



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2025 – 01:02 PM EDT

PDB ID : 4LF2
Title : Hexameric Form II RuBisCO from Rhodospseudomonas palustris, activated and complexed with sulfate and magnesium
Authors : Chan, S.; Satagopan, S.; Sawaya, M.R.; Eisenberg, D.; Tabita, F.R.; Perry, L.J.
Deposited on : 2013-06-26
Resolution : 2.38 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:

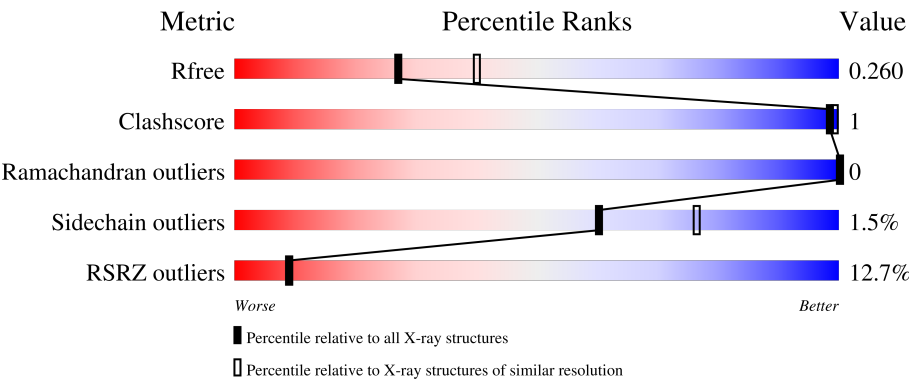
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.4

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.38 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.



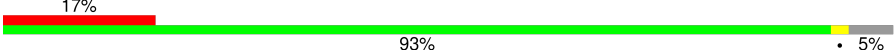
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	6699 (2.40-2.36)
Clashscore	180529	7414 (2.40-2.36)
Ramachandran outliers	177936	7337 (2.40-2.36)
Sidechain outliers	177891	7338 (2.40-2.36)
RSRZ outliers	164620	6699 (2.40-2.36)

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	481	<div><div>7%</div><div>92%</div><div>5%</div></div>
1	B	481	<div><div>12%</div><div>90%</div><div>6%</div></div>
1	C	481	<div><div>13%</div><div>92%</div><div>6%</div></div>
1	D	481	<div><div>8%</div><div>93%</div><div>5%</div></div>
1	E	481	<div><div>15%</div><div>92%</div><div>5%</div></div>

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Mol	Chain	Length	Quality of chain
1	F	481	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: a red segment at the beginning labeled '17%', a long green segment in the middle labeled '93%', and a small yellow segment at the end labeled '5%'. The segments are separated by thin black lines.

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 22617 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	457	Total	C	N	O	S	5	4	0
			3557	2262	614	662	19			
1	B	453	Total	C	N	O	S	3	2	0
			3514	2232	608	655	19			
1	C	453	Total	C	N	O	S	5	1	0
			3513	2231	610	653	19			
1	D	457	Total	C	N	O	S	9	0	0
			3536	2247	613	657	19			
1	E	455	Total	C	N	O	S	6	1	0
			3522	2238	610	656	18			
1	F	456	Total	C	N	O	S	8	2	0
			3537	2249	613	657	18			

