



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 02:21 PM GMT

PDB ID : 3WQP
Title : Crystal structure of Rubisco T289D mutant from *Thermococcus kodakarensis*
Authors : Fujihashi, M.; Nishitani, Y.; Kiriyaama, T.; Miki, K.
Deposited on : 2014-01-29
Resolution : 2.25 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

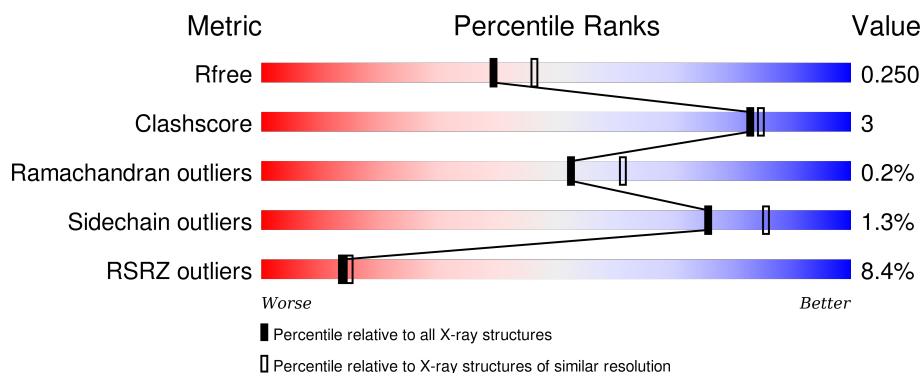
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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.



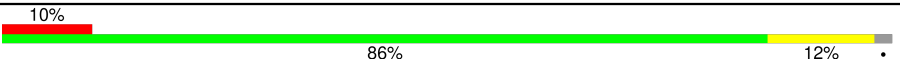

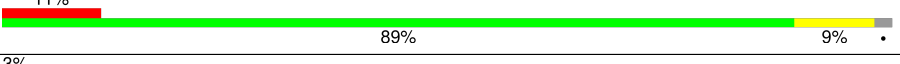
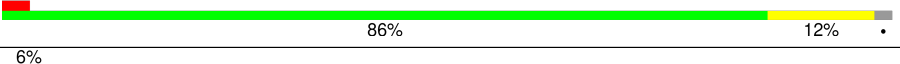
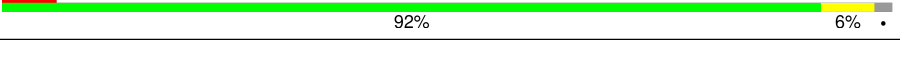
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1640 (2.28-2.24)
Clashscore	102246	1095 (2.26-2.26)
Ramachandran outliers	100387	1063 (2.26-2.26)
Sidechain outliers	100360	1063 (2.26-2.26)
RSRZ outliers	91569	1647 (2.28-2.24)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	444	<div> <div>5%</div> <div>91%</div> <div>8%</div> </div>
1	B	444	<div> <div>11%</div> <div>89%</div> <div>9%</div> </div>
1	C	444	<div> <div>6%</div> <div>91%</div> <div>7%</div> </div>
1	D	444	<div> <div>8%</div> <div>88%</div> <div>10%</div> </div>
1	E	444	<div> <div>7%</div> <div>91%</div> <div>7%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	444	
1	G	444	
1	H	444	
1	I	444	
1	J	444	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	EDO	I	504	-	-	-	X
4	EDO	J	503	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 36577 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 Ribulose biphosphate carboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	437	Total	C	N	O	S	0	0	0
			3425	2200	584	631	10			
1	B	438	Total	C	N	O	S	0	0	0
			3440	2207	587	636	10			
1	C	438	Total	C	N	O	S	0	0	0
			3443	2209	588	636	10			
1	D	436	Total	C	N	O	S	0	0	0
			3441	2209	587	635	10			
1	E	438	Total	C	N	O	S	0	0	0
			3438	2206	586	636	10			
1	F	436	Total	C	N	O	S	0	0	0
			3408	2185	584	629	10			
1	G	436	Total	C	N	O	S	0	0	0
			3416	2192	581	633	10			
1	H	437	Total	C	N	O	S	0	0	0
			3423	2200	586	627	10			
1	I	436	Total	C	N	O	S	0	0	0
			3434	2204	587	633	10			
1	J	437	Total	C	N	O	S	0	0	0
			3438	2209	586	633	10			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	289	ASP	THR	ENGINEERED MUTATION	UNP O93627
B	289	ASP	THR	ENGINEERED MUTATION	UNP O93627
C	289	ASP	THR	ENGINEERED MUTATION	UNP O93627
D	289	ASP	THR	ENGINEERED MUTATION	UNP O93627
E	289	ASP	THR	ENGINEERED MUTATION	UNP O93627
F	289	ASP	THR	ENGINEERED MUTATION	UNP O93627
G	289	ASP	THR	ENGINEERED MUTATION	UNP O93627
H	289	ASP	THR	ENGINEERED MUTATION	UNP O93627
I	289	ASP	THR	ENGINEERED MUTATION	UNP O93627

