



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:15 PM GMT

PDB ID : 4O9C
Title : Crystal structure of Beta-ketothiolase (PhaA) from Ralstonia eutropha H16
Authors : Kim, E.J.; Kim, J.; Kim, S.; Kim, K.J.
Deposited on : 2014-01-02
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<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

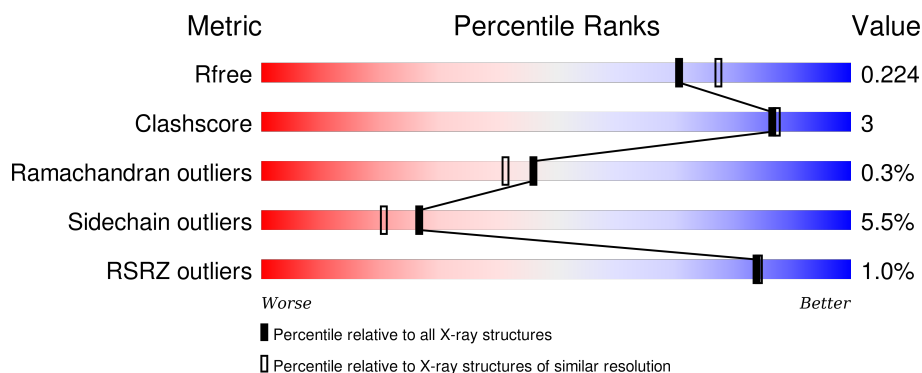
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.




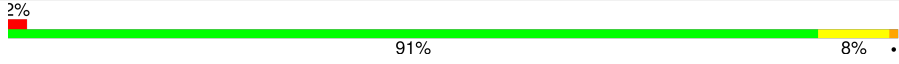

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	393	<div> <div></div> <div>89% 10% .</div> </div>
1	B	393	<div> <div></div> <div>91% 9% .</div> </div>
1	C	393	<div> <div></div> <div>89% 10% .</div> </div>
1	D	393	<div> <div></div> <div>90% 9% .</div> </div>
1	E	393	<div> <div></div> <div>87% 12% .</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	393	
1	G	393	
1	H	393	

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
2	COA	C	401	-	-	-	X

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 23650 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 Acetyl-CoA acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	393	Total	C	N	O	S	0	0	0
			2835	1774	502	539	20			
1	B	393	Total	C	N	O	S	0	0	0
			2835	1774	502	539	20			
1	C	393	Total	C	N	O	S	0	0	0
			2835	1774	502	539	20			
1	D	393	Total	C	N	O	S	0	0	0
			2835	1774	502	539	20			
1	E	393	Total	C	N	O	S	0	0	0
			2835	1774	502	539	20			
1	F	393	Total	C	N	O	S	0	0	0
			2835	1774	502	539	20			
1	G	393	Total	C	N	O	S	0	0	0
			2835	1774	502	539	20			
1	H	393	Total	C	N	O	S	0	0	0
			2835	1774	502	539	20			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	88	SER	CYS	ENGINEERED MUTATION	UNP P14611
B	88	SER	CYS	ENGINEERED MUTATION	UNP P14611
C	88	SER	CYS	ENGINEERED MUTATION	UNP P14611
D	88	SER	CYS	ENGINEERED MUTATION	UNP P14611
E	88	SER	CYS	ENGINEERED MUTATION	UNP P14611
F	88	SER	CYS	ENGINEERED MUTATION	UNP P14611
G	88	SER	CYS	ENGINEERED MUTATION	UNP P14611
H	88	SER	CYS	ENGINEERED MUTATION	UNP P14611

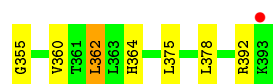
- Molecule 2 is COENZYME A (three-letter code: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S).



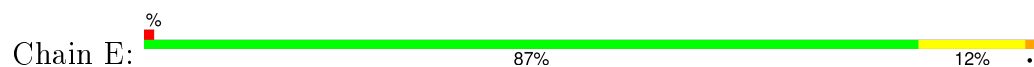
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	C	1	48	21	7	16	3	0	0

- Molecule 3 is water.

