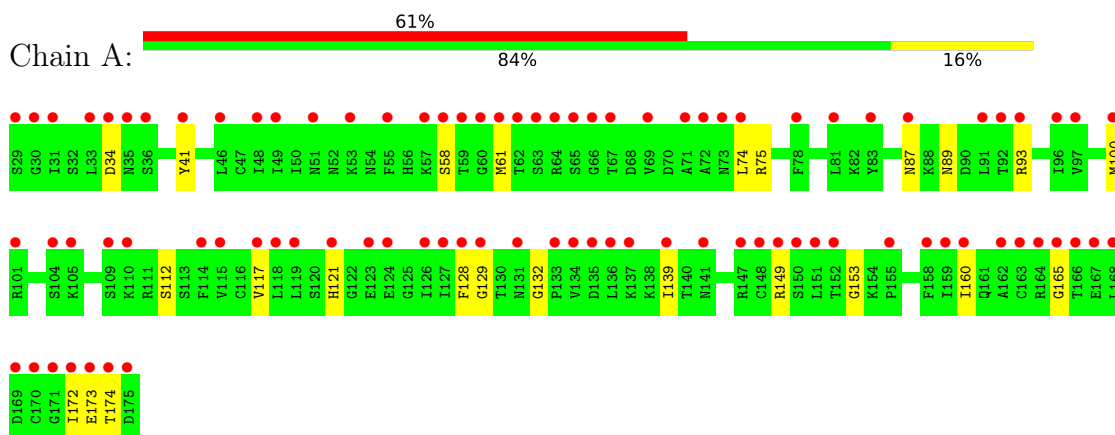
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	231	Total 231	O 231	0	0
4	B	126	Total 126	O 126	0	0
4	I	6	Total 6	O 6	0	0

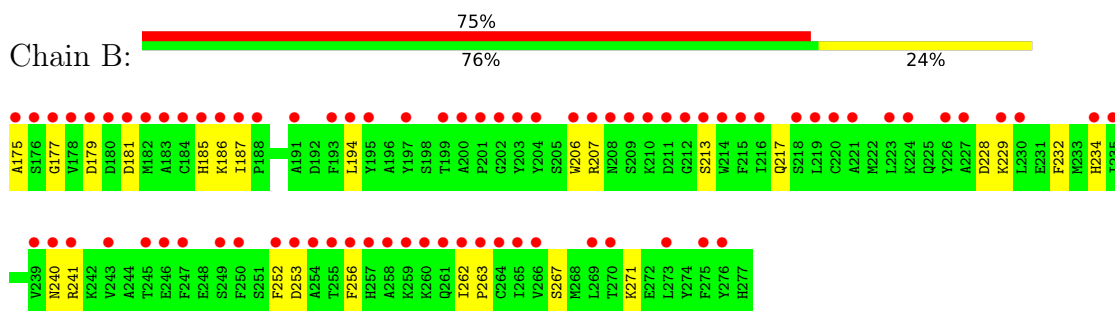
3 Residue-property plots [i](#)

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.

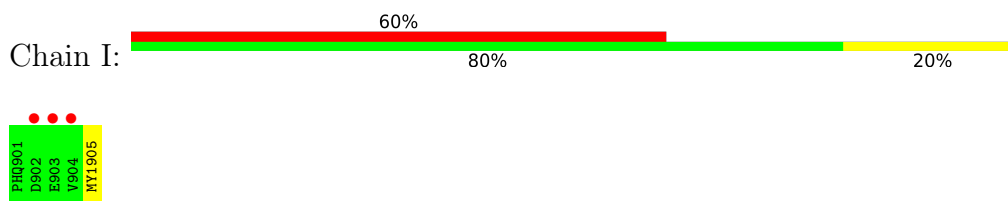
- Molecule 1: CASPASE-3 SUBUNIT P17



- Molecule 2: CASPASE-3 SUBUNIT P12



- Molecule 3: AZA-PEPTIDE EXPOXIDE



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	67.47Å 83.78Å 96.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.49 – 1.70 19.49 – 1.70	Depositor EDS
% Data completeness (in resolution range)	97.9 (19.49-1.70) 95.5 (19.49-1.70)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.37 (at 1.70Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.177 , 0.204 0.368 , 0.367	Depositor DCC
R_{free} test set	2876 reflections (9.97%)	wwPDB-VP
Wilson B-factor (Å ²)	17.8	Xtrriage
Anisotropy	0.655	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 60.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.82	EDS
Total number of atoms	2429	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.48% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PHQ, MY1