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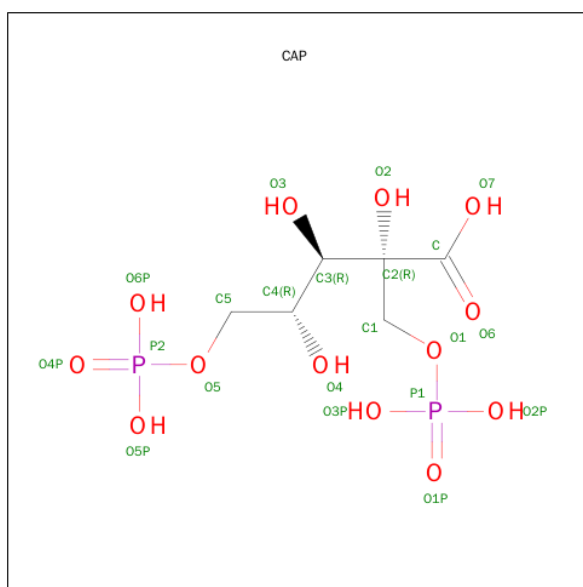
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Chain	Residue	Modelled	Actual	Comment	Reference
J	289	ASP	THR	ENGINEERED MUTATION	UNP O93627

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	1	Total Mg 1 1	0	0
2	J	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0
2	E	1	Total Mg 1 1	0	0
2	H	1	Total Mg 1 1	0	0
2	B	1	Total Mg 1 1	0	0
2	I	1	Total Mg 1 1	0	0
2	C	1	Total Mg 1 1	0	0
2	A	1	Total Mg 1 1	0	0
2	F	1	Total Mg 1 1	0	0

- Molecule 3 is 2-CARBOXYARABINITOL-1,5-DIPHOSPHATE (three-letter code: CAP) (formula: C₆H₁₄O₁₃P₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			21	6	13	2		
3	B	1	Total	C	O	P	0	0
			21	6	13	2		
3	C	1	Total	C	O	P	0	0
			21	6	13	2		
3	D	1	Total	C	O	P	0	0
			21	6	13	2		
3	E	1	Total	C	O	P	0	0
			21	6	13	2		
3	F	1	Total	C	O	P	0	0
			21	6	13	2		
3	G	1	Total	C	O	P	0	0
			21	6	13	2		
3	H	1	Total	C	O	P	0	0
			21	6	13	2		
3	I	1	Total	C	O	P	0	0
			21	6	13	2		
3	J	1	Total	C	O	P	0	0
			21	6	13	2		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	E	1	Total C O 4 2 2	0	0
4	H	1	Total C O 4 2 2	0	0
4	H	1	Total C O 4 2 2	0	0
4	I	1	Total C O 4 2 2	0	0
4	I	1	Total C O 4 2 2	0	0
4	J	1	Total C O 4 2 2	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	183	Total O 183 183	0	0
5	B	127	Total O 127 127	0	0

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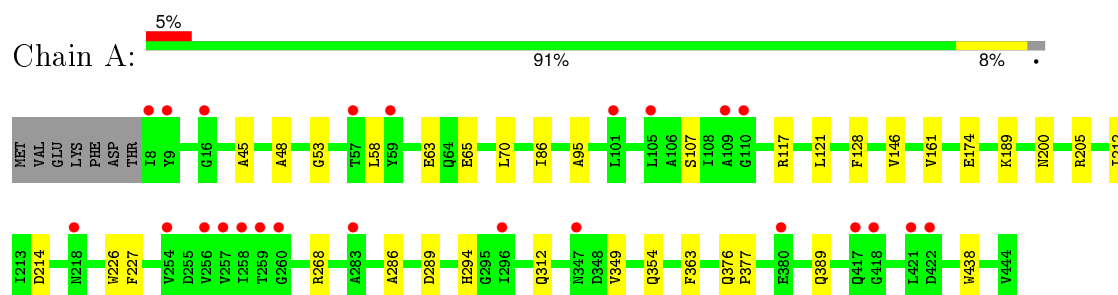
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	223	Total 223	O 223	0	0
5	D	240	Total 240	O 240	0	0
5	E	252	Total 252	O 252	0	0
5	F	170	Total 170	O 170	0	0
5	G	133	Total 133	O 133	0	0
5	H	184	Total 184	O 184	0	0
5	I	244	Total 244	O 244	0	0
5	J	255	Total 255	O 255	0	0