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP Q6N0W9
A	-18	GLY	-	expression tag	UNP Q6N0W9
A	-17	SER	-	expression tag	UNP Q6N0W9
A	-16	SER	-	expression tag	UNP Q6N0W9
A	-15	HIS	-	expression tag	UNP Q6N0W9
A	-14	HIS	-	expression tag	UNP Q6N0W9
A	-13	HIS	-	expression tag	UNP Q6N0W9
A	-12	HIS	-	expression tag	UNP Q6N0W9
A	-11	HIS	-	expression tag	UNP Q6N0W9
A	-10	HIS	-	expression tag	UNP Q6N0W9
A	-9	SER	-	expression tag	UNP Q6N0W9
A	-8	SER	-	expression tag	UNP Q6N0W9
A	-7	GLY	-	expression tag	UNP Q6N0W9
A	-6	LEU	-	expression tag	UNP Q6N0W9
A	-5	VAL	-	expression tag	UNP Q6N0W9
A	-4	PRO	-	expression tag	UNP Q6N0W9
A	-3	ARG	-	expression tag	UNP Q6N0W9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q6N0W9
A	-1	SER	-	expression tag	UNP Q6N0W9
A	0	HIS	-	expression tag	UNP Q6N0W9
B	-19	MET	-	initiating methionine	UNP Q6N0W9
B	-18	GLY	-	expression tag	UNP Q6N0W9
B	-17	SER	-	expression tag	UNP Q6N0W9
B	-16	SER	-	expression tag	UNP Q6N0W9
B	-15	HIS	-	expression tag	UNP Q6N0W9
B	-14	HIS	-	expression tag	UNP Q6N0W9
B	-13	HIS	-	expression tag	UNP Q6N0W9
B	-12	HIS	-	expression tag	UNP Q6N0W9
B	-11	HIS	-	expression tag	UNP Q6N0W9
B	-10	HIS	-	expression tag	UNP Q6N0W9
B	-9	SER	-	expression tag	UNP Q6N0W9
B	-8	SER	-	expression tag	UNP Q6N0W9
B	-7	GLY	-	expression tag	UNP Q6N0W9
B	-6	LEU	-	expression tag	UNP Q6N0W9
B	-5	VAL	-	expression tag	UNP Q6N0W9
B	-4	PRO	-	expression tag	UNP Q6N0W9
B	-3	ARG	-	expression tag	UNP Q6N0W9
B	-2	GLY	-	expression tag	UNP Q6N0W9
B	-1	SER	-	expression tag	UNP Q6N0W9
B	0	HIS	-	expression tag	UNP Q6N0W9
C	-19	MET	-	initiating methionine	UNP Q6N0W9
C	-18	GLY	-	expression tag	UNP Q6N0W9
C	-17	SER	-	expression tag	UNP Q6N0W9
C	-16	SER	-	expression tag	UNP Q6N0W9
C	-15	HIS	-	expression tag	UNP Q6N0W9
C	-14	HIS	-	expression tag	UNP Q6N0W9
C	-13	HIS	-	expression tag	UNP Q6N0W9
C	-12	HIS	-	expression tag	UNP Q6N0W9
C	-11	HIS	-	expression tag	UNP Q6N0W9
C	-10	HIS	-	expression tag	UNP Q6N0W9
C	-9	SER	-	expression tag	UNP Q6N0W9
C	-8	SER	-	expression tag	UNP Q6N0W9
C	-7	GLY	-	expression tag	UNP Q6N0W9
C	-6	LEU	-	expression tag	UNP Q6N0W9
C	-5	VAL	-	expression tag	UNP Q6N0W9
C	-4	PRO	-	expression tag	UNP Q6N0W9
C	-3	ARG	-	expression tag	UNP Q6N0W9
C	-2	GLY	-	expression tag	UNP Q6N0W9
C	-1	SER	-	expression tag	UNP Q6N0W9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	0	HIS	-	expression tag	UNP Q6N0W9
D	-19	MET	-	initiating methionine	UNP Q6N0W9
D	-18	GLY	-	expression tag	UNP Q6N0W9
D	-17	SER	-	expression tag	UNP Q6N0W9
D	-16	SER	-	expression tag	UNP Q6N0W9
D	-15	HIS	-	expression tag	UNP Q6N0W9
D	-14	HIS	-	expression tag	UNP Q6N0W9
D	-13	HIS	-	expression tag	UNP Q6N0W9
D	-12	HIS	-	expression tag	UNP Q6N0W9
D	-11	HIS	-	expression tag	UNP Q6N0W9
D	-10	HIS	-	expression tag	UNP Q6N0W9
D	-9	SER	-	expression tag	UNP Q6N0W9
D	-8	SER	-	expression tag	UNP Q6N0W9
D	-7	GLY	-	expression tag	UNP Q6N0W9
D	-6	LEU	-	expression tag	UNP Q6N0W9
D	-5	VAL	-	expression tag	UNP Q6N0W9
D	-4	PRO	-	expression tag	UNP Q6N0W9
D	-3	ARG	-	expression tag	UNP Q6N0W9
D	-2	GLY	-	expression tag	UNP Q6N0W9
D	-1	SER	-	expression tag	UNP Q6N0W9
D	0	HIS	-	expression tag	UNP Q6N0W9
E	-19	MET	-	initiating methionine	UNP Q6N0W9
E	-18	GLY	-	expression tag	UNP Q6N0W9
E	-17	SER	-	expression tag	UNP Q6N0W9
E	-16	SER	-	expression tag	UNP Q6N0W9
E	-15	HIS	-	expression tag	UNP Q6N0W9
E	-14	HIS	-	expression tag	UNP Q6N0W9
E	-13	HIS	-	expression tag	UNP Q6N0W9
E	-12	HIS	-	expression tag	UNP Q6N0W9
E	-11	HIS	-	expression tag	UNP Q6N0W9
E	-10	HIS	-	expression tag	UNP Q6N0W9
E	-9	SER	-	expression tag	UNP Q6N0W9
E	-8	SER	-	expression tag	UNP Q6N0W9
E	-7	GLY	-	expression tag	UNP Q6N0W9
E	-6	LEU	-	expression tag	UNP Q6N0W9
E	-5	VAL	-	expression tag	UNP Q6N0W9
E	-4	PRO	-	expression tag	UNP Q6N0W9
E	-3	ARG	-	expression tag	UNP Q6N0W9
E	-2	GLY	-	expression tag	UNP Q6N0W9
E	-1	SER	-	expression tag	UNP Q6N0W9
E	0	HIS	-	expression tag	UNP Q6N0W9
F	-19	MET	-	initiating methionine	UNP Q6N0W9

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-18	GLY	-	expression tag	UNP Q6N0W9
F	-17	SER	-	expression tag	UNP Q6N0W9
F	-16	SER	-	expression tag	UNP Q6N0W9
F	-15	HIS	-	expression tag	UNP Q6N0W9
F	-14	HIS	-	expression tag	UNP Q6N0W9
F	-13	HIS	-	expression tag	UNP Q6N0W9
F	-12	HIS	-	expression tag	UNP Q6N0W9
F	-11	HIS	-	expression tag	UNP Q6N0W9
F	-10	HIS	-	expression tag	UNP Q6N0W9
F	-9	SER	-	expression tag	UNP Q6N0W9
F	-8	SER	-	expression tag	UNP Q6N0W9
F	-7	GLY	-	expression tag	UNP Q6N0W9
F	-6	LEU	-	expression tag	UNP Q6N0W9
F	-5	VAL	-	expression tag	UNP Q6N0W9
F	-4	PRO	-	expression tag	UNP Q6N0W9
F	-3	ARG	-	expression tag	UNP Q6N0W9
F	-2	GLY	-	expression tag	UNP Q6N0W9
F	-1	SER	-	expression tag	UNP Q6N0W9
F	0	HIS	-	expression tag	UNP Q6N0W9