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	0.32	0/1176	0.87	6/1574 (0.4%)
2	B	0.34	0/868	0.91	3/1171 (0.3%)
3	I	0.19	0/23	0.62	0/30
All	All	0.33	0/2067	0.88	9/2775 (0.3%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	129	GLY	N-CA-C	-7.06	101.23	112.66
1	A	160	ILE	N-CA-C	7.05	118.48	107.28
1	A	121	HIS	N-CA-C	-6.18	102.21	110.55
1	A	128	PHE	N-CA-C	5.61	118.39	109.24
2	B	267	SER	N-CA-C	5.54	117.99	109.07
1	A	132	GLY	CA-C-N	5.42	125.33	119.85
1	A	132	GLY	C-N-CA	5.42	125.33	119.85
2	B	179	ASP	N-CA-C	5.19	119.15	112.41
2	B	232	PHE	N-CA-C	5.11	117.25	111.11

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	1161	0	1152	19	12
2	B	843	0	807	15	15
3	I	62	0	43	3	0
4	A	231	0	0	8	6
4	B	126	0	0	7	4
4	I	6	0	0	0	0
All	All	2429	0	2002	33	21

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 (33) 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:A:174:THR:OG1	4:A:2221:HOH:O	1.60	1.15
2:B:185:HIS:O	4:B:2044:HOH:O	1.77	1.01
1:A:61:MET:HG2	3:I:905:MY1:H20	1.48	0.92
2:B:185:HIS:HB2	4:B:2044:HOH:O	1.88	0.74
1:A:87:ASN:HB2	4:A:2121:HOH:O	1.89	0.71
2:B:241:ARG:NH1	4:B:2096:HOH:O	2.19	0.70
2:B:252:PHE:HB2	4:B:2110:HOH:O	1.90	0.70
2:B:175:ALA:N	4:B:2028:HOH:O	2.27	0.67
2:B:228:ASP:OD1	2:B:229:LYS:HG3	1.97	0.64
1:A:100:MET:HG3	1:A:139:ILE:HG23	1.84	0.59
2:B:177:GLY:HA3	4:B:2035:HOH:O	2.04	0.58
1:A:74:LEU:HD13	1:A:117:VAL:HG11	1.87	0.57
1:A:153:GLY:HA3	4:A:2196:HOH:O	2.07	0.54
1:A:149:ARG:HH11	1:A:149:ARG:HA	1.74	0.53
1:A:165:GLY:HA2	3:I:905:MY1:H27	1.94	0.50
2:B:240:ASN:OD1	2:B:263:PRO:HB2	2.12	0.50
1:A:93:ARG:NH1	4:A:2131:HOH:O	2.45	0.50
2:B:206:TRP:HH2	2:B:256:PHE:HB3	1.76	0.50
2:B:213:SER:O	2:B:217:GLN:HG3	2.12	0.49
2:B:207:ARG:HA	2:B:213:SER:HA	1.96	0.47
1:A:34:ASP:OD1	2:B:271:LYS:HE2	2.15	0.46
1:A:89:ASN:O	4:A:2124:HOH:O	2.20	0.46
2:B:262:ILE:HG23	2:B:262:ILE:O	2.15	0.46
1:A:75:ARG:HD2	4:A:2121:HOH:O	2.16	0.45
1:A:149:ARG:NH1	1:A:149:ARG:HB3	2.32	0.45
1:A:149:ARG:HH11	1:A:149:ARG:CA	2.31	0.43
1:A:89:ASN:HB3	4:A:2038:HOH:O	2.18	0.43
1:A:153:GLY:CA	4:A:2196:HOH:O	2.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:LEU:CD1	1:A:117:VAL:HG11	2.48	0.42
1:A:41:TYR:HB2	1:A:112:SER:OG	2.21	0.41
1:A:61:MET:SD	3:I:905:MY1:H19	2.60	0.41
2:B:185:HIS:C	4:B:2044:HOH:O	2.47	0.41
2:B:194:LEU:C	2:B:194:LEU:HD23	2.47	0.40

