



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:36 PM UTC

PDB ID : 8UGC / pdb_00008ugc
Title : FD15: Flat repeat helix-turn-helix-turn protein
Authors : Davila-Hernandez, F.; Bera, A.K.; Kang, A.; Baker, D.
Deposited on : 2023-10-05
Resolution : 4.00 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
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

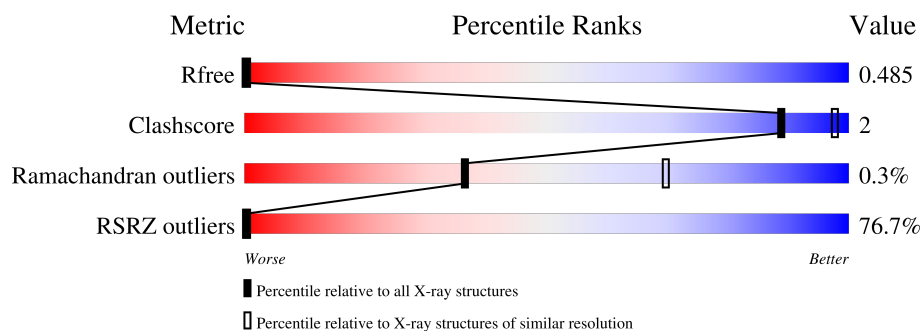
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.00 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	1082 (4.20-3.80)
Clashscore	190562	1129 (4.20-3.80)
Ramachandran outliers	187476	1064 (4.20-3.80)
RSRZ outliers	180081	1082 (4.20-3.80)

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	393	75% 94%
1	B	393	75% 95%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3816 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.

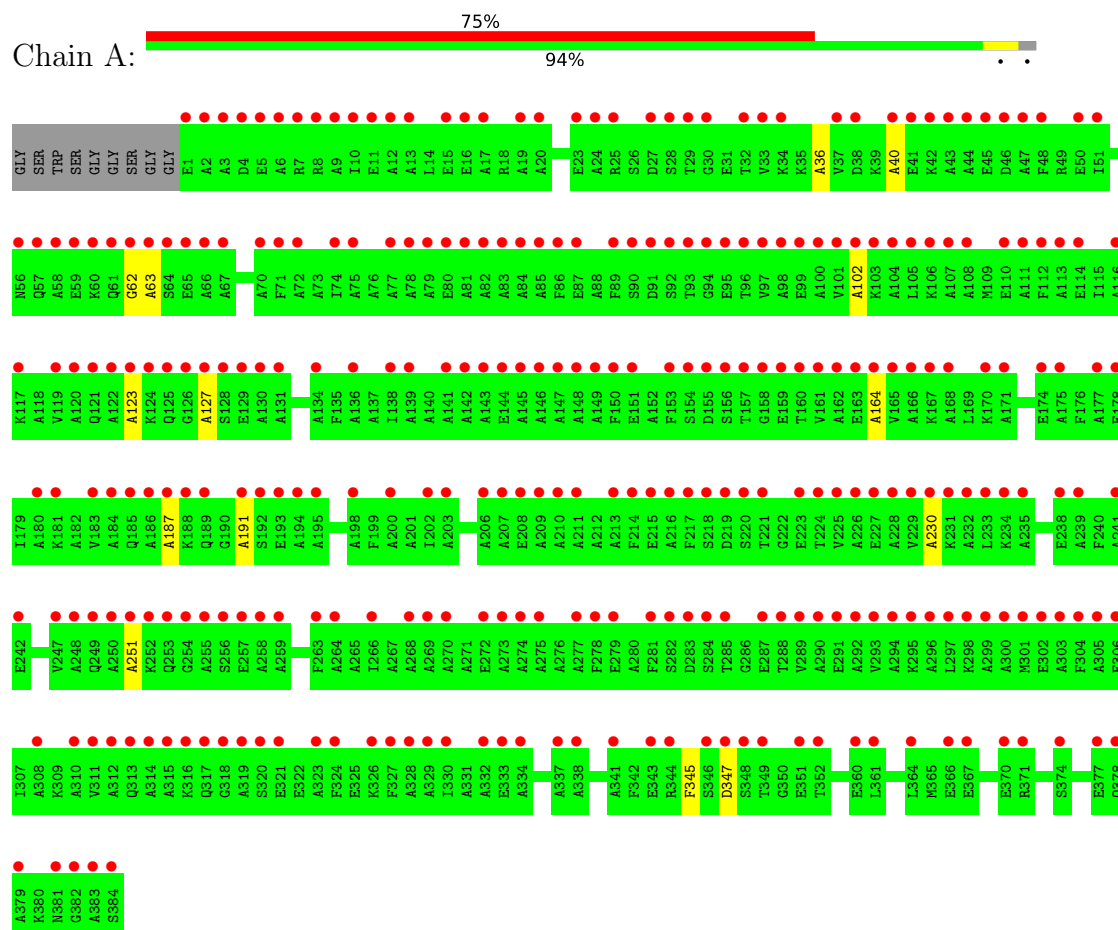
- Molecule 1 is a protein called FD15.