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

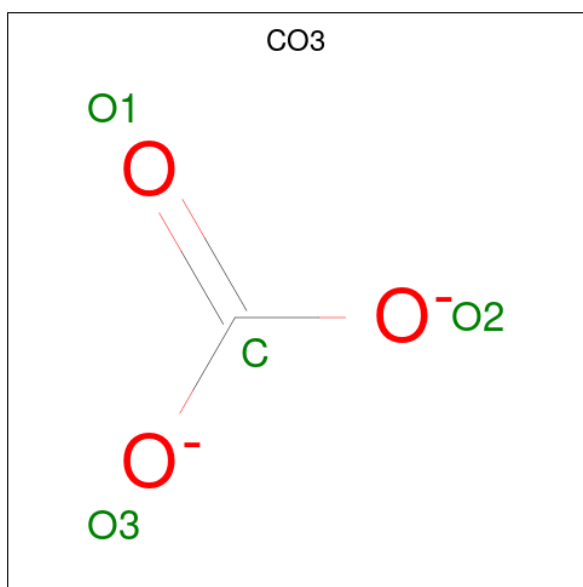
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mg 1 1	0	0
2	B	1	Total Mg 1 1	0	0
2	C	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is CARBONATE ION (three-letter code: CO3) (formula: CO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	1	3		
4	B	1	Total	C	O	0	0
			4	1	3		
4	C	1	Total	C	O	0	0
			4	1	3		

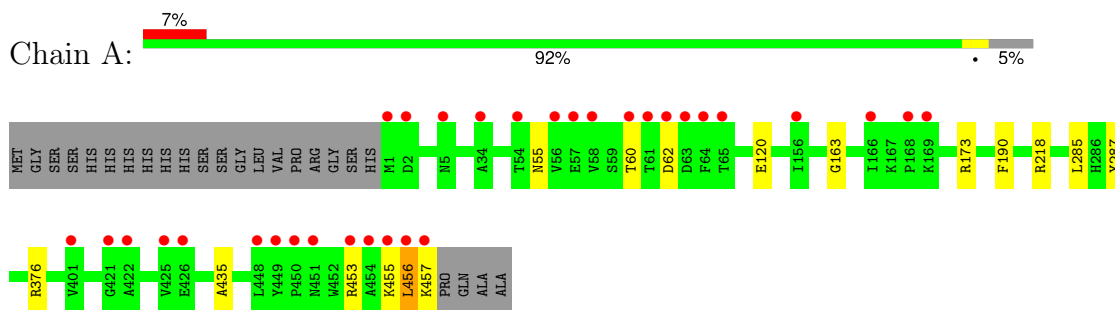
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	239	Total	O	0	0
			239	239		
5	B	243	Total	O	0	0
			243	243		
5	C	254	Total	O	0	0
			254	254		
5	D	245	Total	O	0	0
			245	245		
5	E	197	Total	O	0	0
			197	197		
5	F	184	Total	O	0	0
			184	184		

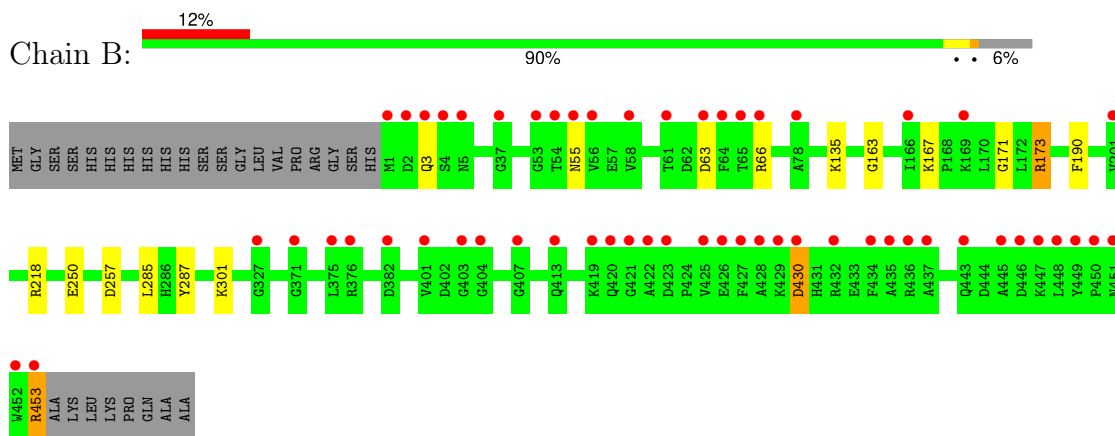
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

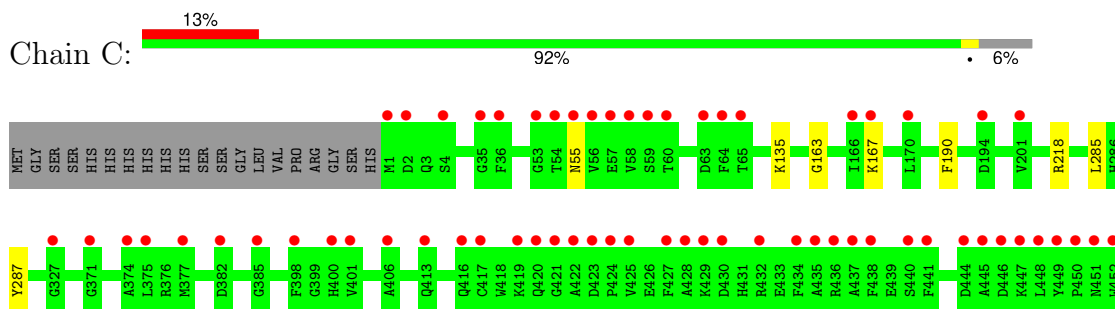
- Molecule 1: Ribulose biphosphate carboxylase