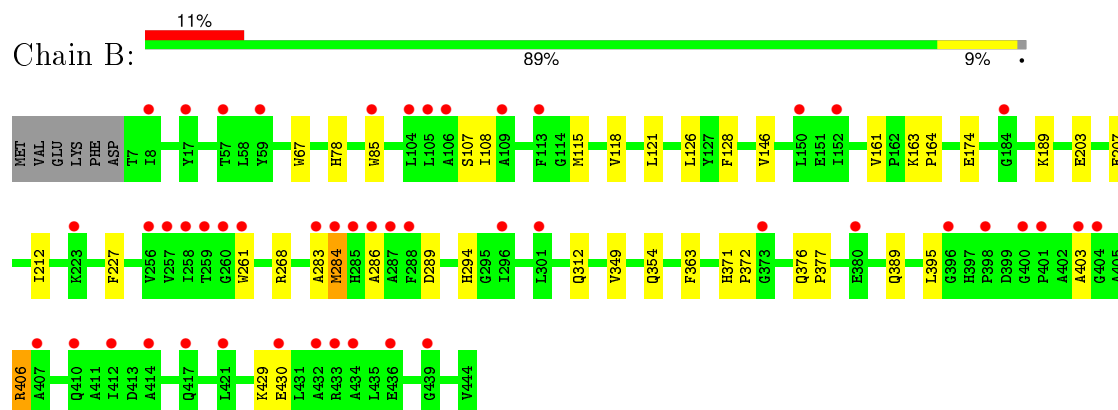
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

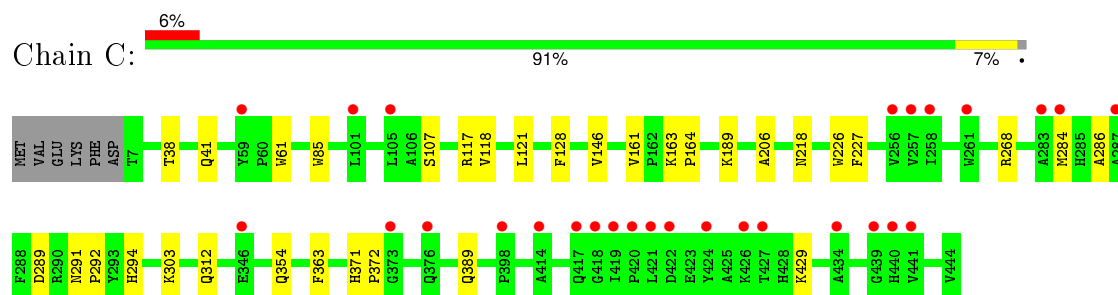
- Molecule 1: Ribulose biphosphate carboxylase



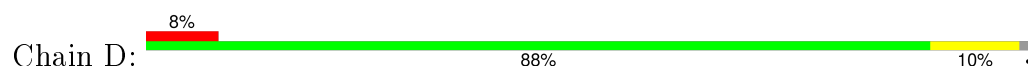
- Molecule 1: Ribulose biphosphate carboxylase

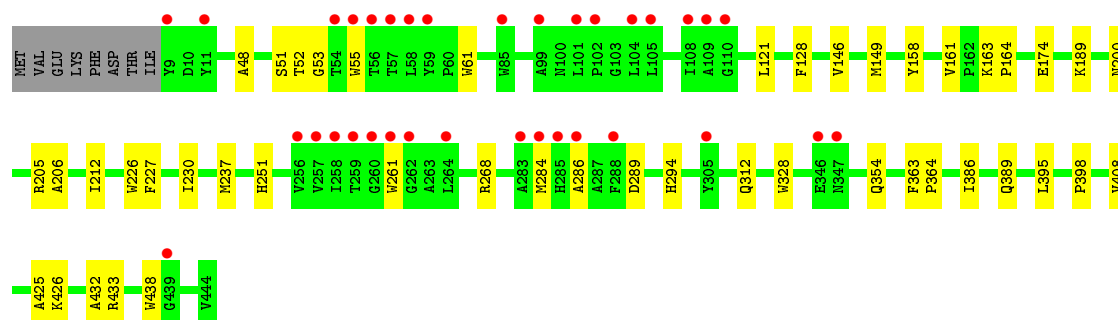


- Molecule 1: Ribulose biphosphate carboxylase

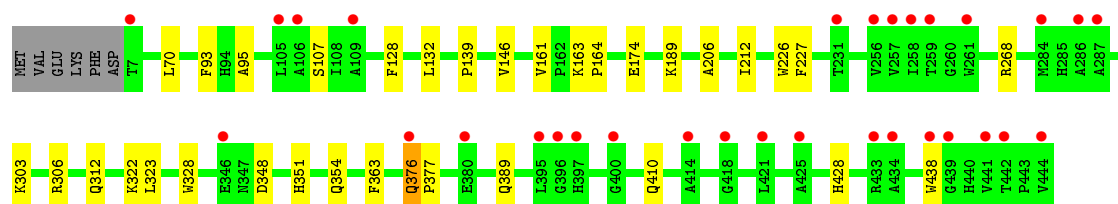
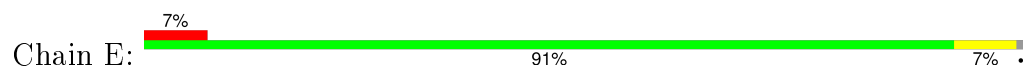


