



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:58 AM UTC

PDB ID : 1FHU / pdb_00001fhu
Title : CRYSTAL STRUCTURE ANALYSIS OF O-SUCCINYLBENZOATE SYNTHASE FROM E. COLI
Authors : Rayment, I.; Thompson, T.B.; Gerlt, J.A.
Deposited on : 2000-08-02
Resolution : 1.65 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

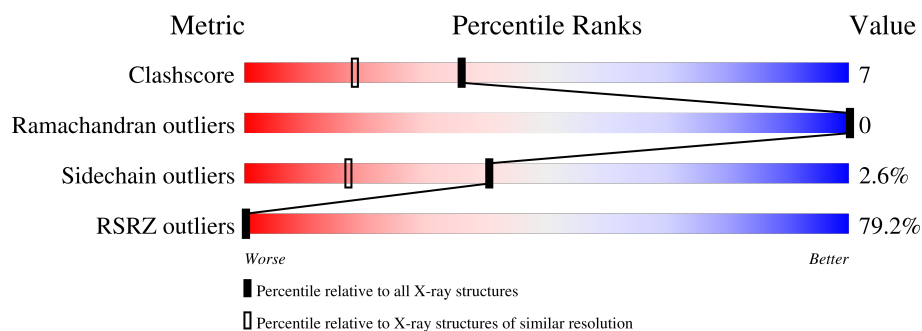
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)
RSRZ outliers	180081	2564 (1.66-1.66)

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	320	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2632 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 O-SUCCINYLBENZOATE SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	298	Total	C	N	O	S	0	0	0
			2281	1447	394	430	10			

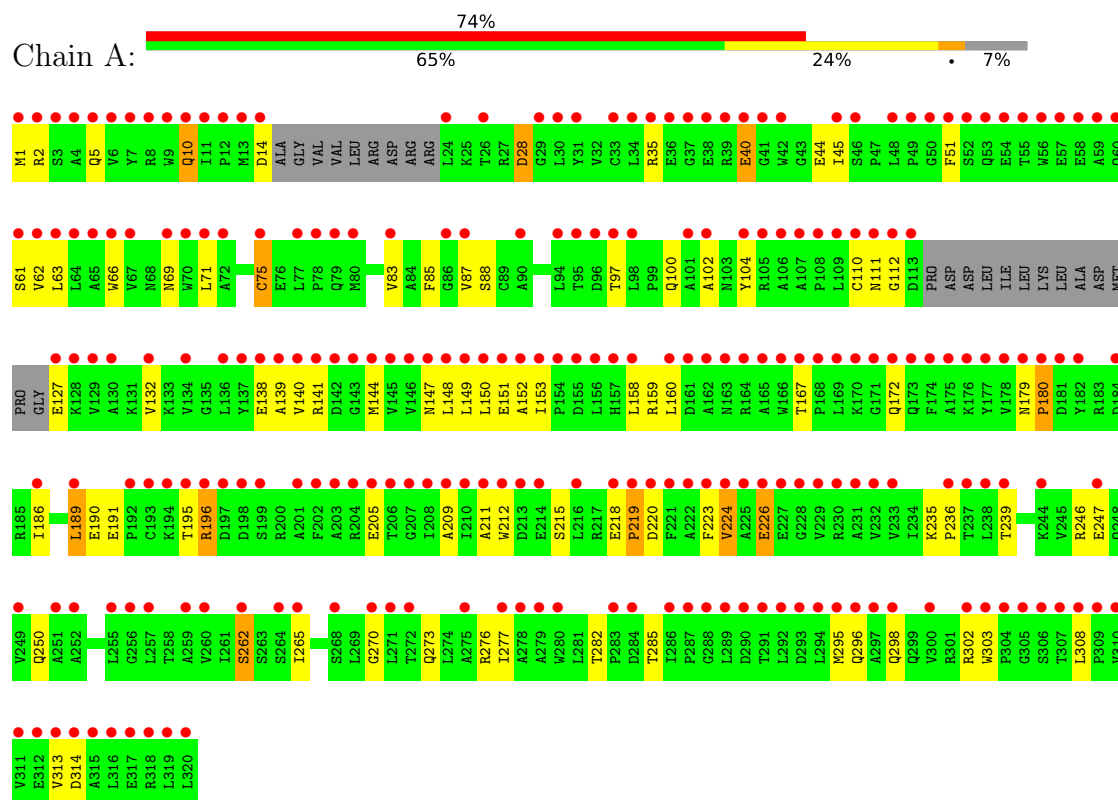
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	351	Total	O	0	0
			351	351		