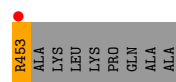


- Molecule 1: Ribulose biphosphate carboxylase

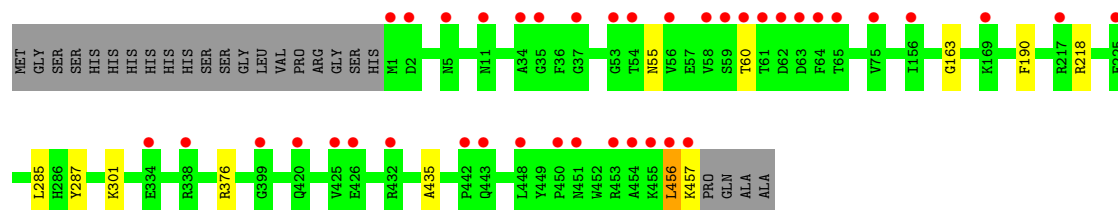


- Molecule 1: Ribulose biphosphate carboxylase

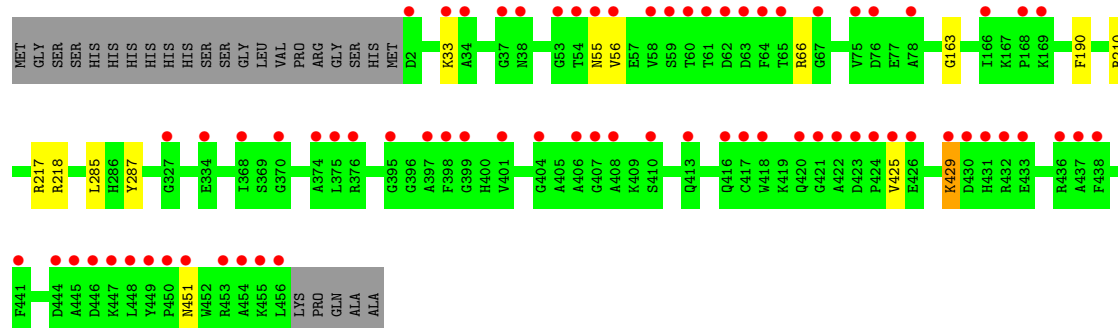
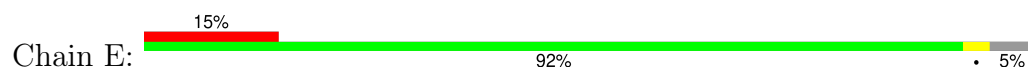




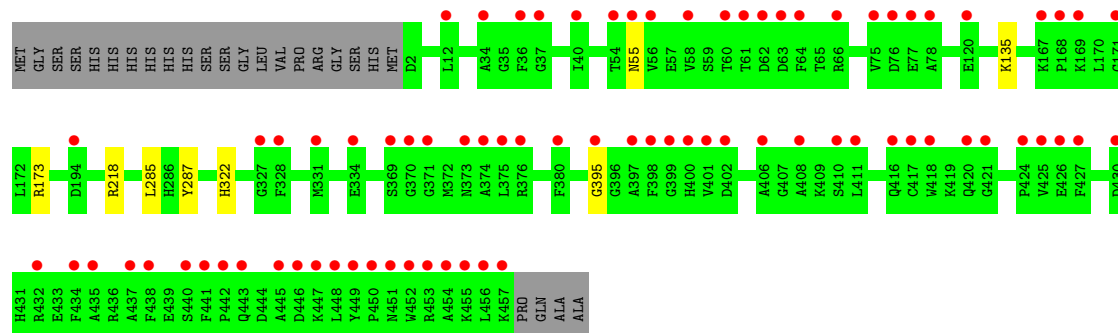
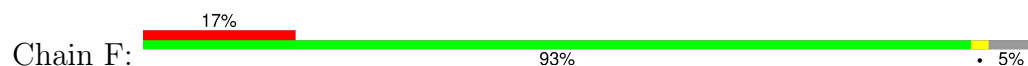
- Molecule 1: Ribulose biphosphate carboxylase



- Molecule 1: Ribulose biphosphate carboxylase



- Molecule 1: Ribulose biphosphate carboxylase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	74.22Å 99.78Å 100.00Å 67.30° 71.28° 86.63°	Depositor
Resolution (Å)	87.43 – 2.38 87.43 – 2.38	Depositor EDS
% Data completeness (in resolution range)	96.6 (87.43-2.38) 96.6 (87.43-2.38)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 1.86Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.203 , 0.258 0.207 , 0.260	Depositor DCC
R_{free} test set	4851 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	17.1	Xtrriage
Anisotropy	0.156	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 43.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	22617	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 23.72 % 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 4.4135e-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 ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, CO3, KCX, MG

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	0.53	0/3645	0.78	5/4929 (0.1%)
1	B	0.54	0/3596	0.79	3/4866 (0.1%)
1	C	0.54	0/3592	0.79	3/4860 (0.1%)
1	D	0.52	0/3612	0.75	2/4886 (0.0%)
1	E	0.54	0/3601	0.78	4/4873 (0.1%)
1	F	0.54	0/3619	0.78	2/4895 (0.0%)
All	All	0.53	0/21665	0.78	19/29309 (0.1%)