- Molecule 1: Ribulose biphosphate carboxylase

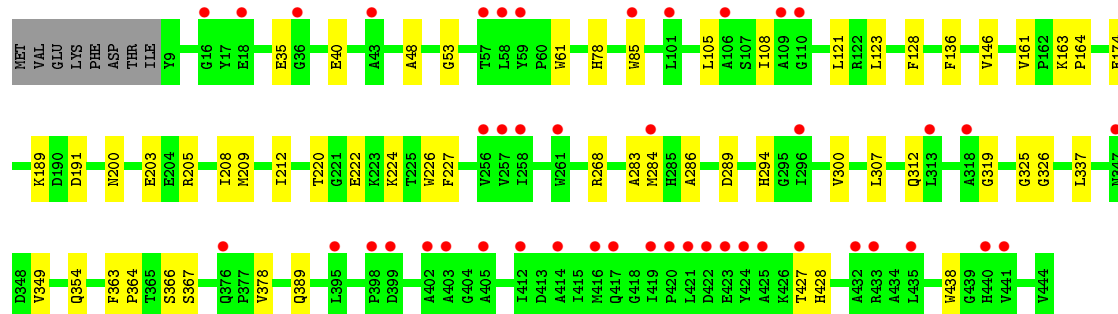
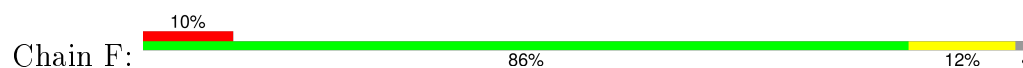




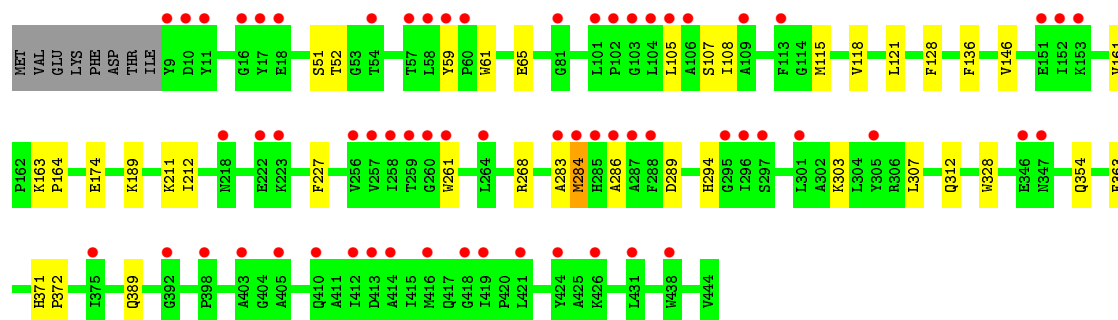
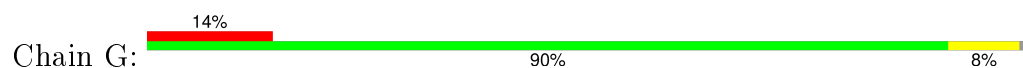
- Molecule 1: Ribulose biphosphate carboxylase



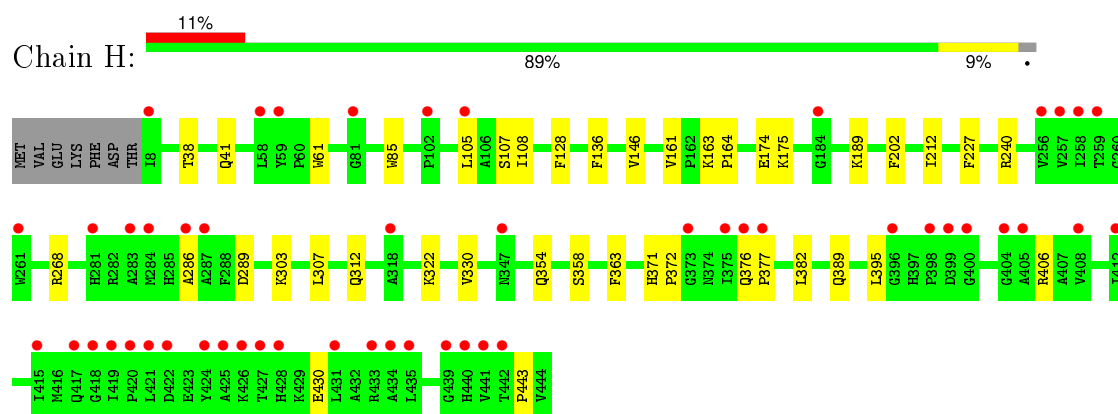
- Molecule 1: Ribulose biphosphate carboxylase