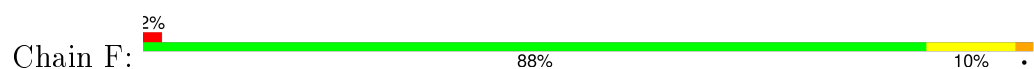
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	131	Total	O	0	0
			131	131		
3	B	119	Total	O	0	0
			119	119		
3	C	134	Total	O	0	0
			134	134		
3	D	122	Total	O	0	0
			122	122		
3	E	114	Total	O	0	0
			114	114		
3	F	98	Total	O	0	0
			98	98		
3	G	95	Total	O	0	0
			95	95		
3	H	109	Total	O	0	0
			109	109		



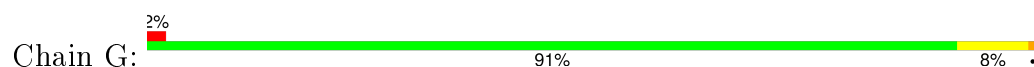
• Molecule 1: Acetyl-CoA acetyltransferase



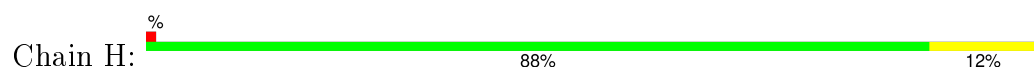
• Molecule 1: Acetyl-CoA acetyltransferase



• Molecule 1: Acetyl-CoA acetyltransferase



• Molecule 1: Acetyl-CoA acetyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	102.09 Å 157.44 Å 114.87 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	102.09 – 2.00 27.71 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.4 (102.09-2.00) 98.4 (27.71-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	16.72 (at 2.01 Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.173 , 0.213 0.186 , 0.224	Depositor DCC
R_{free} test set	11968 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	19.7	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 28.3	EDS
Estimated twinning fraction	0.478 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 238332 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	23650	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.16% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: COA

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	0.91	2/2875 (0.1%)	0.97	8/3886 (0.2%)
1	B	0.90	1/2875 (0.0%)	0.97	6/3886 (0.2%)
1	C	0.92	3/2875 (0.1%)	0.97	10/3886 (0.3%)
1	D	0.91	1/2875 (0.0%)	0.97	12/3886 (0.3%)
1	E	0.93	2/2875 (0.1%)	0.99	9/3886 (0.2%)
1	F	0.92	0/2875	1.00	15/3886 (0.4%)
1	G	0.93	0/2875	1.02	18/3886 (0.5%)
1	H	0.93	1/2875 (0.0%)	0.98	6/3886 (0.2%)
All	All	0.92	10/23000 (0.0%)	0.98	84/31088 (0.3%)

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	E	0	1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	86	LYS	CD-CE	6.33	1.67	1.51
1	D	86	LYS	CD-CE	5.87	1.66	1.51
1	E	336	SER	CB-OG	-5.76	1.34	1.42
1	C	86	LYS	CD-CE	5.71	1.65	1.51
1	A	86	LYS	CD-CE	5.60	1.65	1.51
1	E	86	LYS	CE-NZ	5.55	1.62	1.49
1	C	86	LYS	CE-NZ	5.32	1.62	1.49
1	H	336	SER	CB-OG	-5.24	1.35	1.42
1	C	333	TRP	CB-CG	5.05	1.59	1.50
1	A	333	TRP	CB-CG	5.03	1.59	1.50