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	453	ARG	NE-CZ-NH1	10.42	125.51	120.30
1	B	453	ARG	NE-CZ-NH1	9.51	125.06	120.30
1	A	453	ARG	NE-CZ-NH2	7.36	123.98	120.30
1	A	173	ARG	NE-CZ-NH1	6.26	123.43	120.30
1	F	218	ARG	NE-CZ-NH1	6.10	123.35	120.30
1	A	218	ARG	NE-CZ-NH1	6.08	123.34	120.30
1	B	218	ARG	NE-CZ-NH1	5.86	123.23	120.30
1	C	218	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	D	218	ARG	NE-CZ-NH1	5.60	123.10	120.30
1	E	66	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	B	453	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	A	376	ARG	NE-CZ-NH1	5.32	122.96	120.30
1	F	173	ARG	NE-CZ-NH1	5.27	122.93	120.30
1	A	453	ARG	NE-CZ-NH1	-5.26	117.67	120.30
1	E	218	ARG	NE-CZ-NH1	5.23	122.92	120.30
1	E	217	ARG	NE-CZ-NH1	5.23	122.91	120.30
1	D	376	ARG	NE-CZ-NH1	5.19	122.89	120.30
1	E	210	ARG	NE-CZ-NH1	5.08	122.84	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	453	ARG	CD-NE-CZ	5.02	130.63	123.60

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	3557	0	3444	4	0
1	B	3514	0	3385	10	0
1	C	3513	0	3385	3	0
1	D	3536	0	3414	4	0
1	E	3522	0	3394	3	0
1	F	3537	0	3420	3	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
3	A	10	0	0	0	0
3	B	10	0	0	0	0
3	C	10	0	0	0	0
3	D	10	0	0	0	0
3	E	10	0	0	0	0
3	F	10	0	0	0	0
4	A	4	0	0	0	0
4	B	4	0	0	0	0
4	C	4	0	0	0	0
5	A	239	0	0	0	0
5	B	243	0	0	2	0
5	C	254	0	0	0	0
5	D	245	0	0	1	0
5	E	197	0	0	0	0
5	F	184	0	0	2	0
All	All	22617	0	20442	22	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 1.

All (22) 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:3[B]:GLN:HE21	1:B:3[B]:GLN:HA	1.62	0.64
1:A:62:ASP:OD2	1:B:173:ARG:NH2	2.30	0.64
1:B:135:LYS:NZ	5:B:784:HOH:O	2.33	0.62
1:D:301:LYS:NZ	5:D:935:HOH:O	2.33	0.59
1:E:425:VAL:O	1:E:429:LYS:NZ	2.38	0.56
1:E:56:VAL:HG11	1:F:395:GLY:HA3	1.88	0.54
1:F:135:LYS:NZ	5:F:902:HOH:O	2.43	0.51
1:A:435:ALA:HB1	1:A:456:LEU:HD21	1.96	0.47
1:A:60:THR:OG1	1:B:167:LYS:O	2.22	0.46
1:C:167:LYS:O	1:D:60:THR:OG1	2.23	0.46
1:B:301:LYS:NZ	5:B:767:HOH:O	2.34	0.45
1:B:430:ASP:OD1	1:B:430:ASP:N	2.51	0.44
1:F:322:HIS:ND1	5:F:904:HOH:O	2.32	0.43
1:A:163:GLY:HA2	1:A:190:PHE:O	2.20	0.42
1:B:171:GLY:O	1:B:173:ARG:NH1	2.52	0.42
1:D:163:GLY:HA2	1:D:190:PHE:O	2.20	0.42
1:B:63:ASP:OD1	1:B:66:ARG:NH1	2.53	0.42
1:D:435:ALA:HB1	1:D:456:LEU:HD21	2.01	0.41
1:B:163:GLY:HA2	1:B:190:PHE:O	2.21	0.41
1:C:163:GLY:HA2	1:C:190:PHE:O	2.21	0.41
1:E:163:GLY:HA2	1:E:190:PHE:O	2.21	0.41
1:B:257:ASP:OD2	1:C:135:LYS:NZ	2.47	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	458/481 (95%)	447 (98%)	11 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	452/481 (94%)	442 (98%)	10 (2%)	0	100	100
1	C	451/481 (94%)	442 (98%)	9 (2%)	0	100	100
1	D	454/481 (94%)	444 (98%)	10 (2%)	0	100	100
1	E	453/481 (94%)	441 (97%)	12 (3%)	0	100	100
1	F	455/481 (95%)	443 (97%)	12 (3%)	0	100	100
All	All	2723/2886 (94%)	2659 (98%)	64 (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	357/372 (96%)	350 (98%)	7 (2%)	50	68
1	B	352/372 (95%)	345 (98%)	7 (2%)	50	68
1	C	351/372 (94%)	347 (99%)	4 (1%)	70	83
1	D	353/372 (95%)	348 (99%)	5 (1%)	62	78
1	E	352/372 (95%)	346 (98%)	6 (2%)	56	73
1	F	354/372 (95%)	351 (99%)	3 (1%)	79	89
All	All	2119/2232 (95%)	2087 (98%)	32 (2%)	60	76

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	ASN
1	A	120	GLU
1	A	285	LEU
1	A	287	TYR
1	A	455	LYS
1	A	456	LEU
1	A	457	LYS
1	B	55	ASN

