



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 06:01 PM UTC

PDB ID : 4X8F / pdb_00004x8f
Title : Vibrio cholerae O395 Ribokinase in apo form
Authors : Paul, R.; Patra, M.D.; Sen, U.
Deposited on : 2014-12-10
Resolution : 3.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

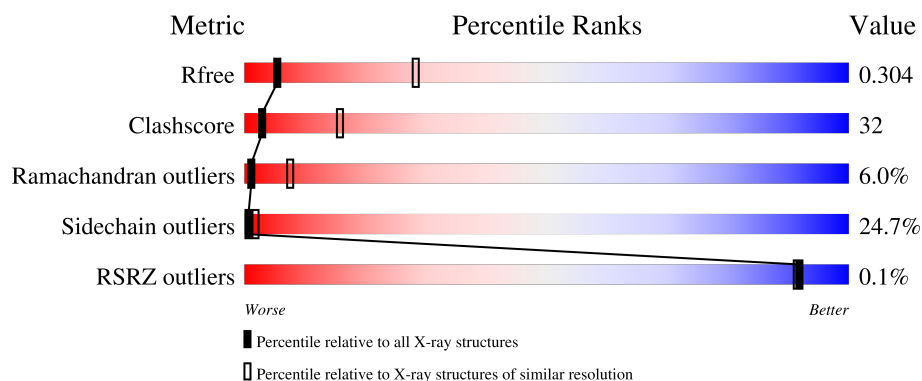
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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.



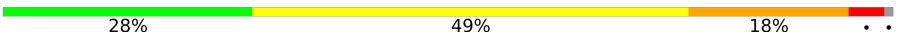
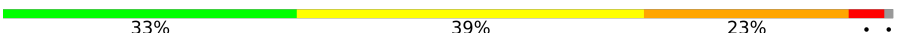
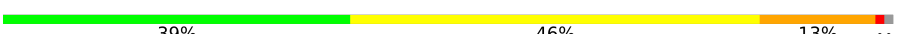
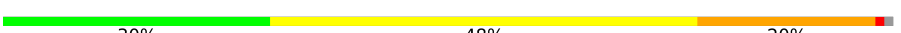
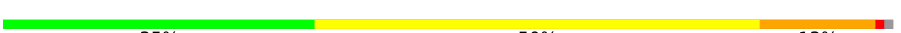
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1001 (3.44-3.36)
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)
RSRZ outliers	180081	1001 (3.44-3.36)

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	309	40% 46% 12% ..
1	B	309	34% 45% 17% ..
1	C	309	38% 41% 19% ..
1	D	309	35% 46% 16% ..
1	E	309	42% 43% 13% ..

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Mol	Chain	Length	Quality of chain
1	F	309	 33% 49% 16% ..
1	G	309	 28% 49% 18% . .
1	H	309	 33% 39% 23% . .
1	I	309	 39% 45% 14% ..
1	J	309	 39% 46% 13% ..
1	K	309	 30% 48% 20% ..
1	L	309	 35% 50% 13% ..
1	M	309	 43% 42% 13% ..
1	N	309	 38% 45% 16% ..
1	O	309	 37% 43% 19% .
1	P	309	 39% 45% 13% ..

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 36000 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 Ribokinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	306	Total	C	N	O	S	0	0	0
			2250	1408	391	441	10			
1	B	306	Total	C	N	O	S	0	0	0
			2250	1408	391	441	10			
1	C	306	Total	C	N	O	S	0	0	0
			2250	1408	391	441	10			
1	D	306	Total	C	N	O	S	0	0	0
			2250	1408	391	441	10			
1	E	306	Total	C	N	O	S	0	0	0
			2250	1408	391	441	10			
1	F	306	Total	C	N	O	S	0	0	0
			2250	1408	391	441	10			
1	G	306	Total	C	N	O	S	0	0	0
			2250	1408	391	441	10			
1	H	306	Total	C	N	O	S	0	0	0
			2250	1408	391	441	10			
1	I	306	Total	C	N	O	S	0	0	0
			2250	1408	391	441	10			
1	J	306	Total	C	N	O	S	0	0	0
			2250	1408	391	441	10			
1	K	306	Total	C	N	O	S	0	0	0
			2250	1408	391	441	10			
1	L	306	Total	C	N	O	S	0	0	0
			2250	1408	391	441	10			
1	M	306	Total	C	N	O	S	0	0	0
			2250	1408	391	441	10			
1	N	306	Total	C	N	O	S	0	0	0
			2250	1408	391	441	10			
1	O	306	Total	C	N	O	S	0	0	0
			2250	1408	391	441	10			
1	P	306	Total	C	N	O	S	0	0	0
			2250	1408	391	441	10			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP A5F1B7
A	-1	SER	-	expression tag	UNP A5F1B7
A	0	HIS	-	expression tag	UNP A5F1B7
B	-2	GLY	-	expression tag	UNP A5F1B7
B	-1	SER	-	expression tag	UNP A5F1B7
B	0	HIS	-	expression tag	UNP A5F1B7
C	-2	GLY	-	expression tag	UNP A5F1B7
C	-1	SER	-	expression tag	UNP A5F1B7
C	0	HIS	-	expression tag	UNP A5F1B7
D	-2	GLY	-	expression tag	UNP A5F1B7
D	-1	SER	-	expression tag	UNP A5F1B7
D	0	HIS	-	expression tag	UNP A5F1B7
E	-2	GLY	-	expression tag	UNP A5F1B7
E	-1	SER	-	expression tag	UNP A5F1B7
E	0	HIS	-	expression tag	UNP A5F1B7
F	-2	GLY	-	expression tag	UNP A5F1B7
F	-1	SER	-	expression tag	UNP A5F1B7
F	0	HIS	-	expression tag	UNP A5F1B7
G	-2	GLY	-	expression tag	UNP A5F1B7
G	-1	SER	-	expression tag	UNP A5F1B7
G	0	HIS	-	expression tag	UNP A5F1B7
H	-2	GLY	-	expression tag	UNP A5F1B7
H	-1	SER	-	expression tag	UNP A5F1B7
H	0	HIS	-	expression tag	UNP A5F1B7
I	-2	GLY	-	expression tag	UNP A5F1B7
I	-1	SER	-	expression tag	UNP A5F1B7
I	0	HIS	-	expression tag	UNP A5F1B7
J	-2	GLY	-	expression tag	UNP A5F1B7
J	-1	SER	-	expression tag	UNP A5F1B7
J	0	HIS	-	expression tag	UNP A5F1B7
K	-2	GLY	-	expression tag	UNP A5F1B7
K	-1	SER	-	expression tag	UNP A5F1B7
K	0	HIS	-	expression tag	UNP A5F1B7
L	-2	GLY	-	expression tag	UNP A5F1B7
L	-1	SER	-	expression tag	UNP A5F1B7
L	0	HIS	-	expression tag	UNP A5F1B7
M	-2	GLY	-	expression tag	UNP A5F1B7
M	-1	SER	-	expression tag	UNP A5F1B7
M	0	HIS	-	expression tag	UNP A5F1B7
N	-2	GLY	-	expression tag	UNP A5F1B7
N	-1	SER	-	expression tag	UNP A5F1B7
N	0	HIS	-	expression tag	UNP A5F1B7