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: O-SUCCINYLBENZOATE SYNTHASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	56.10Å 70.00Å 80.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 1.65 30.00 – 1.65	Depositor EDS
% Data completeness (in resolution range)	99.0 (30.00-1.65) 98.6 (30.00-1.65)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.03 (at 1.52Å)	Xtriage
Refinement program	TNT	Depositor
R, R_{free}	0.195 , 0.265 0.378 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	12.8	Xtriage
Anisotropy	0.654	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 151.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.80	EDS
Total number of atoms	2632	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.74% 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

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	1.87	34/2328 (1.5%)	1.79	33/3175 (1.0%)

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	191	GLU	CA-CB	10.06	1.61	1.52
1	A	149	LEU	CA-C	-7.03	1.44	1.52
1	A	63	LEU	CA-C	6.64	1.61	1.52
1	A	69	ASN	C-N	6.44	1.42	1.34
1	A	189	LEU	CA-C	6.37	1.60	1.52
1	A	285	THR	CA-C	-6.33	1.45	1.52
1	A	2	ARG	N-CA	6.33	1.53	1.46
1	A	273	GLN	N-CA	-6.23	1.38	1.46
1	A	270	GLY	CA-C	6.22	1.59	1.52
1	A	83	VAL	CA-CB	6.15	1.62	1.54
1	A	45	ILE	CA-C	-6.01	1.46	1.52
1	A	239	THR	N-CA	-5.96	1.39	1.46
1	A	295	MET	CA-C	-5.80	1.45	1.52
1	A	61	SER	CA-C	-5.75	1.45	1.52
1	A	88	SER	CA-C	5.69	1.60	1.52
1	A	276	ARG	N-CA	-5.69	1.39	1.46
1	A	211	ALA	CA-C	5.67	1.59	1.52
1	A	247	GLU	CA-C	5.65	1.60	1.52
1	A	172	GLN	N-CA	5.61	1.53	1.46
1	A	150	LEU	C-N	-5.60	1.25	1.33
1	A	66	TRP	CA-CB	5.58	1.62	1.53
1	A	139	ALA	CA-C	5.49	1.60	1.52
1	A	167	THR	CA-C	5.47	1.59	1.52
1	A	44	GLU	C-N	5.36	1.41	1.33
1	A	141	ARG	NE-CZ	5.33	1.39	1.33
1	A	97	THR	CB-OG1	-5.28	1.35	1.43
1	A	236	PRO	N-CD	5.24	1.55	1.47
1	A	28	ASP	CA-C	-5.18	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	226	GLU	CA-C	-5.18	1.46	1.52
1	A	191	GLU	CA-C	-5.16	1.49	1.53
1	A	158	LEU	CA-C	5.12	1.58	1.52
1	A	223	PHE	C-N	-5.11	1.26	1.33
1	A	112	GLY	CA-C	5.06	1.59	1.51
1	A	62	VAL	N-CA	-5.04	1.40	1.46

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	196	ARG	CD-NE-CZ	9.98	138.37	124.40
1	A	196	ARG	NE-CZ-NH1	8.72	130.22	121.50
1	A	191	GLU	N-CA-CB	-7.54	103.30	111.66
1	A	219	PRO	CA-C-N	-6.88	112.90	125.02
1	A	219	PRO	C-N-CA	-6.88	112.90	125.02
1	A	262	SER	N-CA-CB	-6.76	99.06	111.37
1	A	40	GLU	CB-CG-CD	-6.72	101.18	112.60
1	A	282	THR	O-C-N	6.66	127.36	121.17
1	A	191	GLU	CB-CA-C	-6.27	106.75	111.20
1	A	296	GLN	N-CA-C	6.15	120.86	113.23
1	A	51	PHE	CA-CB-CG	-5.93	107.87	113.80
1	A	314	ASP	N-CA-CB	5.74	119.22	110.14
1	A	277	ILE	O-C-N	5.68	127.68	121.83
1	A	303	TRP	N-CA-C	-5.56	100.59	109.04
1	A	85	PHE	CA-CB-CG	-5.55	108.25	113.80
1	A	313	VAL	O-C-N	5.52	127.46	121.94
1	A	87	VAL	N-CA-C	5.51	116.24	110.62
1	A	159	ARG	N-CA-C	-5.50	100.22	109.07
1	A	180	PRO	N-CA-CB	5.49	109.45	103.30
1	A	314	ASP	CB-CA-C	5.48	121.09	110.46
1	A	186	ILE	N-CA-C	-5.48	99.19	107.73
1	A	190	GLU	O-C-N	5.37	129.33	123.04
1	A	138	GLU	CB-CG-CD	5.34	121.68	112.60
1	A	209	ALA	CA-C-N	-5.31	115.39	122.77
1	A	209	ALA	C-N-CA	-5.31	115.39	122.77
1	A	191	GLU	CA-C-O	5.27	124.47	120.26
1	A	172	GLN	CA-CB-CG	-5.24	103.63	114.10
1	A	247	GLU	CB-CG-CD	-5.03	104.04	112.60
1	A	75	CYS	CA-CB-SG	-5.03	102.83	114.40
1	A	10	GLN	CA-C-N	-5.03	118.41	123.04
1	A	10	GLN	C-N-CA	-5.03	118.41	123.04
1	A	151	GLU	CA-C-N	5.02	127.01	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	151	GLU	C-N-CA	5.02	127.01	120.28