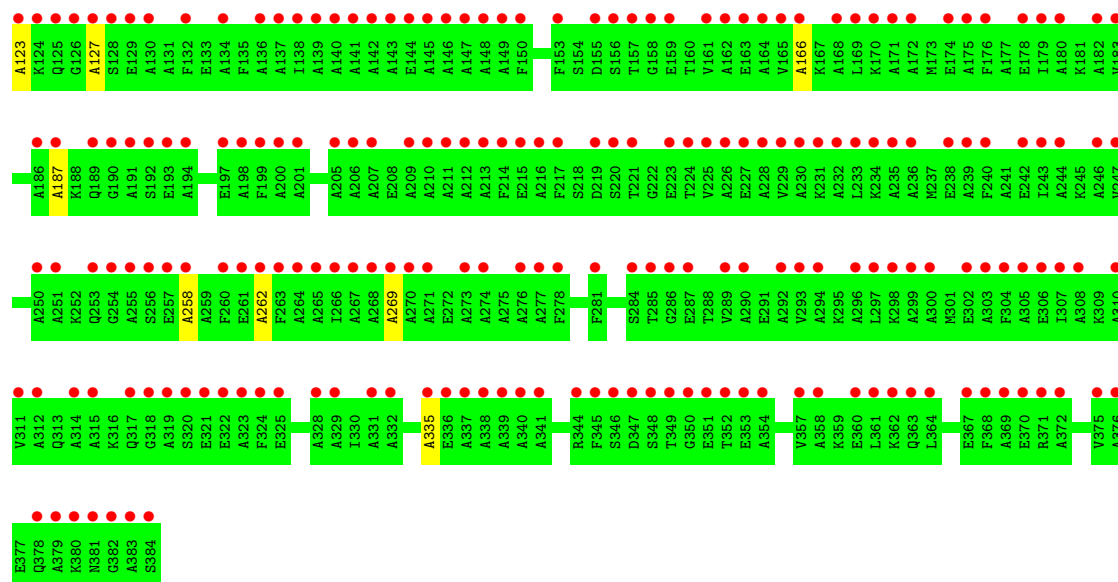
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	384	Total	C	N	O	0	0	0
			1908	1140	384	384			
1	B	384	Total	C	N	O	0	0	0
			1908	1140	384	384			

3 Residue-property plots

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: FD15





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.67Å 122.78Å 90.00Å 90.00° 97.61° 90.00°	Depositor
Resolution (Å)	89.20 – 4.00 89.20 – 4.00	Depositor EDS
% Data completeness (in resolution range)	93.2 (89.20-4.00) 97.6 (89.20-4.00)	Depositor EDS
R_{merge}	0.45	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.54 (at 4.01Å)	Xtriage
Refinement program	PHENIX dev_4761, PHENIX dev_4761	Depositor
R, R_{free}	0.465 , 0.492 0.467 , 0.485	Depositor DCC
R_{free} test set	560 reflections (4.64%)	wwPDB-VP
Wilson B-factor (Å ²)	108.0	Xtriage
Anisotropy	0.801	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 288.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.74	EDS
Total number of atoms	3816	wwPDB-VP
Average B, all atoms (Å ²)	103.0	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 28.01 % 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 1.9872e-03. 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

5.1 Standard geometry

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	0.10	0/1907	0.27	0/2661
1	B	0.09	0/1907	0.24	0/2661
All	All	0.10	0/3814	0.26	0/5322

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

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	1908	0	1256	7	0
1	B	1908	0	1256	5	0
All	All	3816	0	2512	12	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 2.