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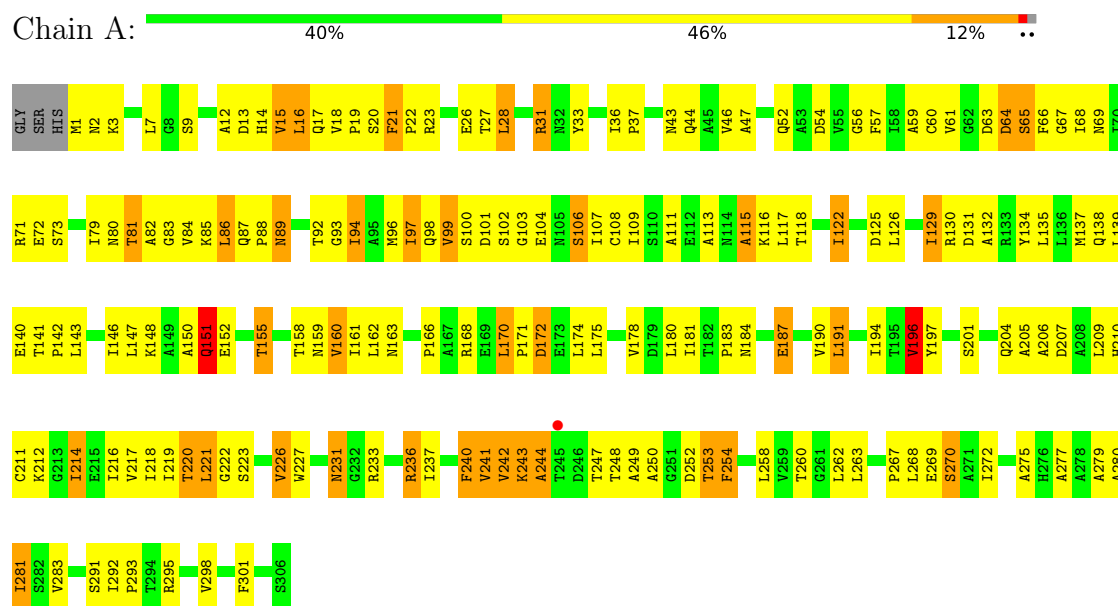
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Chain	Residue	Modelled	Actual	Comment	Reference
O	-2	GLY	-	expression tag	UNP A5F1B7
O	-1	SER	-	expression tag	UNP A5F1B7
O	0	HIS	-	expression tag	UNP A5F1B7
P	-2	GLY	-	expression tag	UNP A5F1B7
P	-1	SER	-	expression tag	UNP A5F1B7
P	0	HIS	-	expression tag	UNP A5F1B7