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	2281	0	2234	33	0
2	A	351	0	0	11	5
All	All	2632	0	2234	33	5

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 7.

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:140:VAL:HG12	1:A:144:MET:HE2	1.47	0.96
1:A:224:VAL:O	2:A:850:HOH:O	1.98	0.80
1:A:196:ARG:HD2	1:A:212:TRP:CH2	2.17	0.79
1:A:1:MET:HE2	2:A:743:HOH:O	1.86	0.75
1:A:5:GLN:HE22	1:A:35:ARG:HE	1.35	0.73
1:A:180:PRO:HB3	2:A:654:HOH:O	1.87	0.73
1:A:144:MET:HE1	2:A:705:HOH:O	1.92	0.69
1:A:302:ARG:NH2	2:A:848:HOH:O	2.24	0.69
1:A:147:ASN:ND2	1:A:179:ASN:H	1.89	0.68
1:A:35:ARG:HD2	2:A:502:HOH:O	2.00	0.62
1:A:219:PRO:O	1:A:220:ASP:HB2	1.99	0.61
1:A:196:ARG:HD2	1:A:212:TRP:CZ3	2.37	0.60
1:A:110:CYS:SG	1:A:111:ASN:N	2.75	0.60
1:A:218:GLU:OE1	2:A:622:HOH:O	2.17	0.59
1:A:10:GLN:HG2	1:A:28:ASP:OD1	2.04	0.58
1:A:196:ARG:HD3	1:A:215:SER:OG	2.08	0.53
1:A:205:GLU:HG2	2:A:727:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:ALA:HB3	1:A:104:TYR:CE1	2.45	0.51
1:A:196:ARG:CD	1:A:212:TRP:CZ3	2.93	0.51
1:A:224:VAL:HG13	1:A:226:GLU:HG3	1.94	0.49
1:A:205:GLU:CG	2:A:727:HOH:O	2.60	0.49
1:A:246:ARG:HE	1:A:250:GLN:NE2	2.12	0.48
1:A:195:THR:HB	2:A:665:HOH:O	2.14	0.47
1:A:298:GLN:HG3	1:A:308:LEU:HB2	1.98	0.46
1:A:75:CYS:SG	2:A:557:HOH:O	2.39	0.45
1:A:235:LYS:HE2	1:A:262:SER:OG	2.17	0.44
1:A:110:CYS:HB3	1:A:132:VAL:HG22	1.99	0.44
1:A:224:VAL:CG1	1:A:226:GLU:HG3	2.48	0.43
1:A:160:LEU:HB2	1:A:189:LEU:HG	2.00	0.43
1:A:219:PRO:O	1:A:220:ASP:CB	2.62	0.42
1:A:152:ALA:C	1:A:153:ILE:HG13	2.45	0.41
1:A:71:LEU:HD23	1:A:71:LEU:HA	1.89	0.41
1:A:100:GLN:HE21	1:A:100:GLN:HB2	1.71	0.40

All (5) 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)
2:A:767:HOH:O	2:A:843:HOH:O[2_564]	1.69	0.51
2:A:663:HOH:O	2:A:724:HOH:O[2_464]	1.77	0.43
2:A:620:HOH:O	2:A:665:HOH:O[2_564]	1.89	0.31
2:A:639:HOH:O	2:A:681:HOH:O[4_455]	1.97	0.23
2:A:575:HOH:O	2:A:598:HOH:O[2_464]	2.14	0.06