All (21) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:58:SER:OG	2:B:253:ASP:OD2[2_665]	1.16	1.04
1:A:173:GLU:OE2	2:B:186:LYS:CG[3_656]	1.49	0.71
1:A:173:GLU:OE2	2:B:186:LYS:CD[3_656]	1.53	0.67
1:A:172:ILE:N	2:B:187:ILE:O[3_656]	1.59	0.61
2:B:234:HIS:CE1	2:B:234:HIS:CE1[3_656]	1.74	0.46
1:A:172:ILE:O	2:B:187:ILE:N[3_656]	1.75	0.45
1:A:173:GLU:CD	2:B:186:LYS:CG[3_656]	1.76	0.44
2:B:234:HIS:NE2	2:B:234:HIS:NE2[3_656]	1.78	0.42
4:A:2126:HOH:O	4:B:2043:HOH:O[6_554]	1.79	0.41
4:A:2063:HOH:O	4:B:2060:HOH:O[2_665]	1.85	0.35
1:A:58:SER:OG	2:B:253:ASP:CG[2_665]	1.86	0.34
1:A:174:THR:CG2	2:B:187:ILE:CG2[3_656]	1.87	0.33
1:A:89:ASN:N	2:B:181:ASP:OD2[6_554]	1.90	0.30
4:A:2085:HOH:O	4:A:2085:HOH:O[3_656]	1.91	0.29
1:A:173:GLU:OE1	2:B:185:HIS:O[3_656]	2.00	0.20
4:A:2156:HOH:O	4:A:2156:HOH:O[3_656]	2.06	0.14
1:A:87:ASN:ND2	2:B:181:ASP:O[6_554]	2.09	0.11
4:A:2079:HOH:O	4:B:2045:HOH:O[6_554]	2.09	0.11
2:B:234:HIS:CE1	2:B:234:HIS:NE2[3_656]	2.13	0.07
1:A:173:GLU:OE1	2:B:186:LYS:CG[3_656]	2.14	0.06
4:A:2059:HOH:O	4:B:2107:HOH:O[2_665]	2.17	0.03

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	145/147 (99%)	140 (97%)	5 (3%)	0	100	100
2	B	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
3	I	2/5 (40%)	2 (100%)	0	0	100	100
All	All	248/255 (97%)	242 (98%)	6 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	132/132 (100%)	132 (100%)	0	100	100
2	B	90/90 (100%)	90 (100%)	0	100	100
3	I	3/3 (100%)	3 (100%)	0	100	100
All	All	225/225 (100%)	225 (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. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	80	ASN

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	147/147 (100%)	2.41	89 (60%) 0 0	12, 18, 29, 56	0
2	B	103/103 (100%)	2.80	77 (74%) 0 0	11, 15, 28, 34	0
3	I	3/5 (60%)	3.76	3 (100%) 0 0	23, 23, 26, 31	0
All	All	253/255 (99%)	2.58	169 (66%) 0 0	11, 17, 29, 56	0

All (169) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	168	LEU	7.2
2	B	204	TYR	6.7
1	A	174	THR	6.7
2	B	180	ASP	6.1
1	A	172	ILE	5.8
1	A	173	GLU	5.6
2	B	256	PHE	5.5
2	B	177	GLY	5.5
2	B	210	LYS	5.5
1	A	61	MET	5.3
3	I	904	VAL	5.1
2	B	206	TRP	5.0
1	A	175	ASP	4.9
1	A	128	PHE	4.8
2	B	253	ASP	4.7
2	B	176	SER	4.7
2	B	262	ILE	4.7
2	B	255	THR	4.6
1	A	170	CYS	4.6
2	B	201	PRO	4.6
2	B	175	ALA	4.5
1	A	169	ASP	4.5
1	A	58	SER	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	34	ASP	4.4
2	B	250	PHE	4.3
2	B	252	PHE	4.3
1	A	171	GLY	4.1
2	B	203	TYR	4.1
1	A	123	GLU	4.0
2	B	200	ALA	4.0
2	B	183	ALA	4.0
2	B	185	HIS	3.9
1	A	62	THR	3.8
1	A	30	GLY	3.7
1	A	139	ILE	3.7
2	B	247	PHE	3.7
2	B	265	ILE	3.7
1	A	29	SER	3.6
2	B	215	PHE	3.6
1	A	134	VAL	3.6
1	A	165	GLY	3.6
2	B	258	ALA	3.6
1	A	163	CYS	3.6
2	B	246	GLU	3.5
1	A	33	LEU	3.5
2	B	184	CYS	3.5
1	A	155	PRO	3.5
1	A	127	ILE	3.5
2	B	276	TYR	3.5
2	B	230	LEU	3.5
1	A	162	ALA	3.4
3	I	903	GLU	3.4
1	A	126	ILE	3.4
2	B	214	TRP	3.4
2	B	209	SER	3.4
2	B	195	TYR	3.3
1	A	65	SER	3.3
1	A	72	ALA	3.3
1	A	97	VAL	3.3
1	A	71	ALA	3.2
2	B	227	ALA	3.2
2	B	254	ALA	3.2
2	B	241	ARG	3.2
1	A	55	PHE	3.2
2	B	208	ASN	3.2