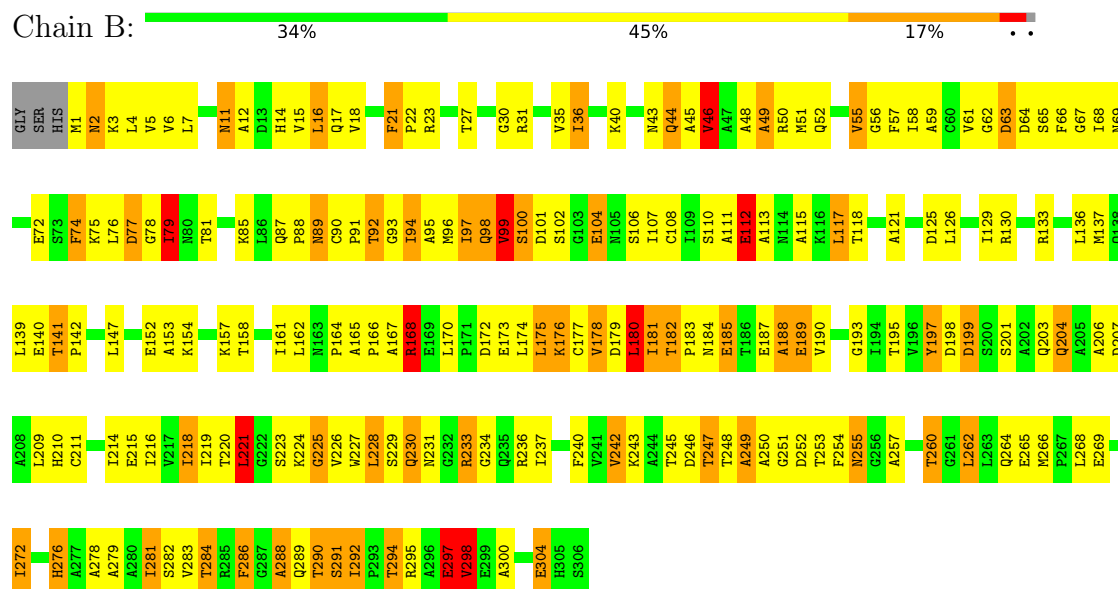
3 Residue-property plots

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.