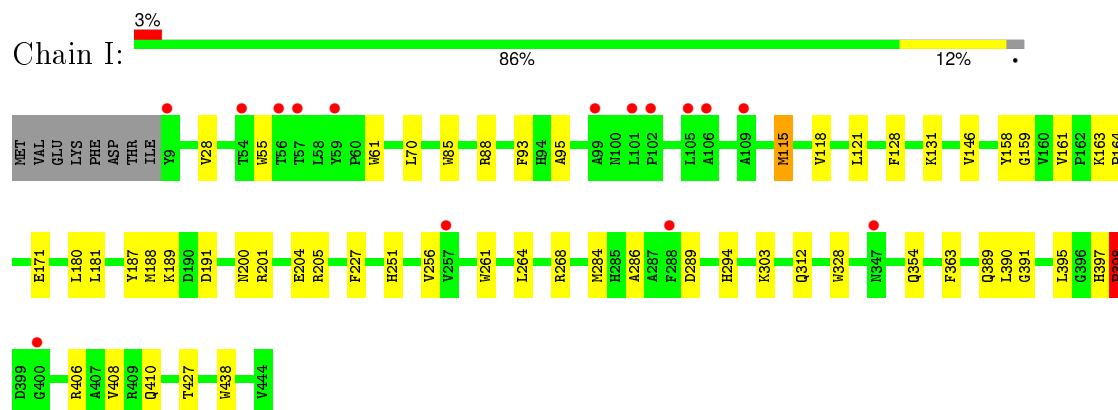
- Molecule 1: Ribulose biphosphate carboxylase



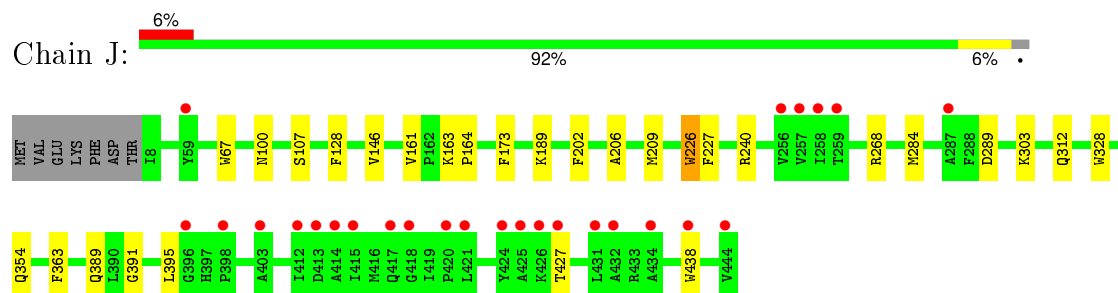
- Molecule 1: Ribulose biphosphate carboxylase



• Molecule 1: Ribulose biphosphate carboxylase



• Molecule 1: Ribulose biphosphate carboxylase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	170.57Å 246.24Å 144.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.25 47.18 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.6 (50.00-2.25) 99.7 (47.18-2.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 2.24Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.220 , 0.258 0.215 , 0.250	Depositor DCC
R_{free} test set	14436 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	33.8	Xtriage
Anisotropy	1.150	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 45.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Outliers	1 of 286386 reflections (0.000%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	36577	wwPDB-VP
Average B, all atoms (Å ²)	51.0	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 48.73 % 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 8.2523e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, CAP, EDO, KCX

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	0.48	2/3502 (0.1%)	0.51	0/4753
1	B	0.48	3/3517 (0.1%)	0.50	0/4770
1	C	0.48	2/3520 (0.1%)	0.51	0/4773
1	D	0.50	5/3517 (0.1%)	0.52	0/4766
1	E	0.50	2/3515 (0.1%)	0.52	0/4767
1	F	0.49	4/3483 (0.1%)	0.51	0/4724
1	G	0.48	3/3493 (0.1%)	0.49	0/4742
1	H	0.48	2/3500 (0.1%)	0.49	0/4748
1	I	0.50	6/3510 (0.2%)	0.53	0/4757
1	J	0.50	4/3515 (0.1%)	0.52	0/4766
All	All	0.49	33/35072 (0.1%)	0.51	0/47566

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	438	TRP	CD2-CE2	5.26	1.47	1.41
1	I	438	TRP	CD2-CE2	5.19	1.47	1.41
1	F	438	TRP	CD2-CE2	5.18	1.47	1.41
1	F	226	TRP	CD2-CE2	5.18	1.47	1.41
1	C	61	TRP	CD2-CE2	5.17	1.47	1.41

There are no bond angle outliers.