All (12) 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:63:ALA:HB2	1:B:123:ALA:HB1	1.76	0.68
1:A:63:ALA:HB2	1:A:123:ALA:HB1	1.78	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:ALA:HB2	1:A:187:ALA:HB1	1.77	0.66
1:B:127:ALA:HB2	1:B:187:ALA:HB1	1.87	0.55
1:A:40:ALA:HB2	1:A:102:ALA:HA	1.96	0.47
1:A:191:ALA:HB2	1:A:251:ALA:HB1	1.97	0.46
1:B:269:ALA:HB1	1:B:335:ALA:HB2	2.00	0.43
1:B:258:ALA:O	1:B:262:ALA:N	2.50	0.42
1:B:100:ALA:HB1	1:B:166:ALA:HB2	2.01	0.42
1:A:164:ALA:HB1	1:A:230:ALA:HB2	2.01	0.42
1:A:36:ALA:HB1	1:A:102:ALA:HB2	2.01	0.41
1:A:345:PHE:C	1:A:347:ASP:H	2.29	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	382/393 (97%)	366 (96%)	15 (4%)	1 (0%)	36	70
1	B	382/393 (97%)	371 (97%)	10 (3%)	1 (0%)	36	70
All	All	764/786 (97%)	737 (96%)	25 (3%)	2 (0%)	36	70

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	62	GLY
1	B	93	THR

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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	384/393 (97%)	3.11	296 (77%) 0 0	56, 104, 136, 153	0
1	B	384/393 (97%)	3.11	293 (76%) 0 0	55, 103, 135, 177	0
All	All	768/786 (97%)	3.11	589 (76%) 0 0	55, 103, 137, 177	0