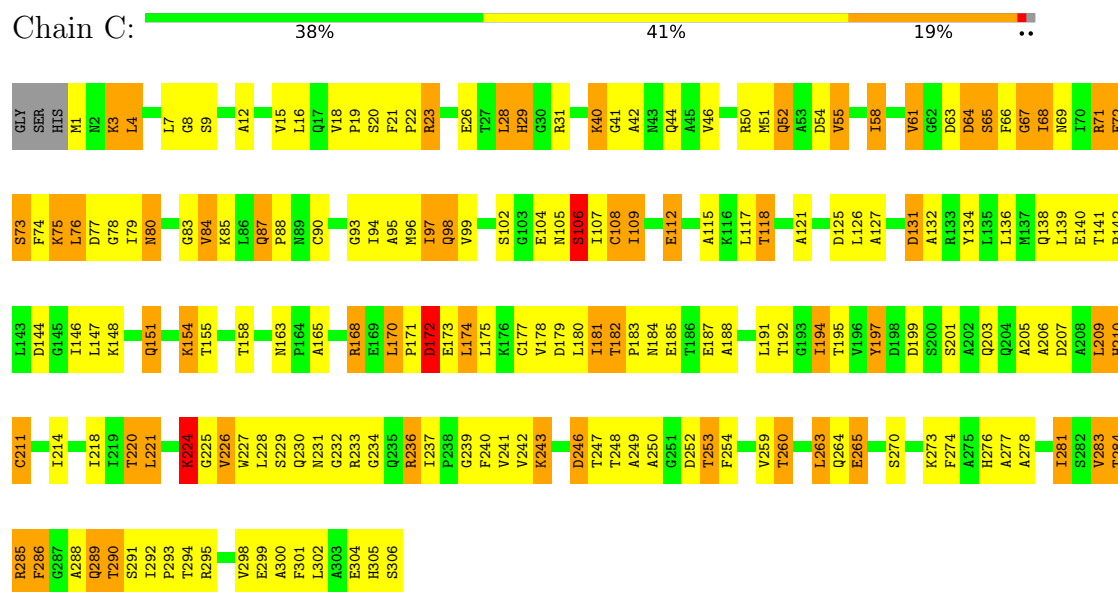
• Molecule 1: Ribokinase



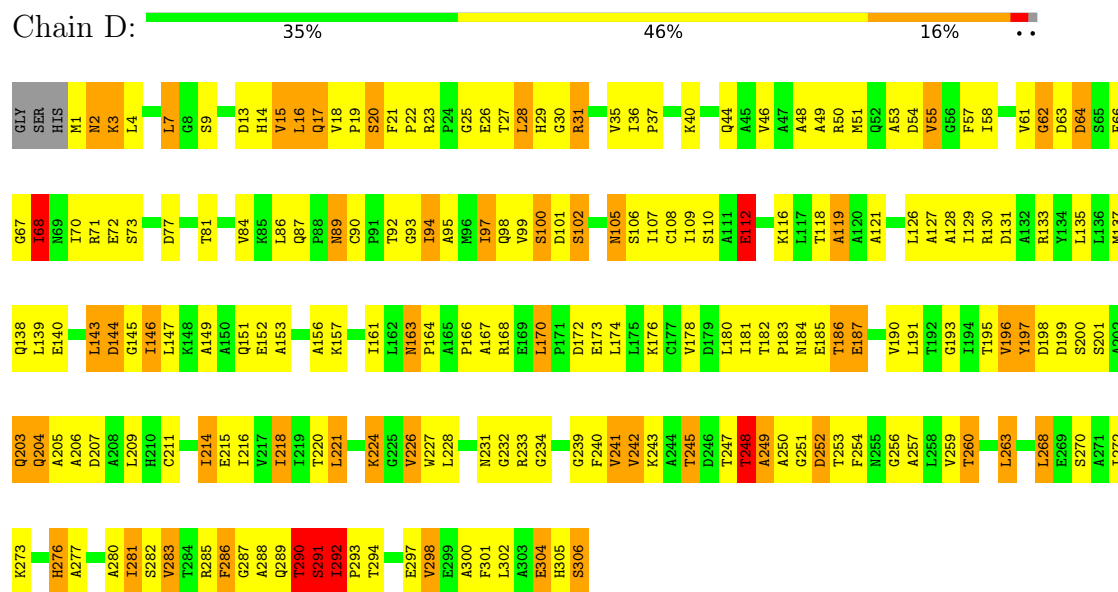
• Molecule 1: Ribokinase



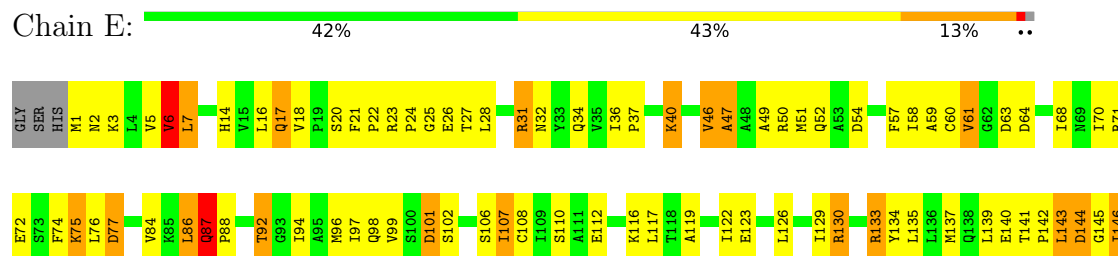
• Molecule 1: Ribokinase

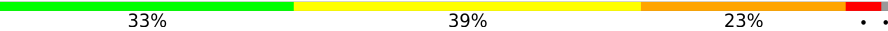


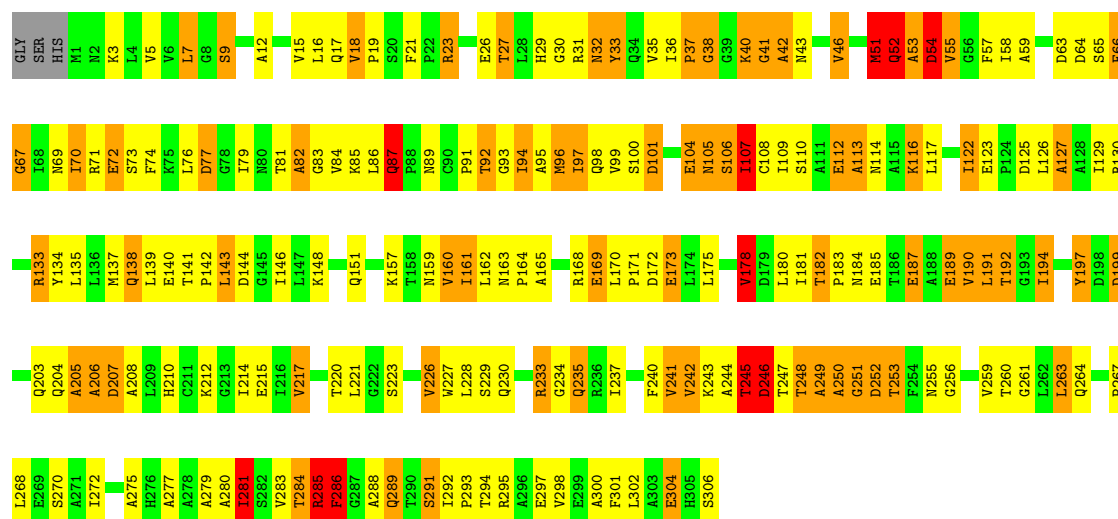
• Molecule 1: Ribokinase