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	3425	0	3321	16	0
1	B	3440	0	3335	25	0
1	C	3443	0	3344	17	0
1	D	3441	0	3368	22	0
1	E	3438	0	3328	17	0
1	F	3408	0	3301	31	0
1	G	3416	0	3299	18	0
1	H	3423	0	3328	21	0
1	I	3434	0	3355	35	0
1	J	3438	0	3346	12	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
3	A	21	0	8	0	0
3	B	21	0	9	0	0
3	C	21	0	9	0	0
3	D	21	0	8	0	0
3	E	21	0	9	0	0
3	F	21	0	9	1	0
3	G	21	0	8	0	0
3	H	21	0	9	1	0
3	I	21	0	7	0	0
3	J	21	0	9	0	0
4	A	4	0	6	1	0
4	B	4	0	6	0	0
4	C	4	0	6	0	0
4	D	4	0	6	0	0
4	E	4	0	6	0	0
4	H	8	0	12	0	0
4	I	8	0	12	0	0
4	J	4	0	6	1	0
5	A	183	0	0	0	0
5	B	127	0	0	0	0
5	C	223	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	240	0	0	0	0
5	E	252	0	0	1	0
5	F	170	0	0	3	0
5	G	133	0	0	1	0
5	H	184	0	0	0	0
5	I	244	0	0	2	0
5	J	255	0	0	0	0
All	All	36577	0	33470	212	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 3.

The worst 5 of 212 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:406:ARG:HH11	1:B:406:ARG:HG2	1.06	1.06
1:F:174:GLU:HG3	1:F:212:ILE:HD11	1.52	0.90
1:B:108:ILE:HD12	1:B:126:LEU:HD11	1.52	0.90
1:A:128:PHE:H	1:A:354:GLN:HE22	1.24	0.86
1:B:406:ARG:NH1	1:B:406:ARG:HG2	1.86	0.86

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	434/444 (98%)	415 (96%)	19 (4%)	0	100	100
1	B	435/444 (98%)	414 (95%)	20 (5%)	1 (0%)	52	61
1	C	435/444 (98%)	419 (96%)	15 (3%)	1 (0%)	52	61
1	D	433/444 (98%)	416 (96%)	16 (4%)	1 (0%)	52	61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	435/444 (98%)	420 (97%)	15 (3%)	0	100	100
1	F	433/444 (98%)	417 (96%)	15 (4%)	1 (0%)	52	61
1	G	433/444 (98%)	416 (96%)	16 (4%)	1 (0%)	52	61
1	H	434/444 (98%)	417 (96%)	17 (4%)	0	100	100
1	I	433/444 (98%)	415 (96%)	16 (4%)	2 (0%)	34	34
1	J	434/444 (98%)	419 (96%)	14 (3%)	1 (0%)	52	61
All	All	4339/4440 (98%)	4168 (96%)	163 (4%)	8 (0%)	52	61

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	284	MET
1	D	284	MET
1	I	284	MET
1	C	284	MET
1	G	284	MET

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	339/355 (96%)	335 (99%)	4 (1%)	78	87
1	B	341/355 (96%)	336 (98%)	5 (2%)	72	82
1	C	342/355 (96%)	338 (99%)	4 (1%)	78	87
1	D	345/355 (97%)	343 (99%)	2 (1%)	90	94
1	E	340/355 (96%)	336 (99%)	4 (1%)	78	87
1	F	336/355 (95%)	331 (98%)	5 (2%)	72	82
1	G	338/355 (95%)	333 (98%)	5 (2%)	72	82
1	H	338/355 (95%)	334 (99%)	4 (1%)	78	87
1	I	343/355 (97%)	338 (98%)	5 (2%)	72	82
1	J	341/355 (96%)	336 (98%)	5 (2%)	72	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3403/3550 (96%)	3360 (99%)	43 (1%)	76 85

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	35	GLU
1	G	59	TYR
1	J	268	ARG
1	F	40	GLU
1	F	191	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	354	GLN
1	F	312	GLN
1	I	389	GLN
1	E	410	GLN
1	F	354	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