All (589) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	348	SER	11.8
1	A	383	ALA	11.7
1	B	384	SER	11.3
1	A	16	GLU	10.2
1	A	1	GLU	10.0
1	B	59	GLU	9.6
1	A	63	ALA	8.9
1	A	28	SER	8.8
1	A	59	GLU	8.6
1	A	44	ALA	8.4
1	B	315	ALA	8.4
1	A	92	SER	8.2
1	A	284	SER	8.0
1	B	123	ALA	8.0
1	B	251	ALA	7.8
1	B	55	VAL	7.8
1	B	187	ALA	7.6
1	B	348	SER	7.5
1	B	353	GLU	7.4
1	B	186	ALA	7.0
1	A	220	SER	7.0
1	A	314	ALA	6.9
1	A	156	SER	6.9
1	B	61	GLN	6.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	378	GLN	6.8
1	A	384	SER	6.8
1	B	368	PHE	6.6
1	A	187	ALA	6.5
1	B	58	ALA	6.4
1	A	79	ALA	6.3
1	A	41	GLU	6.3
1	A	206	ALA	6.2
1	B	247	VAL	6.2
1	B	18	ARG	6.2
1	A	186	ALA	6.2
1	A	334	ALA	6.2
1	B	220	SER	6.1
1	B	379	ALA	6.0
1	B	92	SER	6.0
1	A	319	ALA	6.0
1	B	308	ALA	6.0
1	B	284	SER	6.0
1	B	192	SER	6.0
1	B	229	VAL	6.0
1	B	62	GLY	5.9
1	A	3	ALA	5.9
1	A	80	GLU	5.9
1	B	10	ILE	5.9
1	B	311	VAL	5.9
1	B	361	LEU	5.9
1	A	145	ALA	5.8
1	B	318	GLY	5.7
1	A	175	ALA	5.7
1	B	17	ALA	5.7
1	B	25	ARG	5.7
1	B	294	ALA	5.6
1	A	251	ALA	5.6
1	A	249	GLN	5.6
1	B	14	LEU	5.6
1	A	123	ALA	5.5
1	A	337	ALA	5.5
1	A	185	GLN	5.5
1	B	254	GLY	5.5
1	A	330	ILE	5.5
1	B	142	ALA	5.4
1	B	122	ALA	5.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	6	ALA	5.4
1	B	250	ALA	5.4
1	B	166	ALA	5.3
1	B	232	ALA	5.3
1	A	47	ALA	5.3
1	A	323	ALA	5.3
1	B	190	GLY	5.3
1	B	314	ALA	5.3
1	A	270	ALA	5.2
1	B	156	SER	5.2
1	A	146	ALA	5.2
1	B	293	VAL	5.2
1	B	383	ALA	5.1
1	B	256	SER	5.1
1	A	209	ALA	5.1
1	A	142	ALA	5.0
1	B	372	ALA	5.0
1	A	11	GLU	5.0
1	B	317	GLN	5.0
1	B	210	ALA	5.0
1	B	82	ALA	4.9
1	B	104	ALA	4.9
1	B	322	GLU	4.9
1	B	369	ALA	4.9
1	B	255	ALA	4.9
1	B	357	VAL	4.9
1	B	253	GLN	4.9
1	A	46	ASP	4.8
1	B	206	ALA	4.8
1	A	29	THR	4.8
1	A	210	ALA	4.8
1	A	315	ALA	4.8
1	B	146	ALA	4.8
1	A	347	ASP	4.7
1	B	119	VAL	4.7
1	B	64	SER	4.7
1	B	26	SER	4.7
1	B	153	PHE	4.7
1	B	183	VAL	4.7
1	A	256	SER	4.7
1	B	3	ALA	4.7
1	A	238	GLU	4.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	22	ASP	4.6
1	B	228	ALA	4.6
1	A	382	GLY	4.6
1	B	126	GLY	4.6
1	A	61	GLN	4.5
1	B	230	ALA	4.5
1	B	277	ALA	4.5
1	B	65	GLU	4.5
1	A	250	ALA	4.5
1	A	290	ALA	4.5
1	B	213	ALA	4.5
1	B	165	VAL	4.5
1	A	341	ALA	4.5
1	A	351	GLU	4.5
1	A	162	ALA	4.5
1	B	376	ALA	4.5
1	B	125	GLN	4.5
1	A	252	LYS	4.4
1	B	307	ILE	4.4
1	A	58	ALA	4.4
1	A	98	ALA	4.4
1	A	27	ASP	4.4
1	A	81	ALA	4.3
1	A	122	ALA	4.3
1	B	162	ALA	4.3
1	A	154	SER	4.3
1	A	62	GLY	4.3
1	A	157	THR	4.3
1	A	45	GLU	4.3
1	B	23	GLU	4.3
1	A	127	ALA	4.3
1	B	332	ALA	4.3
1	B	155	ASP	4.3
1	B	168	ALA	4.3
1	B	320	SER	4.3
1	B	235	ALA	4.3
1	A	50	GLU	4.3
1	B	91	ASP	4.3
1	B	200	ALA	4.3