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	292/320 (91%)	286 (98%)	6 (2%)	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	234/264 (89%)	228 (97%)	6 (3%)	40 17

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	ASP
1	A	40	GLU
1	A	127	GLU
1	A	148	LEU
1	A	224	VAL
1	A	265	ILE

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	5	GLN
1	A	68	ASN
1	A	100	GLN
1	A	147	ASN
1	A	250	GLN

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 [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	298/320 (93%)	3.19	236 (79%) 0 0	7, 14, 44, 87	0

All (236) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	24	LEU	9.5
1	A	109	LEU	7.6
1	A	1	MET	7.5
1	A	14	ASP	7.2
1	A	314	ASP	7.0
1	A	75	CYS	6.9
1	A	38	GLU	6.9
1	A	173	GLN	6.7
1	A	148	LEU	6.7
1	A	224	VAL	6.6
1	A	140	VAL	6.6
1	A	182	TYR	6.5
1	A	11	ILE	6.4
1	A	166	TRP	6.4
1	A	316	LEU	6.4
1	A	294	LEU	6.2
1	A	134	VAL	6.2
1	A	111	ASN	6.2
1	A	26	THR	6.1
1	A	113	ASP	5.8
1	A	308	LEU	5.8
1	A	127	GLU	5.7
1	A	137	TYR	5.6
1	A	293	ASP	5.6
1	A	153	ILE	5.5
1	A	12	PRO	5.5
1	A	174	PHE	5.5