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Mol	Chain	Res	Type
1	B	173	ARG
1	B	250	GLU
1	B	285	LEU
1	B	287	TYR
1	B	430	ASP
1	B	453	ARG
1	C	55	ASN
1	C	285	LEU
1	C	287	TYR
1	C	453	ARG
1	D	55	ASN
1	D	285	LEU
1	D	287	TYR
1	D	456	LEU
1	D	457	LYS
1	E	33	LYS
1	E	55	ASN
1	E	285	LEU
1	E	287	TYR
1	E	429	LYS
1	E	451	ASN
1	F	55	ASN
1	F	285	LEU
1	F	287	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	55	ASN
1	F	55	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 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	B	192	1,2	10,11,12	0.51	0	6,12,14	0.53	0
1	KCX	A	192	1,2	10,11,12	0.56	0	6,12,14	0.50	0
1	KCX	E	192	1	10,11,12	0.52	0	6,12,14	0.51	0
1	KCX	C	192	1	10,11,12	0.51	0	6,12,14	0.48	0
1	KCX	D	192	1,2	10,11,12	0.56	0	6,12,14	0.49	0
1	KCX	F	192	1	10,11,12	0.61	0	6,12,14	0.46	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	B	192	1,2	-	0/9/10/12	-
1	KCX	A	192	1,2	-	0/9/10/12	-
1	KCX	E	192	1	-	0/9/10/12	-
1	KCX	C	192	1	-	0/9/10/12	-
1	KCX	D	192	1,2	-	0/9/10/12	-
1	KCX	F	192	1	-	0/9/10/12	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 19 ligands modelled in this entry, 4 are monoatomic - leaving 15 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	$\# Z > 2$
4	CO3	C	604	-	3,3,3	1.10	0	2,3,3	0.23	0
3	SO4	E	701	-	4,4,4	0.39	0	6,6,6	0.32	0
3	SO4	C	603	-	4,4,4	0.42	0	6,6,6	0.11	0
3	SO4	A	602	-	4,4,4	0.46	0	6,6,6	0.50	0
4	CO3	A	604	-	3,3,3	1.13	0	2,3,3	0.15	0
4	CO3	B	604	-	3,3,3	1.13	0	2,3,3	0.14	0
3	SO4	B	602	-	4,4,4	0.40	0	6,6,6	0.35	0
3	SO4	C	602	-	4,4,4	0.45	0	6,6,6	0.41	0
3	SO4	D	602	-	4,4,4	0.38	0	6,6,6	0.58	0
3	SO4	D	603	-	4,4,4	0.39	0	6,6,6	0.10	0
3	SO4	A	603	-	4,4,4	0.41	0	6,6,6	0.21	0
3	SO4	E	702	-	4,4,4	0.37	0	6,6,6	0.13	0
3	SO4	B	603	-	4,4,4	0.40	0	6,6,6	0.26	0
3	SO4	F	701	-	4,4,4	0.33	0	6,6,6	0.49	0
3	SO4	F	702	-	4,4,4	0.42	0	6,6,6	0.08	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	456/481 (94%)	0.41	32 (7%)	24 24	4, 17, 54, 90	6 (1%)
1	B	452/481 (93%)	0.62	56 (12%)	9 9	5, 16, 61, 92	3 (0%)
1	C	452/481 (93%)	0.65	64 (14%)	7 7	4, 16, 61, 102	3 (0%)
1	D	456/481 (94%)	0.43	40 (8%)	17 17	4, 16, 50, 130	6 (1%)
1	E	454/481 (94%)	0.85	73 (16%)	5 6	4, 21, 74, 122	3 (0%)
1	F	455/481 (94%)	0.85	80 (17%)	4 5	5, 21, 69, 112	5 (1%)
All	All	2725/2886 (94%)	0.63	345 (12%)	9 9	4, 18, 63, 130	26 (0%)

All (345) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	450	PRO	6.6
1	C	401	VAL	6.6
1	D	61	THR	6.5
1	B	448	LEU	6.4
1	F	401	VAL	6.4
1	F	437	ALA	6.1
1	F	448	LEU	5.8
1	F	456	LEU	5.8
1	D	62	ASP	5.6
1	C	434	PHE	5.6
1	D	454	ALA	5.6
1	B	58	VAL	5.5
1	E	399	GLY	5.5
1	E	448	LEU	5.5
1	D	451	ASN	5.4
1	A	454	ALA	5.3
1	A	61	THR	5.2
1	C	440	SER	5.0
1	D	456	LEU	5.0

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Mol	Chain	Res	Type	RSRZ
1	C	435	ALA	5.0
1	C	375	LEU	4.9
1	F	449	TYR	4.8
1	C	420	GLN	4.7
1	F	399	GLY	4.6
1	E	437	ALA	4.6
1	B	53	GLY	4.5
1	D	54	THR	4.5
1	F	451	ASN	4.5
1	E	60	THR	4.4
1	B	64	PHE	4.4
1	B	425	VAL	4.4
1	C	2	ASP	4.3
1	E	54	THR	4.3
1	E	63	ASP	4.3
1	F	450	PRO	4.3
1	E	456	LEU	4.3
1	D	63	ASP	4.3
1	A	169	LYS	4.3
1	E	454	ALA	4.2
1	F	425	VAL	4.2
1	C	451	ASN	4.2
1	E	421	GLY	4.2
1	F	370	GLY	4.1
1	F	441	PHE	4.1
1	F	56	VAL	4.1
1	F	454	ALA	4.1
1	B	434	PHE	4.0
1	D	64	PHE	4.0
1	A	58	VAL	4.0
1	F	447	LYS	4.0
1	E	374	ALA	3.9
1	E	426	GLU	3.9
1	D	457	LYS	3.9
1	E	61	THR	3.9
1	D	420	GLN	3.8
1	A	421	GLY	3.8
1	E	53	GLY	3.8
1	F	395	GLY	3.8
1	B	55	ASN	3.7
1	F	438	PHE	3.7
1	A	56	VAL	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	56	VAL	3.7
1	B	420	GLN	3.7
1	E	447	LYS	3.7
1	B	422	ALA	3.7
1	C	424	PRO	3.7
1	E	420	GLN	3.7
1	C	445	ALA	3.7
1	F	424	PRO	3.6
1	C	327	GLY	3.6
1	E	64	PHE	3.6
1	C	421	GLY	3.6
1	A	62	ASP	3.6
1	F	455	LYS	3.6
1	E	55	ASN	3.6
1	F	430	ASP	3.6
1	F	434	PHE	3.6
1	E	425	VAL	3.6
1	D	59	SER	3.6
1	E	418	TRP	3.6
1	A	456	LEU	3.6
1	F	37	GLY	3.5
1	F	457	LYS	3.5
1	B	449	TYR	3.5
1	B	54	THR	3.5
1	C	423	ASP	3.5
1	F	61	THR	3.5
1	D	455	LYS	3.5
1	F	446	ASP	3.4
1	E	406	ALA	3.4
1	B	423	ASP	3.4
1	B	166	ILE	3.4
1	B	451	ASN	3.4
1	E	370	GLY	3.4
1	B	426	GLU	3.4
1	F	60	THR	3.4
1	F	442	PRO	3.4
1	C	371	GLY	3.4
1	C	452	TRP	3.3
1	E	37	GLY	3.3
1	D	60	THR	3.3
1	A	64	PHE	3.3
1	F	421	GLY	3.3