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Mol	Chain	Res	Type	RSRZ
2	B	261	GLN	3.2
1	A	31	ILE	3.1
2	B	273	LEU	3.1
1	A	60	GLY	3.1
1	A	63	SER	3.1
2	B	259	LYS	3.1
1	A	67	THR	3.1
2	B	239	VAL	3.0
1	A	114	PHE	3.0
1	A	135	ASP	3.0
1	A	69	VAL	3.0
2	B	226	TYR	3.0
1	A	136	LEU	3.0
2	B	235	ILE	3.0
1	A	53	LYS	2.9
2	B	249	SER	2.9
2	B	212	GLY	2.9
2	B	181	ASP	2.9
2	B	234	HIS	2.9
2	B	243	VAL	2.9
1	A	152	THR	2.8
2	B	270	THR	2.8
1	A	167	GLU	2.8
1	A	118	LEU	2.8
2	B	219	LEU	2.8
2	B	263	PRO	2.8
2	B	199	THR	2.8
2	B	221	ALA	2.8
1	A	129	GLY	2.8
1	A	115	VAL	2.8
2	B	223	LEU	2.8
3	I	902	ASP	2.8
2	B	264	CYS	2.7
1	A	59	THR	2.7
1	A	93	ARG	2.7
1	A	105	LYS	2.7
1	A	101	ARG	2.6
2	B	207	ARG	2.6
1	A	36	SER	2.6
1	A	147	ARG	2.6
2	B	191	ALA	2.6
2	B	240	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
2	B	257	HIS	2.6
1	A	104	SER	2.6
2	B	188	PRO	2.6
1	A	64	ARG	2.6
1	A	110	LYS	2.5
1	A	119	LEU	2.5
1	A	124	GLU	2.5
2	B	187	ILE	2.5
1	A	166	THR	2.5
2	B	245	THR	2.5
2	B	213	SER	2.5
2	B	266	VAL	2.5
1	A	159	ILE	2.5
1	A	66	GLY	2.5
2	B	186	LYS	2.5
1	A	164	ARG	2.5
1	A	73	ASN	2.5
2	B	179	ASP	2.5
1	A	96	ILE	2.5
1	A	160	ILE	2.5
1	A	150	SER	2.5
1	A	87	ASN	2.4
1	A	151	LEU	2.4
2	B	202	GLY	2.4
2	B	182	MET	2.4
2	B	197	TYR	2.4
1	A	57	LYS	2.4
2	B	178	VAL	2.4
1	A	121	HIS	2.4
1	A	46	LEU	2.3
1	A	74	LEU	2.3
1	A	148	CYS	2.3
1	A	133	PRO	2.3
1	A	81	LEU	2.3
2	B	269	LEU	2.3
2	B	275	PHE	2.3
1	A	83	TYR	2.3
2	B	229	LYS	2.3
1	A	41	TYR	2.2
1	A	35	ASN	2.2
2	B	218	SER	2.2
2	B	220	CYS	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	216	ILE	2.2
2	B	224	LYS	2.2
1	A	78	PHE	2.2
1	A	158	PHE	2.2
1	A	137	LYS	2.2
1	A	92	THR	2.2
1	A	100	MET	2.1
1	A	91	LEU	2.1
1	A	51	ASN	2.1
1	A	131	ASN	2.1
2	B	211	ASP	2.1
1	A	49	ILE	2.1
1	A	117	VAL	2.1
1	A	48	ILE	2.1
1	A	141	ASN	2.0
2	B	194	LEU	2.0
2	B	260	LYS	2.0
1	A	149	ARG	2.0
2	B	193	PHE	2.0
1	A	109	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.