• Molecule 1: Ribokinase

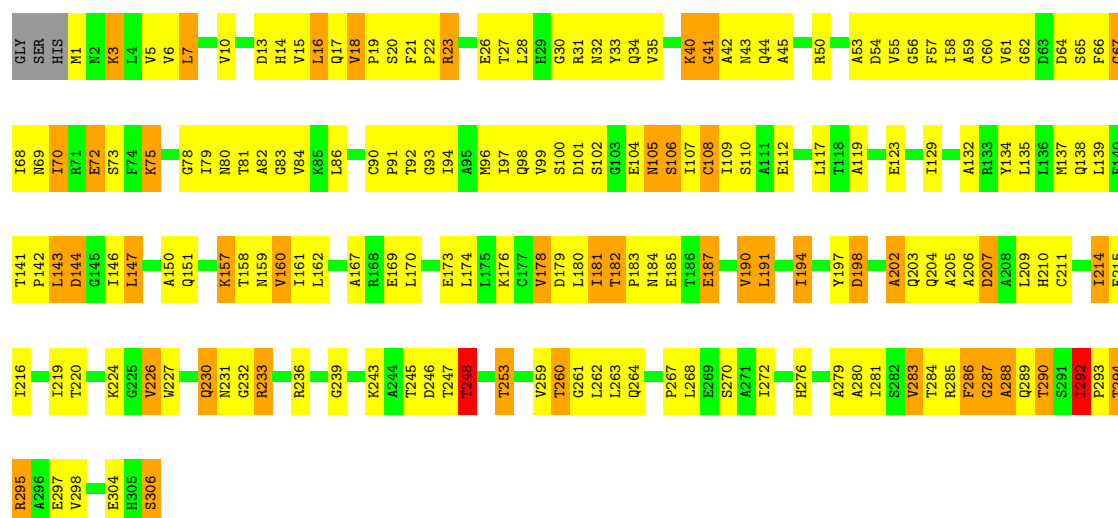


Chain H:  33% 39% 23% ..



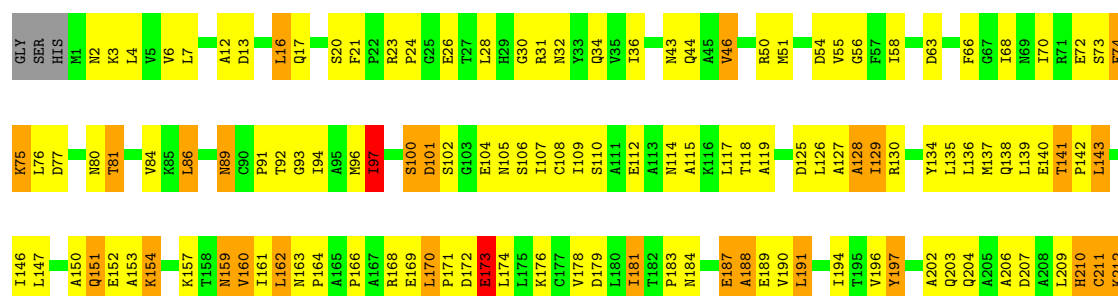
• Molecule 1: Ribokinase

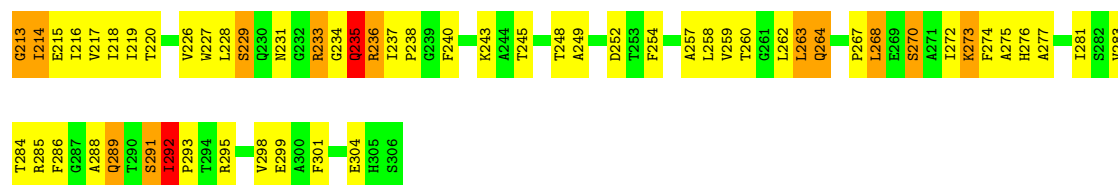
Chain I:  39% 45% 14% ..



• Molecule 1: Ribokinase

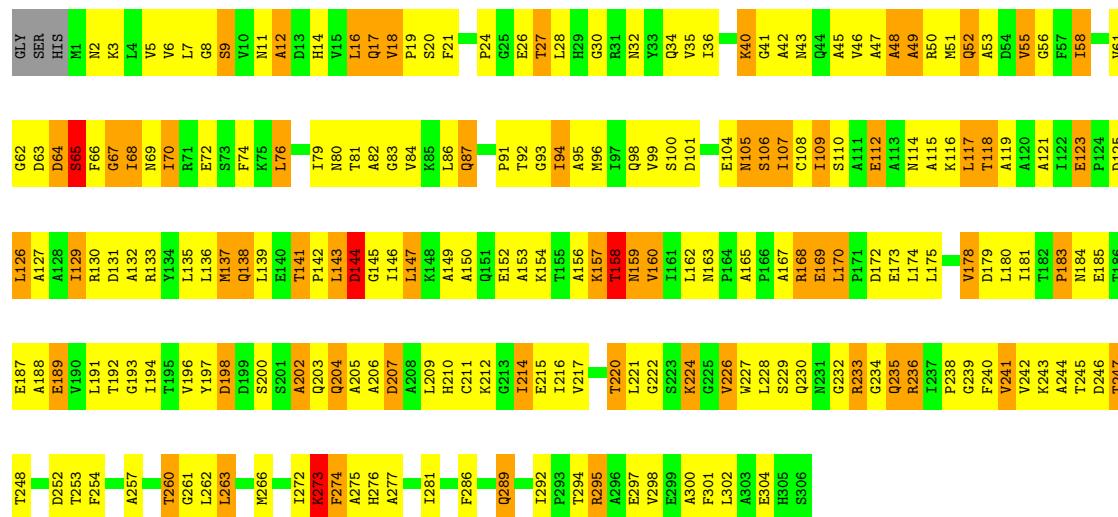
Chain J:  39% 46% 13% ..