All (84) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	375	LEU	CA-CB-CG	8.56	134.99	115.30
1	D	299	ARG	NE-CZ-NH1	8.23	124.42	120.30
1	F	303	ARG	NE-CZ-NH2	-7.93	116.34	120.30
1	B	299	ARG	NE-CZ-NH1	7.77	124.19	120.30
1	G	303	ARG	NE-CZ-NH2	-7.67	116.47	120.30
1	B	136	ASP	CB-CG-OD1	7.65	125.18	118.30
1	G	299	ARG	NE-CZ-NH1	7.59	124.10	120.30
1	G	129	ARG	NE-CZ-NH1	7.46	124.03	120.30
1	B	136	ASP	CB-CG-OD2	-7.38	111.65	118.30
1	G	129	ARG	NE-CZ-NH2	-7.35	116.62	120.30
1	H	375	LEU	CA-CB-CG	7.17	131.78	115.30
1	H	299	ARG	NE-CZ-NH1	7.12	123.86	120.30
1	F	299	ARG	NE-CZ-NH1	7.10	123.85	120.30
1	A	299	ARG	NE-CZ-NH1	7.09	123.85	120.30
1	H	285	ASP	CB-CG-OD1	7.06	124.65	118.30
1	A	375	LEU	CA-CB-CG	6.87	131.09	115.30
1	C	362	LEU	CB-CG-CD2	6.86	122.65	111.00
1	B	375	LEU	CA-CB-CG	6.79	130.91	115.30
1	G	375	LEU	CA-CB-CG	6.70	130.72	115.30
1	F	129	ARG	NE-CZ-NH1	6.69	123.65	120.30
1	A	373	LYS	CD-CE-NZ	-6.68	96.33	111.70
1	E	299	ARG	NE-CZ-NH1	6.63	123.61	120.30
1	C	299	ARG	NE-CZ-NH1	6.62	123.61	120.30
1	G	314	MET	CG-SD-CE	-6.60	89.64	100.20
1	D	129	ARG	NE-CZ-NH1	6.58	123.59	120.30
1	G	11	ARG	NE-CZ-NH1	6.57	123.59	120.30
1	E	375	LEU	CA-CB-CG	6.53	130.32	115.30
1	C	375	LEU	CA-CB-CG	6.49	130.23	115.30
1	G	312	ASP	CB-CG-OD1	-6.44	112.51	118.30
1	D	136	ASP	CB-CG-OD1	6.37	124.03	118.30
1	F	378	LEU	CA-CB-CG	6.32	129.83	115.30
1	E	285	ASP	CB-CG-OD1	6.29	123.96	118.30
1	D	375	LEU	CA-CB-CG	6.29	129.76	115.30
1	C	86	LYS	CD-CE-NZ	6.25	126.08	111.70
1	E	136	ASP	CB-CG-OD1	6.19	123.87	118.30
1	D	86	LYS	CD-CE-NZ	6.05	125.62	111.70
1	F	136	ASP	CB-CG-OD1	6.02	123.72	118.30
1	F	303	ARG	NE-CZ-NH1	5.97	123.29	120.30
1	E	196	ASP	CB-CG-OD1	5.96	123.66	118.30
1	C	373	LYS	CD-CE-NZ	-5.95	98.02	111.70
1	G	106	ASP	CB-CG-OD2	-5.93	112.97	118.30
1	B	303	ARG	NE-CZ-NH1	5.92	123.26	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	136	ASP	CB-CG-OD1	5.91	123.61	118.30
1	F	368	ARG	NE-CZ-NH2	5.83	123.22	120.30
1	A	362	LEU	CA-CB-CG	5.75	128.53	115.30
1	F	11	ARG	NE-CZ-NH1	5.73	123.16	120.30
1	H	392	ARG	NE-CZ-NH2	5.69	123.15	120.30