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Mol	Chain	Res	Type	RSRZ
1	C	448	LEU	3.3
1	C	447	LYS	3.2
1	E	445	ALA	3.2
1	F	435	ALA	3.2
1	F	169	LYS	3.2
1	A	60	THR	3.2
1	D	1	MET	3.2
1	B	327	GLY	3.2
1	B	401	VAL	3.2
1	E	376	ARG	3.2
1	B	446	ASP	3.2
1	F	63	ASP	3.2
1	B	5	ASN	3.1
1	F	168	PRO	3.1
1	B	435	ALA	3.1
1	E	417	CYS	3.1
1	B	419	LYS	3.1
1	E	56	VAL	3.1
1	E	449	TYR	3.1
1	A	54	THR	3.1
1	C	166	ILE	3.1
1	C	441	PHE	3.1
1	C	425	VAL	3.1
1	B	2	ASP	3.1
1	A	448	LEU	3.0
1	C	53	GLY	3.0
1	D	56	VAL	3.0
1	E	58	VAL	3.0
1	E	423	ASP	3.0
1	E	166	ILE	3.0
1	B	63	ASP	3.0
1	B	428	ALA	3.0
1	D	156	ILE	3.0
1	A	1	MET	3.0
1	C	1	MET	3.0
1	C	438	PHE	3.0
1	E	446	ASP	3.0
1	B	450	PRO	3.0
1	D	5	ASN	3.0
1	E	59	SER	3.0
1	B	201	VAL	3.0
1	F	402	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	422	ALA	3.0
1	B	375	LEU	2.9
1	B	4	SER	2.9
1	C	59	SER	2.9
1	E	2	ASP	2.9
1	C	437	ALA	2.9
1	E	78	ALA	2.9
1	E	422	ALA	2.9
1	C	427	PHE	2.9
1	A	426	GLU	2.9
1	D	65	THR	2.9
1	E	327	GLY	2.9
1	D	432	ARG	2.9
1	B	452	TRP	2.9
1	C	36	PHE	2.9
1	F	420	GLN	2.9
1	C	417	CYS	2.9
1	E	62	ASP	2.9
1	D	426	GLU	2.9
1	E	451	ASN	2.9
1	C	4	SER	2.9
1	F	410	SER	2.9
1	F	440	SER	2.9
1	F	398	PHE	2.8
1	F	427	PHE	2.8
1	C	56	VAL	2.8
1	D	450	PRO	2.8
1	E	168	PRO	2.8
1	D	334	GLU	2.8
1	A	451	ASN	2.8
1	B	429	LYS	2.8
1	F	406	ALA	2.8
1	F	66	ARG	2.8
1	D	37	GLY	2.8
1	A	57	GLU	2.8
1	A	450	PRO	2.8
1	E	424	PRO	2.8
1	E	444	ASP	2.8
1	F	62	ASP	2.8
1	F	194	ASP	2.8
1	B	445	ALA	2.8
1	D	448	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	457	LYS	2.8
1	E	438	PHE	2.8
1	E	401	VAL	2.8
1	F	75	VAL	2.8
1	F	452	TRP	2.8
1	B	447	LYS	2.7
1	C	429	LYS	2.7
1	C	430	ASP	2.7
1	E	34	ALA	2.7
1	F	417	CYS	2.7
1	E	404	GLY	2.7
1	B	1	MET	2.7
1	B	453	ARG	2.7
1	F	120	GLU	2.7
1	A	63	ASP	2.7
1	A	425	VAL	2.7
1	F	34	ALA	2.7
1	F	397	ALA	2.7
1	E	429	LYS	2.7
1	A	34	ALA	2.7
1	C	54	THR	2.7
1	E	334	GLU	2.7
1	D	2	ASP	2.7
1	A	401	VAL	2.7
1	C	64	PHE	2.7
1	A	422	ALA	2.7
1	B	66	ARG	2.6
1	F	54	THR	2.6
1	E	76	ASP	2.6
1	F	328	PHE	2.6
1	E	397	ALA	2.6
1	F	334	GLU	2.6
1	B	432	ARG	2.6
1	E	398	PHE	2.6
1	C	406	ALA	2.6
1	C	60	THR	2.6
1	E	455	LYS	2.6
1	F	36	PHE	2.6
1	C	57	GLU	2.6
1	E	375	LEU	2.6
1	C	416	GLN	2.6
1	F	418	TRP	2.6