10 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	KCX	A	189	1,2	7,11,12	0.49	0	7,12,14	0.99	0
1	KCX	B	189	1,2	7,11,12	0.44	0	7,12,14	0.92	0
1	KCX	C	189	1,2	7,11,12	0.41	0	7,12,14	0.84	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	KCX	D	189	1,2	7,11,12	0.47	0	7,12,14	0.89	1 (14%)
1	KCX	E	189	1,2	7,11,12	0.49	0	7,12,14	0.97	0
1	KCX	F	189	1,2	7,11,12	0.57	0	7,12,14	1.04	0
1	KCX	G	189	1,2	7,11,12	0.41	0	7,12,14	0.95	0
1	KCX	H	189	1,2	7,11,12	0.42	0	7,12,14	0.97	0
1	KCX	I	189	1,2	7,11,12	0.47	0	7,12,14	0.74	0
1	KCX	J	189	1,2	7,11,12	0.44	0	7,12,14	0.92	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	KCX	A	189	1,2	-	0/6/10/12	0/0/0/0
1	KCX	B	189	1,2	-	0/6/10/12	0/0/0/0
1	KCX	C	189	1,2	-	0/6/10/12	0/0/0/0
1	KCX	D	189	1,2	-	0/6/10/12	0/0/0/0
1	KCX	E	189	1,2	-	0/6/10/12	0/0/0/0
1	KCX	F	189	1,2	-	0/6/10/12	0/0/0/0
1	KCX	G	189	1,2	-	0/6/10/12	0/0/0/0
1	KCX	H	189	1,2	-	0/6/10/12	0/0/0/0
1	KCX	I	189	1,2	-	0/6/10/12	0/0/0/0
1	KCX	J	189	1,2	-	0/6/10/12	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	189	KCX	O-C-CA	-2.09	120.05	125.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	189	KCX	1	0
1	B	189	KCX	1	0
1	C	189	KCX	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	189	KCX	1	0
1	E	189	KCX	1	0
1	F	189	KCX	2	0
1	G	189	KCX	1	0
1	H	189	KCX	2	0
1	I	189	KCX	1	0
1	J	189	KCX	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 30 ligands modelled in this entry, 10 are monoatomic - leaving 20 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	CAP	A	502	2	14,20,20	0.59	0	15,31,31	1.17	0
4	EDO	A	503	-	3,3,3	0.53	0	2,2,2	0.22	0
3	CAP	B	502	2	14,20,20	0.64	0	15,31,31	1.12	0
4	EDO	B	503	-	3,3,3	0.44	0	2,2,2	0.45	0
3	CAP	C	502	2	14,20,20	0.58	0	15,31,31	1.15	0
4	EDO	C	503	-	3,3,3	0.51	0	2,2,2	0.33	0
3	CAP	D	502	2	14,20,20	0.68	0	15,31,31	1.14	1 (6%)
4	EDO	D	503	-	3,3,3	0.45	0	2,2,2	0.49	0
3	CAP	E	502	2	14,20,20	0.69	0	15,31,31	1.07	0
4	EDO	E	503	-	3,3,3	0.56	0	2,2,2	0.23	0
3	CAP	F	502	2	14,20,20	0.60	0	15,31,31	1.17	1 (6%)
3	CAP	G	502	2	14,20,20	0.63	0	15,31,31	1.16	0
3	CAP	H	502	2	14,20,20	0.60	0	15,31,31	1.10	0
4	EDO	H	503	-	3,3,3	0.48	0	2,2,2	0.35	0
4	EDO	H	504	-	3,3,3	0.53	0	2,2,2	0.29	0
3	CAP	I	502	2	14,20,20	0.63	0	15,31,31	1.22	3 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	I	503	-	3,3,3	0.51	0	2,2,2	0.29	0
4	EDO	I	504	-	3,3,3	0.55	0	2,2,2	0.23	0
3	CAP	J	502	2	14,20,20	0.67	0	15,31,31	1.08	0
4	EDO	J	503	-	3,3,3	0.68	0	2,2,2	0.24	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CAP	A	502	2	-	0/23/29/29	0/0/0/0
4	EDO	A	503	-	-	0/1/1/1	0/0/0/0
3	CAP	B	502	2	-	0/23/29/29	0/0/0/0
4	EDO	B	503	-	-	0/1/1/1	0/0/0/0
3	CAP	C	502	2	-	0/23/29/29	0/0/0/0
4	EDO	C	503	-	-	0/1/1/1	0/0/0/0
3	CAP	D	502	2	-	0/23/29/29	0/0/0/0
4	EDO	D	503	-	-	0/1/1/1	0/0/0/0
3	CAP	E	502	2	-	0/23/29/29	0/0/0/0
4	EDO	E	503	-	-	0/1/1/1	0/0/0/0
3	CAP	F	502	2	-	0/23/29/29	0/0/0/0
3	CAP	G	502	2	-	0/23/29/29	0/0/0/0
3	CAP	H	502	2	-	0/23/29/29	0/0/0/0
4	EDO	H	503	-	-	0/1/1/1	0/0/0/0
4	EDO	H	504	-	-	0/1/1/1	0/0/0/0
3	CAP	I	502	2	-	0/23/29/29	0/0/0/0
4	EDO	I	503	-	-	0/1/1/1	0/0/0/0
4	EDO	I	504	-	-	0/1/1/1	0/0/0/0
3	CAP	J	502	2	-	0/23/29/29	0/0/0/0
4	EDO	J	503	-	-	0/1/1/1	0/0/0/0

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	502	CAP	O5-P2-O4P	-2.18	101.59	107.14
3	D	502	CAP	O3P-P1-O2P	2.01	115.04	107.38
3	I	502	CAP	O3P-P1-O2P	2.02	115.07	107.38
3	I	502	CAP	O6P-P2-O5P	2.18	115.69	107.38
3	F	502	CAP	O6P-P2-O5P	2.48	116.81	107.38