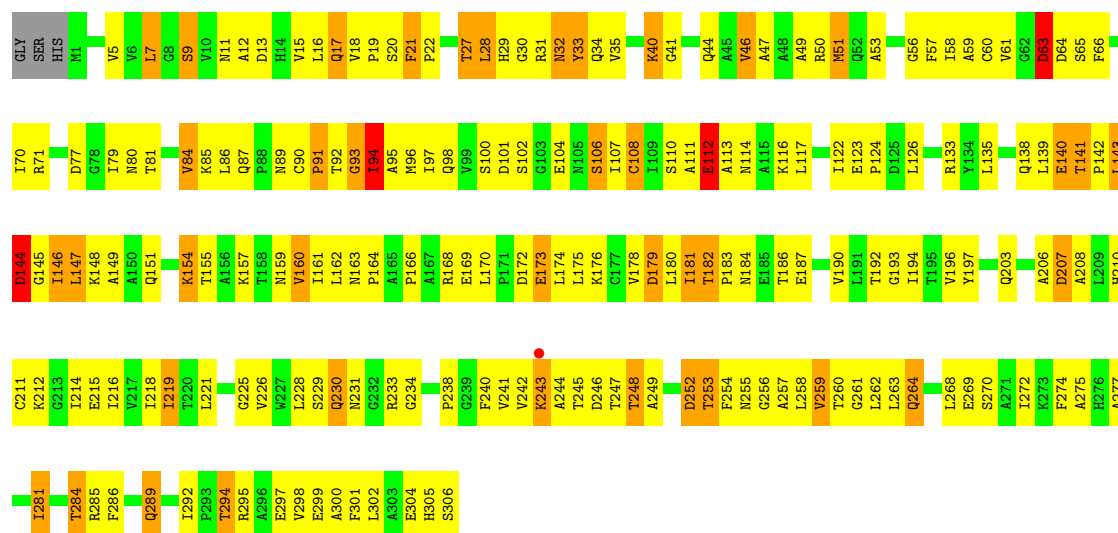
• Molecule 1: Ribokinase

Chain K: 30% 48% 20% ..



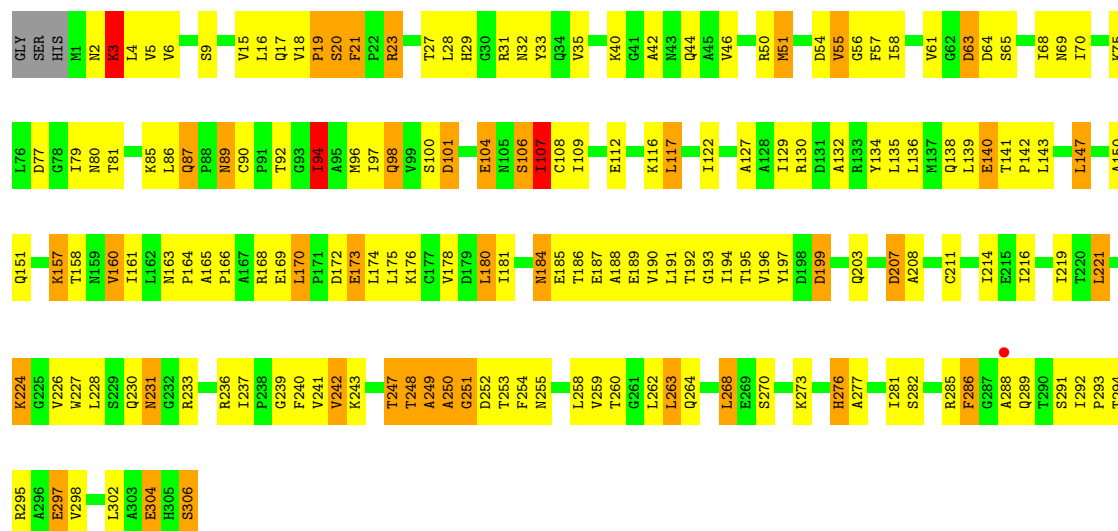
• Molecule 1: Ribokinase

Chain L: 35% 50% 13% ..



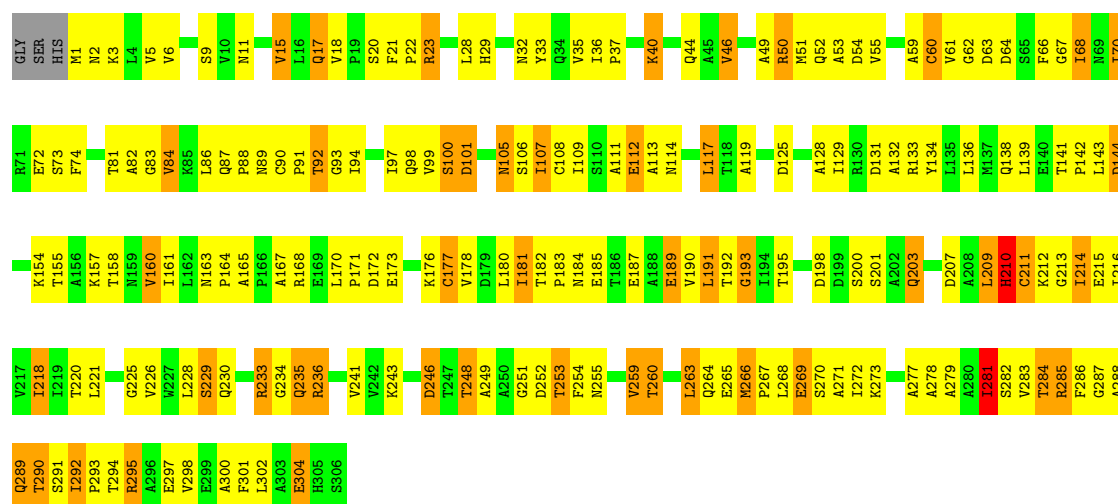
• Molecule 1: Ribokinase

Chain M: 43% 42% 13% ..