1	G	106	ASP	CB-CG-OD1	5.63	123.36	118.30
1	E	106	ASP	CB-CG-OD1	5.61	123.35	118.30
1	F	106	ASP	CB-CG-OD1	5.61	123.35	118.30
1	D	299	ARG	NE-CZ-NH2	-5.61	117.50	120.30
1	E	106	ASP	CB-CG-OD2	-5.60	113.26	118.30
1	G	299	ARG	NE-CZ-NH2	-5.59	117.51	120.30
1	G	368	ARG	NE-CZ-NH2	5.55	123.07	120.30
1	A	136	ASP	CB-CG-OD1	5.55	123.29	118.30
1	B	210	ASP	CB-CG-OD1	5.51	123.26	118.30
1	A	86	LYS	CD-CE-NZ	5.50	124.36	111.70
1	C	334	ASP	CB-CG-OD1	5.50	123.25	118.30
1	C	285	ASP	CB-CG-OD1	5.49	123.24	118.30
1	G	86	LYS	CB-CG-CD	5.43	125.71	111.60
1	D	362	LEU	CA-CB-CG	5.40	127.72	115.30
1	G	303	ARG	NE-CZ-NH1	5.39	122.99	120.30
1	F	299	ARG	NE-CZ-NH2	-5.34	117.63	120.30
1	D	67	ARG	NE-CZ-NH1	-5.33	117.64	120.30
1	E	299	ARG	NE-CZ-NH2	-5.26	117.67	120.30
1	G	369	ARG	NE-CZ-NH2	5.22	122.91	120.30
1	H	129	ARG	NE-CZ-NH1	5.21	122.91	120.30
1	D	232	LEU	CB-CG-CD1	5.21	119.86	111.00
1	F	312	ASP	CB-CG-OD1	-5.21	113.61	118.30
1	C	136	ASP	CB-CG-OD1	5.20	122.98	118.30
1	F	129	ARG	NE-CZ-NH2	-5.20	117.70	120.30
1	F	86	LYS	CD-CE-NZ	5.20	123.65	111.70
1	C	40	ARG	NE-CZ-NH2	-5.20	117.70	120.30
1	A	133	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	G	86	LYS	CD-CE-NZ	5.13	123.51	111.70
1	F	86	LYS	CB-CG-CD	5.11	124.88	111.60
1	G	357	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	D	392	ARG	NE-CZ-NH1	-5.08	117.76	120.30
1	D	136	ASP	CB-CG-OD2	-5.07	113.74	118.30
1	D	129	ARG	NE-CZ-NH2	-5.06	117.77	120.30
1	A	40	ARG	NE-CZ-NH1	5.05	122.82	120.30
1	G	378	LEU	CA-CB-CG	5.05	126.91	115.30
1	C	40	ARG	NE-CZ-NH1	5.02	122.81	120.30
1	E	232	LEU	CB-CG-CD1	5.01	119.52	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	1	MET	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	2835	0	2907	23	0
1	B	2835	0	2907	17	1
1	C	2835	0	2907	18	0
1	D	2835	0	2907	13	0
1	E	2835	0	2907	18	0
1	F	2835	0	2907	17	1
1	G	2835	0	2907	13	0
1	H	2835	0	2907	19	0
2	C	48	0	32	0	0
3	A	131	0	0	2	0
3	B	119	0	0	2	0
3	C	134	0	0	2	0
3	D	122	0	0	3	0
3	E	114	0	0	3	0
3	F	98	0	0	1	0
3	G	95	0	0	1	0
3	H	109	0	0	2	0
All	All	23650	0	23288	125	1