1	B	78	ALA	4.3
1	B	290	ALA	4.3
1	B	328	ALA	4.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	304	PHE	4.2
1	A	64	SER	4.2
1	B	349	THR	4.2
1	A	302	GLU	4.2
1	B	129	GLU	4.2
1	B	225	VAL	4.2
1	B	274	ALA	4.2
1	A	110	GLU	4.1
1	B	296	ALA	4.1
1	A	273	ALA	4.1
1	A	320	SER	4.1
1	A	96	THR	4.1
1	A	318	GLY	4.1
1	B	15	GLU	4.1
1	B	143	ALA	4.1
1	A	147	ALA	4.1
1	B	341	ALA	4.1
1	A	374	SER	4.1
1	B	30	GLY	4.1
1	B	38	ASP	4.0
1	B	145	ALA	4.0
1	A	57	GLN	4.0
1	B	257	GLU	4.0
1	A	224	THR	4.0
1	A	214	PHE	4.0
1	A	51	ILE	4.0
1	A	7	ARG	4.0
1	B	381	ASN	4.0
1	B	128	SER	4.0
1	B	35	LYS	4.0
1	B	243	ILE	4.0
1	A	19	ALA	4.0
1	B	85	ALA	4.0
1	B	303	ALA	3.9
1	B	31	GLU	3.9
1	A	170	LYS	3.9
1	A	255	ALA	3.9
1	B	264	ALA	3.9
1	A	30	GLY	3.9
1	B	19	ALA	3.9
1	A	327	PHE	3.9
1	A	15	GLU	3.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	192	SER	3.9
1	B	7	ARG	3.9
1	A	366	GLU	3.9
1	B	149	ALA	3.8
1	B	378	GLN	3.8
1	A	278	PHE	3.8
1	B	98	ALA	3.8
1	B	338	ALA	3.8
1	A	160	THR	3.8
1	A	313	GLN	3.8
1	A	296	ALA	3.8
1	B	306	GLU	3.8
1	A	219	ASP	3.8
1	A	24	ALA	3.8
1	A	332	ALA	3.8
1	A	213	ALA	3.8
1	B	299	ALA	3.8
1	A	234	LYS	3.8
1	A	228	ALA	3.8
1	A	379	ALA	3.8
1	B	81	ALA	3.7
1	B	89	PHE	3.7
1	A	283	ASP	3.7
1	A	275	ALA	3.7
1	A	294	ALA	3.7
1	B	244	ALA	3.7
1	B	217	PHE	3.7
1	A	257	GLU	3.7
1	A	274	ALA	3.7
1	A	48	PHE	3.7
1	A	107	ALA	3.7
1	B	101	VAL	3.6
1	A	114	GLU	3.6
1	B	209	ALA	3.6
1	A	211	ALA	3.6
1	A	277	ALA	3.6
1	A	338	ALA	3.6
1	B	226	ALA	3.6
1	B	189	GLN	3.6
1	A	125	GLN	3.6
1	B	380	LYS	3.6
1	A	166	ALA	3.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	299	ALA	3.6
1	A	97	VAL	3.6
1	B	300	ALA	3.6
1	A	178	GLU	3.6
1	A	84	ALA	3.5
1	A	65	GLU	3.5
1	B	370	GLU	3.5
1	A	300	ALA	3.5
1	B	346	SER	3.5
1	A	121	GLN	3.5
1	A	4	ASP	3.5
1	A	129	GLU	3.5
1	B	86	PHE	3.5
1	A	191	ALA	3.5
1	B	28	SER	3.5
1	B	263	PHE	3.5
1	B	281	PHE	3.5
1	B	193	GLU	3.5
1	A	128	SER	3.5
1	A	317	GLN	3.5
1	B	21	ALA	3.5
1	A	370	GLU	3.5
1	B	11	GLU	3.5
1	B	351	GLU	3.5
1	B	221	THR	3.5
1	A	100	ALA	3.5
1	A	113	ALA	3.5
1	A	131	ALA	3.5
1	B	201	ALA	3.5
1	B	242	GLU	3.4
1	A	235	ALA	3.4
1	B	191	ALA	3.4
1	B	344	ARG	3.4
1	B	375	VAL	3.4
1	A	38	ASP	3.4
1	A	174	GLU	3.4
1	B	100	ALA	3.4
1	B	324	PHE	3.4
1	A	67	ALA	3.4
1	B	27	ASP	3.4
1	B	67	ALA	3.4
1	A	25	ARG	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	258	ALA	3.4
1	B	319	ALA	3.4
1	A	143	ALA	3.3
1	A	83	ALA	3.3
1	B	223	GLU	3.3
1	A	148	ALA	3.3
1	A	377	GLU	3.3
1	B	287	GLU	3.3
1	A	149	ALA	3.3
1	A	226	ALA	3.3
1	A	263	PHE	3.3
1	A	8	ARG	3.3
1	A	183	VAL	3.3
1	B	233	LEU	3.3
1	A	106	LYS	3.3
1	A	239	ALA	3.3
1	B	302	GLU	3.3
1	A	139	ALA	3.3