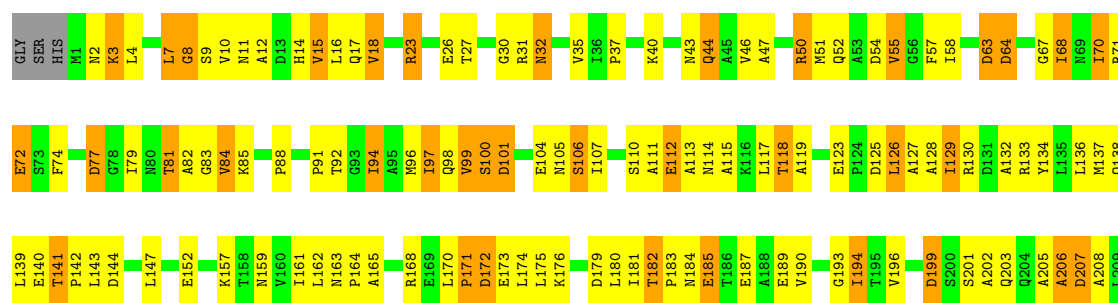
● Molecule 1: Ribokinase

Chain N: 38% 45% 16% ..



● Molecule 1: Ribokinase

Chain O: 37% 43% 19% .



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	129.22Å 130.85Å 145.69Å 110.52° 90.00° 119.59°	Depositor
Resolution (Å)	43.57 – 3.40 43.57 – 3.40	Depositor EDS
% Data completeness (in resolution range)	92.8 (43.57-3.40) 92.9 (43.57-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.15	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.13 (at 3.40Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.239 , 0.308 0.237 , 0.304	Depositor DCC
R_{free} test set	4832 reflections (4.63%)	wwPDB-VP
Wilson B-factor (Å ²)	63.2	Xtriage
Anisotropy	0.563	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 55.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.277 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	36000	wwPDB-VP
Average B, all atoms (Å ²)	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.86% 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	0.67	0/2283	1.17	7/3105 (0.2%)
1	B	0.67	0/2283	1.20	13/3105 (0.4%)
1	C	0.74	0/2283	1.26	17/3105 (0.5%)
1	D	0.79	0/2283	1.34	24/3105 (0.8%)
1	E	0.85	0/2283	1.32	18/3105 (0.6%)
1	F	0.80	1/2283 (0.0%)	1.22	12/3105 (0.4%)
1	G	0.89	2/2283 (0.1%)	1.39	33/3105 (1.1%)
1	H	0.88	0/2283	1.33	19/3105 (0.6%)
1	I	0.79	0/2283	1.24	16/3105 (0.5%)
1	J	0.77	0/2283	1.23	9/3105 (0.3%)
1	K	0.82	1/2283 (0.0%)	1.32	19/3105 (0.6%)
1	L	0.86	0/2283	1.24	14/3105 (0.5%)
1	M	0.80	0/2283	1.24	12/3105 (0.4%)
1	N	0.71	0/2283	1.21	14/3105 (0.5%)
1	O	0.66	0/2283	1.19	15/3105 (0.5%)
1	P	0.62	0/2283	1.20	15/3105 (0.5%)
All	All	0.77	4/36528 (0.0%)	1.26	257/49680 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	1
1	G	0	1
1	J	0	1
1	K	0	2
1	N	0	1
All	All	0	6

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	110	SER	CA-C	-6.12	1.47	1.53
1	G	165	ALA	CA-CB	-5.31	1.46	1.53
1	F	12	ALA	CA-CB	-5.20	1.44	1.53
1	K	91	PRO	CA-C	5.17	1.58	1.53

The worst 5 of 257 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	23	ARG	N-CA-C	-11.44	96.58	110.31
1	G	75	LYS	N-CA-C	-10.91	102.18	114.62
1	D	23	ARG	N-CA-C	-10.31	97.93	110.31
1	F	232	GLY	N-CA-C	-10.14	101.59	114.37
1	G	163	ASN	CA-C-N	-10.08	107.24	119.84

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	290	THR	Peptide
1	G	100	SER	Peptide
1	J	100	SER	Peptide
1	K	156	ALA	Peptide
1	K	157	LYS	Peptide

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	2250	0	2273	151	0
1	B	2250	0	2273	189	0
1	C	2250	0	2273	130	0
1	D	2250	0	2273	168	0
1	E	2250	0	2273	140	0
1	F	2250	0	2273	150	0
1	G	2250	0	2273	169	0
1	H	2250	0	2273	208	0
1	I	2250	0	2273	127	0
1	J	2250	0	2273	129	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	K	2250	0	2273	174	0
1	L	2250	0	2273	169	0
1	M	2250	0	2273	125	0
1	N	2250	0	2273	136	0
1	O	2250	0	2273	143	0
1	P	2250	0	2273	139	0
All	All	36000	0	36368	2335	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 32.