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Mol	Chain	Res	Type	RSRZ
1	A	150	LEU	5.4
1	A	175	ALA	5.4
1	A	220	ASP	5.3
1	A	129	VAL	5.3
1	A	177	TYR	5.3
1	A	310	VAL	5.2
1	A	320	LEU	5.2
1	A	112	GLY	5.2
1	A	172	GLN	5.2
1	A	189	LEU	5.0
1	A	286	ILE	5.0
1	A	110	CYS	4.9
1	A	152	ALA	4.9
1	A	139	ALA	4.8
1	A	307	THR	4.8
1	A	37	GLY	4.8
1	A	313	VAL	4.8
1	A	155	ASP	4.7
1	A	56	TRP	4.7
1	A	156	LEU	4.7
1	A	193	CYS	4.6
1	A	319	LEU	4.6
1	A	201	ALA	4.6
1	A	13	MET	4.5
1	A	65	ALA	4.5
1	A	96	ASP	4.5
1	A	230	ARG	4.5
1	A	149	LEU	4.4
1	A	10	GLN	4.4
1	A	296	GLN	4.4
1	A	209	ALA	4.4
1	A	141	ARG	4.4
1	A	203	ALA	4.3
1	A	35	ARG	4.3
1	A	143	GLY	4.3
1	A	202	PHE	4.3
1	A	305	GLY	4.3
1	A	48	LEU	4.3
1	A	291	THR	4.2
1	A	169	LEU	4.1
1	A	219	PRO	4.1
1	A	304	PRO	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	59	ALA	4.1
1	A	303	TRP	4.1
1	A	295	MET	4.0
1	A	136	LEU	4.0
1	A	206	THR	4.0
1	A	8	ARG	4.0
1	A	71	LEU	3.9
1	A	292	LEU	3.9
1	A	226	GLU	3.9
1	A	192	PRO	3.9
1	A	132	VAL	3.9
1	A	179	ASN	3.9
1	A	9	TRP	3.9
1	A	244	LYS	3.9
1	A	180	PRO	3.8
1	A	311	VAL	3.8
1	A	247	GLU	3.8
1	A	154	PRO	3.8
1	A	229	VAL	3.7
1	A	280	TRP	3.7
1	A	315	ALA	3.7
1	A	204	ARG	3.7
1	A	255	LEU	3.7
1	A	54	GLU	3.6
1	A	106	ALA	3.6
1	A	160	LEU	3.6
1	A	168	PRO	3.6
1	A	223	PHE	3.6
1	A	146	VAL	3.6
1	A	207	GLY	3.6
1	A	205	GLU	3.6
1	A	195	THR	3.5
1	A	171	GLY	3.5
1	A	7	TYR	3.5
1	A	309	PRO	3.5
1	A	297	ALA	3.5
1	A	144	MET	3.5
1	A	302	ARG	3.5
1	A	4	ALA	3.5
1	A	162	ALA	3.5
1	A	145	VAL	3.5
1	A	138	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	227	GLU	3.5
1	A	210	ILE	3.4
1	A	158	LEU	3.4
1	A	142	ASP	3.4
1	A	60	GLN	3.3
1	A	318	ARG	3.3
1	A	147	ASN	3.3
1	A	208	ILE	3.3
1	A	265	ILE	3.3
1	A	98	LEU	3.3
1	A	184	ASP	3.3
1	A	36	GLU	3.3
1	A	34	LEU	3.3
1	A	167	THR	3.2
1	A	58	GLU	3.2
1	A	212	TRP	3.2
1	A	128	LYS	3.1
1	A	94	LEU	3.1
1	A	306	SER	3.1
1	A	198	ASP	3.1
1	A	90	ALA	3.1
1	A	231	ALA	3.1
1	A	6	VAL	3.1
1	A	42	TRP	3.1
1	A	178	VAL	3.1
1	A	186	ILE	3.1
1	A	216	LEU	3.0
1	A	236	PRO	3.0
1	A	30	LEU	3.0
1	A	46	SER	2.9
1	A	165	ALA	2.9
1	A	271	LEU	2.9
1	A	289	LEU	2.9
1	A	3	SER	2.9
1	A	272	THR	2.8
1	A	83	VAL	2.8
1	A	225	ALA	2.8
1	A	45	ILE	2.8
1	A	51	PHE	2.8
1	A	64	LEU	2.8
1	A	33	CYS	2.8
1	A	69	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	214	GLU	2.8
1	A	218	GLU	2.8
1	A	194	LYS	2.8
1	A	164	ARG	2.8
1	A	79	GLN	2.8
1	A	50	GLY	2.8
1	A	300	VAL	2.7
1	A	77	LEU	2.7
1	A	170	LYS	2.7
1	A	197	ASP	2.7
1	A	62	VAL	2.7
1	A	67	VAL	2.7
1	A	55	THR	2.7
1	A	130	ALA	2.7
1	A	196	ARG	2.7
1	A	199	SER	2.7
1	A	5	GLN	2.7
1	A	97	THR	2.6
1	A	86	GLY	2.6
1	A	102	ALA	2.6
1	A	287	PRO	2.6
1	A	262	SER	2.6
1	A	270	GLY	2.6
1	A	161	ASP	2.6
1	A	70	TRP	2.6
1	A	78	PRO	2.6
1	A	80	MET	2.6
1	A	101	ALA	2.6
1	A	41	GLY	2.5
1	A	237	THR	2.5
1	A	157	HIS	2.5
1	A	176	LYS	2.5
1	A	31	TYR	2.5
1	A	105	ARG	2.5
1	A	232	VAL	2.5
1	A	107	ALA	2.5
1	A	108	PRO	2.5
1	A	288	GLY	2.5
1	A	257	LEU	2.5
1	A	251	ALA	2.5
1	A	95	THR	2.5
1	A	284	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	72	ALA	2.5
1	A	252	ALA	2.5
1	A	66	TRP	2.4
1	A	87	VAL	2.4
1	A	277	ILE	2.4
1	A	256	GLY	2.4
1	A	275	ALA	2.4
1	A	278	ALA	2.4
1	A	221	PHE	2.4
1	A	290	ASP	2.4
1	A	317	GLU	2.4
1	A	213	ASP	2.3
1	A	264	SER	2.3
1	A	211	ALA	2.3
1	A	39	ARG	2.3
1	A	249	VAL	2.3
1	A	151	GLU	2.3
1	A	49	PRO	2.2
1	A	53	GLN	2.2
1	A	163	ASN	2.2
1	A	63	LEU	2.2
1	A	238	LEU	2.2
1	A	268	SER	2.2
1	A	40	GLU	2.2
1	A	312	GLU	2.2
1	A	2	ARG	2.2
1	A	61	SER	2.2
1	A	181	ASP	2.1
1	A	222	ALA	2.1
1	A	239	THR	2.1
1	A	283	PRO	2.1
1	A	233	VAL	2.1
1	A	52	SER	2.1
1	A	228	GLY	2.1
1	A	259	ALA	2.1
1	A	104	TYR	2.1
1	A	260	VAL	2.0
1	A	57	GLU	2.0
1	A	29	GLY	2.0
1	A	298	GLN	2.0
1	A	279	ALA	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.