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Mol	Chain	Res	Type	RSRZ
1	E	430	ASP	2.6
1	D	217	ARG	2.6
1	C	35	GLY	2.5
1	C	374	ALA	2.5
1	D	58	VAL	2.5
1	B	61	THR	2.5
1	F	375	LEU	2.5
1	C	413	GLN	2.5
1	E	436	ARG	2.5
1	F	376	ARG	2.5
1	E	33	LYS	2.5
1	B	407	GLY	2.5
1	D	425	VAL	2.5
1	F	58	VAL	2.5
1	F	64	PHE	2.5
1	F	12	LEU	2.5
1	C	453	ARG	2.5
1	F	369	SER	2.5
1	C	444	ASP	2.5
1	C	385	GLY	2.5
1	E	395	GLY	2.5
1	F	408	ALA	2.5
1	D	11	ASN	2.5
1	E	38	ASN	2.5
1	F	400	HIS	2.5
1	D	453	ARG	2.5
1	E	416	GLN	2.5
1	C	382	ASP	2.4
1	F	77	GLU	2.4
1	F	371	GLY	2.4
1	F	432	ARG	2.4
1	A	168	PRO	2.4
1	C	449	TYR	2.4
1	E	368	ILE	2.4
1	C	194	ASP	2.4
1	C	446	ASP	2.4
1	E	453	ARG	2.4
1	C	201	VAL	2.4
1	F	416	GLN	2.4
1	F	445	ALA	2.4
1	C	58	VAL	2.4
1	E	441	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	377	MET	2.4
1	B	404	GLY	2.4
1	E	67	GLY	2.4
1	F	453	ARG	2.4
1	C	55	ASN	2.4
1	D	34	ALA	2.4
1	E	75	VAL	2.3
1	E	410	SER	2.3
1	F	76	ASP	2.3
1	B	371	GLY	2.3
1	E	413	GLN	2.3
1	F	327	GLY	2.3
1	B	437	ALA	2.3
1	B	427	PHE	2.3
1	D	75	VAL	2.3
1	E	450	PRO	2.3
1	A	453	ARG	2.3
1	A	449	TYR	2.3
1	B	403	GLY	2.3
1	A	5	ASN	2.3
1	C	170	LEU	2.3
1	F	426	GLU	2.3
1	C	398	PHE	2.3
1	D	35	GLY	2.3
1	E	407	GLY	2.3
1	B	169	LYS	2.3
1	D	169	LYS	2.3
1	A	2	ASP	2.3
1	A	166	ILE	2.3
1	D	53	GLY	2.3
1	D	225	GLU	2.2
1	C	65	THR	2.2
1	C	436	ARG	2.2
1	F	40	ILE	2.2
1	B	37	GLY	2.2
1	C	419	LYS	2.2
1	B	436	ARG	2.2
1	D	338	ARG	2.2
1	E	408	ALA	2.2
1	C	400	HIS	2.2
1	B	413	GLN	2.2
1	D	443	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	421	GLY	2.2
1	F	55	ASN	2.2
1	A	65	THR	2.2
1	B	430	ASP	2.2
1	B	376	ARG	2.2
1	F	411	LEU	2.2
1	B	65	THR	2.2
1	C	428	ALA	2.1
1	A	455	LYS	2.1
1	E	65	THR	2.1
1	F	380	PHE	2.1
1	D	399	GLY	2.1
1	B	443	GLN	2.1
1	E	169	LYS	2.1
1	F	443	GLN	2.1
1	F	374	ALA	2.1
1	E	431	HIS	2.1
1	F	78	ALA	2.1
1	E	433	GLU	2.1
1	C	432	ARG	2.1
1	C	63	ASP	2.1
1	F	167	LYS	2.1
1	B	3[A]	GLN	2.1
1	B	78	ALA	2.1
1	E	432	ARG	2.0
1	B	382	ASP	2.0
1	F	171	GLY	2.0
1	C	167	LYS	2.0
1	A	156	ILE	2.0
1	D	442	PRO	2.0
1	F	373	ASN	2.0
1	F	331	MET	2.0

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. 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	B-factors(Å ²)	Q<0.9
1	KCX	B	192	12/13	0.88	0.13	14,25,34,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	KCX	C	192	12/13	0.90	0.10	13,22,36,52	0
1	KCX	D	192	12/13	0.90	0.10	15,18,28,31	0
1	KCX	F	192	12/13	0.90	0.10	16,25,45,53	0
1	KCX	E	192	12/13	0.91	0.10	11,17,36,42	0
1	KCX	A	192	12/13	0.92	0.08	11,17,26,28	0

6.3 Carbohydrates [i](#)

There are no monosaccharides 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. 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	B-factors(\AA^2)	Q<0.9
2	MG	C	601	1/1	0.72	0.14	52,52,52,52	0
4	CO3	C	604	4/4	0.81	0.14	28,31,46,64	0
3	SO4	B	602	5/5	0.86	0.13	18,29,42,53	0
3	SO4	C	602	5/5	0.87	0.12	15,31,34,44	0
3	SO4	E	701	5/5	0.87	0.15	25,37,47,72	0
3	SO4	F	702	5/5	0.87	0.11	39,51,62,70	0
2	MG	B	601	1/1	0.87	0.15	62,62,62,62	0
3	SO4	A	602	5/5	0.88	0.14	15,19,39,44	0
4	CO3	B	604	4/4	0.88	0.11	37,38,40,70	0
3	SO4	F	701	5/5	0.88	0.14	35,38,45,63	0
2	MG	A	601	1/1	0.89	0.07	34,34,34,34	0
4	CO3	A	604	4/4	0.89	0.10	29,43,50,57	0
3	SO4	C	603	5/5	0.90	0.11	42,43,59,79	0
3	SO4	E	702	5/5	0.91	0.12	39,44,50,52	0
3	SO4	D	602	5/5	0.91	0.11	15,23,46,47	0
3	SO4	B	603	5/5	0.93	0.15	29,36,44,56	0
2	MG	D	601	1/1	0.95	0.06	44,44,44,44	0
3	SO4	A	603	5/5	0.98	0.06	17,29,32,35	0
3	SO4	D	603	5/5	0.99	0.07	18,24,31,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.