The worst 5 of 2335 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:H:31:ARG:NH2	1:H:101:ASP:OD1	1.89	1.06
1:K:94:ILE:HD12	1:K:95:ALA:H	1.18	1.04
1:L:51:MET:HB2	1:L:260:THR:HG21	1.43	1.00
1:H:243:LYS:HG3	1:K:101:ASP:HA	1.42	1.00
1:E:87:GLN:HG2	1:E:116:LYS:HG3	1.45	0.99

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	304/309 (98%)	242 (80%)	46 (15%)	16 (5%)	1	10
1	B	304/309 (98%)	228 (75%)	50 (16%)	26 (9%)	0	4
1	C	304/309 (98%)	236 (78%)	46 (15%)	22 (7%)	1	5
1	D	304/309 (98%)	251 (83%)	33 (11%)	20 (7%)	1	6
1	E	304/309 (98%)	261 (86%)	34 (11%)	9 (3%)	3	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	304/309 (98%)	239 (79%)	46 (15%)	19 (6%)	1	7
1	G	304/309 (98%)	236 (78%)	50 (16%)	18 (6%)	1	8
1	H	304/309 (98%)	238 (78%)	38 (12%)	28 (9%)	0	3
1	I	304/309 (98%)	264 (87%)	27 (9%)	13 (4%)	2	13
1	J	304/309 (98%)	244 (80%)	46 (15%)	14 (5%)	2	12
1	K	304/309 (98%)	238 (78%)	39 (13%)	27 (9%)	0	3
1	L	304/309 (98%)	259 (85%)	30 (10%)	15 (5%)	1	11
1	M	304/309 (98%)	253 (83%)	31 (10%)	20 (7%)	1	6
1	N	304/309 (98%)	262 (86%)	27 (9%)	15 (5%)	1	11
1	O	304/309 (98%)	245 (81%)	40 (13%)	19 (6%)	1	7
1	P	304/309 (98%)	259 (85%)	36 (12%)	9 (3%)	3	18
All	All	4864/4944 (98%)	3955 (81%)	619 (13%)	290 (6%)	1	7

5 of 290 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	64	ASP
1	A	67	GLY
1	A	82	ALA
1	A	172	ASP
1	A	196	VAL

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	237/239 (99%)	187 (79%)	50 (21%)	1	3
1	B	237/239 (99%)	170 (72%)	67 (28%)	0	1
1	C	237/239 (99%)	173 (73%)	64 (27%)	0	1
1	D	237/239 (99%)	176 (74%)	61 (26%)	0	1
1	E	237/239 (99%)	187 (79%)	50 (21%)	1	3

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	237/239 (99%)	181 (76%)	56 (24%)	1	2
1	G	237/239 (99%)	157 (66%)	80 (34%)	0	0
1	H	237/239 (99%)	169 (71%)	68 (29%)	0	1
1	I	237/239 (99%)	187 (79%)	50 (21%)	1	3
1	J	237/239 (99%)	182 (77%)	55 (23%)	1	2
1	K	237/239 (99%)	177 (75%)	60 (25%)	0	1
1	L	237/239 (99%)	190 (80%)	47 (20%)	1	5
1	M	237/239 (99%)	183 (77%)	54 (23%)	1	3
1	N	237/239 (99%)	180 (76%)	57 (24%)	1	2
1	O	237/239 (99%)	178 (75%)	59 (25%)	0	1
1	P	237/239 (99%)	177 (75%)	60 (25%)	0	1
All	All	3792/3824 (99%)	2854 (75%)	938 (25%)	1	2

5 of 938 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	169	GLU
1	P	50	ARG
1	J	160	VAL
1	O	304	GLU
1	N	230	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 110 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	98	GLN
1	J	305	HIS
1	P	230	GLN
1	O	151	GLN
1	I	289	GLN

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	306/309 (99%)	-0.70	1 (0%) 90 84	61, 108, 179, 294	0
1	B	306/309 (99%)	-0.78	0 100 100	67, 98, 149, 239	0
1	C	306/309 (99%)	-0.87	0 100 100	42, 83, 141, 201	0
1	D	306/309 (99%)	-0.97	0 100 100	34, 76, 134, 179	0
1	E	306/309 (99%)	-1.02	0 100 100	38, 62, 112, 182	0
1	F	306/309 (99%)	-0.88	0 100 100	46, 81, 140, 173	0
1	G	306/309 (99%)	-0.91	0 100 100	40, 79, 131, 162	0
1	H	306/309 (99%)	-0.97	0 100 100	36, 69, 125, 214	0
1	I	306/309 (99%)	-0.87	0 100 100	43, 76, 125, 199	0
1	J	306/309 (99%)	-0.94	0 100 100	43, 80, 130, 202	0
1	K	306/309 (99%)	-0.88	0 100 100	47, 83, 140, 172	0
1	L	306/309 (99%)	-0.99	1 (0%) 90 84	36, 63, 112, 186	0
1	M	306/309 (99%)	-0.85	1 (0%) 90 84	42, 73, 142, 206	0
1	N	306/309 (99%)	-0.88	0 100 100	44, 82, 146, 189	0
1	O	306/309 (99%)	-0.77	0 100 100	59, 96, 163, 215	0
1	P	306/309 (99%)	-0.69	1 (0%) 90 84	61, 107, 170, 202	0
All	All	4896/4944 (99%)	-0.87	4 (0%) 92 91	34, 82, 146, 294	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	288	ALA	3.8
1	L	243	LYS	3.4
1	A	245	THR	3.2
1	P	286	PHE	2.1

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.