1	B	169	LEU	3.3
1	B	219	ASP	3.3
1	A	20	ALA	3.2
1	A	195	ALA	3.2
1	B	24	ALA	3.2
1	B	236	ALA	3.2
1	A	12	ALA	3.2
1	A	102	ALA	3.2
1	B	273	ALA	3.2
1	B	321	GLU	3.2
1	B	179	ILE	3.2
1	B	297	LEU	3.2
1	A	37	VAL	3.2
1	B	41	GLU	3.2
1	B	239	ALA	3.2
1	A	60	LYS	3.2
1	A	364	LEU	3.2
1	A	293	VAL	3.2
1	A	93	THR	3.2
1	A	282	SER	3.2
1	B	207	ALA	3.2
1	A	253	GLN	3.2
1	A	177	ALA	3.2
1	A	70	ALA	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	230	ALA	3.1
1	B	84	ALA	3.1
1	B	1	GLU	3.1
1	B	174	GLU	3.1
1	A	89	PHE	3.1
1	B	289	VAL	3.1
1	A	184	ALA	3.1
1	A	161	VAL	3.1
1	A	371	ARG	3.1
1	A	242	GLU	3.1
1	A	218	SER	3.1
1	A	232	ALA	3.1
1	B	20	ALA	3.1
1	A	136	ALA	3.1
1	B	214	PHE	3.1
1	B	325	GLU	3.1
1	B	350	GLY	3.0
1	B	363	GLN	3.0
1	A	297	LEU	3.0
1	A	223	GLU	3.0
1	A	272	GLU	3.0
1	A	291	GLU	3.0
1	B	360	GLU	3.0
1	A	99	GLU	3.0
1	A	333	GLU	3.0
1	B	367	GLU	3.0
1	A	82	ALA	3.0
1	A	295	LYS	3.0
1	A	326	LYS	3.0
1	B	170	LYS	3.0
1	A	9	ALA	3.0
1	B	83	ALA	3.0
1	B	175	ALA	3.0
1	B	352	THR	3.0
1	A	23	GLU	3.0
1	B	137	ALA	3.0
1	A	13	ALA	3.0
1	B	240	PHE	3.0
1	B	331	ALA	3.0
1	A	101	VAL	3.0
1	A	138	ILE	3.0
1	A	361	LEU	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	34	LYS	3.0
1	B	227	GLU	2.9
1	A	231	LYS	2.9
1	B	4	ASP	2.9
1	B	150	PHE	2.9
1	B	347	ASP	2.9
1	A	164	ALA	2.9
1	A	225	VAL	2.9
1	A	248	ALA	2.9
1	B	371	ARG	2.9
1	A	287	GLU	2.9
1	A	316	LYS	2.9
1	B	234	LYS	2.9
1	A	94	GLY	2.9
1	A	202	ILE	2.9
1	A	259	ALA	2.9
1	B	171	ALA	2.9
1	A	227	GLU	2.9
1	A	367	GLU	2.9
1	A	269	ALA	2.9
1	A	221	THR	2.9
1	A	208	GLU	2.9
1	B	110	GLU	2.9
1	A	266	ILE	2.9
1	A	85	ALA	2.9
1	A	200	ALA	2.9
1	A	141	ALA	2.8
1	A	215	GLU	2.8
1	B	364	LEU	2.8
1	A	72	ALA	2.8
1	B	216	ALA	2.8
1	B	246	ALA	2.8
1	A	346	SER	2.8
1	A	155	ASP	2.8
1	B	382	GLY	2.8
1	B	66	ALA	2.8
1	B	75	ALA	2.8
1	B	87	GLU	2.8
1	A	111	ALA	2.8
1	B	271	ALA	2.8
1	B	292	ALA	2.8
1	A	163	GLU	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	207	ALA	2.8
1	B	111	ALA	2.8
1	A	381	ASN	2.7
1	B	136	ALA	2.7
1	B	194	ALA	2.7
1	A	229	VAL	2.7
1	B	105	LEU	2.7
1	A	78	ALA	2.7
1	A	153	PHE	2.7
1	B	260	PHE	2.7
1	A	56	ASN	2.7
1	A	120	ALA	2.7
1	A	264	ALA	2.7
1	A	268	ALA	2.7
1	A	87	GLU	2.7
1	A	349	THR	2.7
1	B	157	THR	2.7
1	A	217	PHE	2.7
1	A	10	ILE	2.7
1	A	103	LYS	2.7
1	A	104	ALA	2.7
1	B	102	ALA	2.7
1	B	267	ALA	2.7
1	A	66	ALA	2.6
1	B	262	ALA	2.6
1	B	72	ALA	2.6
1	B	182	ALA	2.6
1	A	279	GLU	2.6
1	A	304	PHE	2.6
1	B	286	GLY	2.6
1	A	90	SER	2.6
1	B	212	ALA	2.6
1	B	337	ALA	2.6
1	A	189	GLN	2.6
1	A	321	GLU	2.6
1	B	298	LYS	2.6
1	A	134	ALA	2.6
1	A	310	ALA	2.6
1	B	37	VAL	2.6
1	B	358	ALA	2.6
1	B	261	GLU	2.6