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	503	EDO	1	0
3	F	502	CAP	1	0
3	H	502	CAP	1	0
4	J	503	EDO	1	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	436/444 (98%)	0.23	24 (5%) 29 32	30, 49, 71, 89	0
1	B	437/444 (98%)	0.54	48 (10%) 7 7	38, 58, 90, 108	0
1	C	437/444 (98%)	0.13	28 (6%) 23 25	28, 43, 76, 95	0
1	D	435/444 (97%)	0.35	34 (7%) 16 17	26, 50, 80, 93	0
1	E	437/444 (98%)	0.19	31 (7%) 19 20	24, 42, 84, 101	0
1	F	435/444 (97%)	0.59	45 (10%) 9 9	32, 62, 94, 123	0
1	G	435/444 (97%)	0.71	63 (14%) 3 4	40, 58, 87, 109	0
1	H	436/444 (98%)	0.45	51 (11%) 6 6	32, 53, 95, 122	0
1	I	435/444 (97%)	0.14	15 (3%) 49 53	25, 46, 77, 92	0
1	J	436/444 (98%)	0.13	26 (5%) 25 27	25, 40, 79, 96	0
All	All	4359/4440 (98%)	0.35	365 (8%) 14 15	24, 50, 85, 123	0

The worst 5 of 365 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	421	LEU	6.4
1	J	414	ALA	5.7
1	A	59	TYR	5.7
1	G	421	LEU	5.6
1	I	9	TYR	5.5

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy

less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
1	KCX	G	189	12/13	0.97	0.12	-	48,49,50,51	0
1	KCX	C	189	12/13	0.98	0.11	-	39,41,42,42	0
1	KCX	I	189	12/13	0.96	0.15	-	26,27,28,29	0
1	KCX	F	189	12/13	0.95	0.18	-	42,43,44,46	0
1	KCX	D	189	12/13	0.98	0.15	-	30,31,32,33	0
1	KCX	B	189	12/13	0.97	0.12	-	48,49,50,51	0
1	KCX	J	189	12/13	0.96	0.10	-	37,38,39,39	0
1	KCX	E	189	12/13	0.97	0.12	-	38,40,41,41	0
1	KCX	H	189	12/13	0.97	0.10	-	48,49,51,52	0
1	KCX	A	189	12/13	0.98	0.14	-	34,35,36,36	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	EDO	J	503	4/4	0.58	0.27	4.28	32,32,33,33	0
4	EDO	I	504	4/4	0.79	0.17	2.06	48,48,49,50	0
4	EDO	H	504	4/4	0.88	0.18	1.74	50,53,53,54	0
4	EDO	E	503	4/4	0.76	0.18	1.40	42,43,44,44	0
4	EDO	A	503	4/4	0.71	0.14	1.01	62,62,63,64	0
2	MG	H	501	1/1	0.93	0.18	0.50	58,58,58,58	0
2	MG	D	501	1/1	0.98	0.16	0.21	31,31,31,31	0
4	EDO	H	503	4/4	0.97	0.16	0.16	29,29,30,32	0
3	CAP	I	502	21/21	0.97	0.14	0.03	31,33,35,36	0
3	CAP	J	502	21/21	0.94	0.15	-0.17	41,47,53,54	0
3	CAP	D	502	21/21	0.98	0.14	-0.23	32,35,38,39	0
2	MG	J	501	1/1	0.91	0.16	-0.24	43,43,43,43	0
3	CAP	A	502	21/21	0.97	0.12	-0.25	37,39,42,43	0
2	MG	A	501	1/1	0.96	0.13	-0.33	36,36,36,36	0
4	EDO	C	503	4/4	0.97	0.13	-0.37	24,25,25,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	CAP	G	502	21/21	0.95	0.15	-0.39	52,56,62,62	0
3	CAP	B	502	21/21	0.95	0.14	-0.42	55,59,65,66	0
3	CAP	E	502	21/21	0.95	0.14	-0.48	45,50,57,58	0
2	MG	I	501	1/1	0.97	0.12	-0.59	28,28,28,28	0
3	CAP	C	502	21/21	0.97	0.12	-0.65	43,47,51,52	0
2	MG	E	501	1/1	0.92	0.16	-0.69	45,45,45,45	0
3	CAP	F	502	21/21	0.96	0.13	-0.75	49,53,56,57	0
2	MG	G	501	1/1	0.97	0.15	-0.87	57,57,57,57	0
3	CAP	H	502	21/21	0.95	0.13	-0.96	56,60,67,68	0
2	MG	F	501	1/1	0.97	0.13	-1.03	46,46,46,46	0
2	MG	B	501	1/1	0.88	0.13	-1.24	59,59,59,59	0
4	EDO	B	503	4/4	0.98	0.13	-1.24	31,31,31,33	0
4	EDO	I	503	4/4	0.95	0.15	-1.28	26,26,26,28	0
4	EDO	D	503	4/4	0.96	0.14	-1.87	28,28,29,30	0
2	MG	C	501	1/1	0.95	0.10	-2.54	46,46,46,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.