1	B	312	ALA	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	34	LYS	2.6
1	B	270	ALA	2.6
1	B	335	ALA	2.6
1	A	43	ALA	2.5
1	A	308	ALA	2.5
1	B	178	GLU	2.5
1	B	238	GLU	2.5
1	A	194	ALA	2.5
1	B	127	ALA	2.5
1	B	198	ALA	2.5
1	A	167	LYS	2.5
1	A	188	LYS	2.5
1	B	224	THR	2.5
1	B	90	SER	2.5
1	A	203	ALA	2.5
1	B	147	ALA	2.5
1	A	151	GLU	2.5
1	A	165	VAL	2.5
1	B	340	ALA	2.5
1	B	141	ALA	2.5
1	B	345	PHE	2.5
1	B	73	ALA	2.5
1	B	134	ALA	2.5
1	A	281	PHE	2.5
1	A	116	ALA	2.5
1	A	130	ALA	2.5
1	A	171	ALA	2.5
1	A	292	ALA	2.5
1	A	298	LYS	2.4
1	B	106	LYS	2.4
1	A	2	ALA	2.4
1	A	40	ALA	2.4
1	B	323	ALA	2.4
1	A	112	PHE	2.4
1	A	344	ARG	2.4
1	A	126	GLY	2.4
1	A	328	ALA	2.4
1	B	354	ALA	2.4
1	B	158	GLY	2.4
1	B	305	ALA	2.4
1	A	144	GLU	2.4
1	A	352	THR	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	75	ALA	2.4
1	A	77	ALA	2.4
1	B	79	ALA	2.4
1	B	107	ALA	2.4
1	B	265	ALA	2.4
1	B	310	ALA	2.4
1	A	159	GLU	2.4
1	A	193	GLU	2.4
1	B	57	GLN	2.4
1	B	112	PHE	2.4
1	B	60	LYS	2.4
1	A	306	GLU	2.3
1	B	70	ALA	2.3
1	B	77	ALA	2.3
1	B	172	ALA	2.3
1	A	181	LYS	2.3
1	B	180	ALA	2.3
1	B	32	THR	2.3
1	B	164	ALA	2.3
1	A	74	ILE	2.3
1	A	198	ALA	2.3
1	A	258	ALA	2.3
1	B	44	ALA	2.3
1	A	289	VAL	2.3
1	B	43	ALA	2.3
1	B	88	ALA	2.3
1	A	311	VAL	2.3
1	B	80	GLU	2.3
1	B	144	GLU	2.3
1	A	285	THR	2.3
1	B	197	GLU	2.3
1	B	336	GLU	2.3
1	B	115	ILE	2.3
1	B	116	ALA	2.3
1	B	139	ALA	2.3
1	A	247	VAL	2.2
1	A	303	ALA	2.2
1	A	343	GLU	2.2
1	A	42	LYS	2.2
1	A	168	ALA	2.2
1	B	40	ALA	2.2
1	B	42	LYS	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	231	LYS	2.2
1	A	119	VAL	2.2
1	A	288	THR	2.2
1	B	33	VAL	2.2
1	B	148	ALA	2.2
1	B	269	ALA	2.2
1	A	86	PHE	2.2
1	A	150	PHE	2.2
1	B	95	GLU	2.2
1	B	159	GLU	2.2
1	B	132	PHE	2.2
1	A	91	ASP	2.2
1	B	176	PHE	2.2
1	A	233	LEU	2.2
1	B	16	GLU	2.2
1	B	215	GLU	2.2
1	A	216	ALA	2.1
1	B	362	LYS	2.1
1	B	113	ALA	2.1
1	B	74	ILE	2.1
1	A	32	THR	2.1
1	B	121	GLN	2.1
1	A	180	ALA	2.1
1	A	312	ALA	2.1
1	A	360	GLU	2.1
1	B	268	ALA	2.1
1	B	48	PHE	2.1
1	B	140	ALA	2.1
1	B	211	ALA	2.1
1	B	329	ALA	2.1
1	A	33	VAL	2.1
1	B	161	VAL	2.1
1	B	276	ALA	2.1
1	B	278	PHE	2.1
1	A	158	GLY	2.1
1	A	254	GLY	2.1
1	B	63	ALA	2.1
1	B	205	ALA	2.1
1	A	95	GLU	2.1
1	B	163	GLU	2.1
1	B	46	ASP	2.1
1	A	117	LYS	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	17	ALA	2.1
1	A	108	ALA	2.1
1	A	241	ALA	2.1
1	B	266	ILE	2.1
1	A	5	GLU	2.1
1	A	301	MET	2.0
1	A	71	PHE	2.0
1	B	130	ALA	2.0
1	B	285	THR	2.0
1	A	105	LEU	2.0
1	A	329	ALA	2.0
1	B	339	ALA	2.0
1	B	138	ILE	2.0
1	A	305	ALA	2.0
1	B	118	ALA	2.0
1	A	124	LYS	2.0
1	B	124	LYS	2.0
1	A	324	PHE	2.0
1	B	199	PHE	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.