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.

All (125) 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:200:VAL:CG2	3:A:605:HOH:O	2.29	0.81
1:C:200:VAL:CG2	3:C:602:HOH:O	2.30	0.80
1:E:2:THR:HG22	3:E:575:HOH:O	1.88	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:368:ARG:HB3	1:C:368:ARG:CZ	2.17	0.74
1:A:368:ARG:CZ	1:A:368:ARG:HB3	2.19	0.71
1:H:2:THR:HG22	3:H:604:HOH:O	1.91	0.69
1:G:44:LYS:H	1:G:47:GLN:HE21	1.44	0.64
1:A:122:PRO:CG	1:B:124:VAL:HG21	2.28	0.63
1:G:46:GLU:HB2	1:G:78:MET:CE	2.31	0.61
1:D:2:THR:HG22	3:D:470:HOH:O	2.01	0.59
1:B:200:VAL:HG23	1:B:201:PRO:HD2	1.84	0.59
1:E:229:MET:HA	1:E:232:LEU:HD22	1.84	0.59
1:F:44:LYS:H	1:F:47:GLN:HE21	1.51	0.57
1:C:140:VAL:CG1	1:C:145:VAL:HG21	2.35	0.57
1:D:229:MET:HA	1:D:232:LEU:HD22	1.86	0.56
1:A:7:VAL:HG12	1:A:7:VAL:O	2.05	0.56
1:A:149:TRP:HE1	1:A:154:GLN:NE2	2.06	0.54
1:E:368:ARG:CB	1:E:368:ARG:CZ	2.85	0.54
1:E:206:GLN:CG	1:E:212:VAL:HG23	2.37	0.54
1:H:140:VAL:CG1	1:H:145:VAL:HG21	2.37	0.54
1:B:44:LYS:H	1:B:47:GLN:NE2	2.06	0.53
1:A:122:PRO:HG2	1:B:124:VAL:HG21	1.91	0.53
1:E:44:LYS:H	1:E:47:GLN:NE2	2.08	0.52
1:D:200:VAL:HG23	1:D:201:PRO:HD2	1.92	0.52
1:B:360:VAL:O	1:B:364:HIS:HD2	1.93	0.52
1:C:368:ARG:HB3	1:C:368:ARG:NH2	2.24	0.51
1:A:122:PRO:CG	1:B:124:VAL:CG2	2.88	0.51
1:A:44:LYS:H	1:A:47:GLN:NE2	2.08	0.51
1:E:16:LYS:HG3	1:E:218:GLU:HG3	1.93	0.51
1:D:44:LYS:H	1:D:47:GLN:NE2	2.07	0.51
1:C:7:VAL:HG12	1:C:7:VAL:O	2.08	0.51
1:A:368:ARG:NH2	1:A:368:ARG:HB3	2.26	0.51
1:H:368:ARG:CB	1:H:368:ARG:CZ	2.88	0.51
1:C:149:TRP:HE1	1:C:154:GLN:NE2	2.09	0.51
1:B:7:VAL:HG11	1:B:270:LEU:HD13	1.92	0.51
1:C:44:LYS:H	1:C:47:GLN:NE2	2.08	0.51
1:F:216:THR:HG22	3:F:553:HOH:O	2.11	0.51
1:H:229:MET:HA	1:H:232:LEU:HD22	1.93	0.50
1:A:200:VAL:HG22	3:A:605:HOH:O	2.01	0.50
1:H:149:TRP:HE1	1:H:154:GLN:NE2	2.09	0.49
1:H:44:LYS:H	1:H:47:GLN:NE2	2.10	0.49
1:A:16:LYS:HG3	1:A:218:GLU:HG3	1.93	0.49
1:E:2:THR:CG2	3:E:575:HOH:O	2.55	0.49
1:E:315:GLU:O	1:E:376:ALA:HA	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:200:VAL:HG23	1:C:201:PRO:HD2	1.95	0.48
1:A:30:GLY:HA3	1:A:115:GLN:NE2	2.27	0.48
1:C:360:VAL:O	1:C:364:HIS:HD2	1.96	0.48
1:B:229:MET:HA	1:B:232:LEU:HD22	1.94	0.48
1:D:216:THR:HG22	3:D:437:HOH:O	2.14	0.48
1:H:206:GLN:CG	1:H:212:VAL:HG23	2.44	0.48
1:A:140:VAL:CG1	1:A:145:VAL:HG21	2.44	0.47
1:A:360:VAL:O	1:A:364:HIS:HD2	1.97	0.47
1:B:140:VAL:CG1	1:B:145:VAL:HG21	2.45	0.47
1:A:7:VAL:O	1:A:7:VAL:CG1	2.63	0.46
1:C:125:LEU:HD21	1:H:139:LEU:HD12	1.97	0.46
1:C:30:GLY:HA3	1:C:115:GLN:NE2	2.29	0.46
1:H:360:VAL:O	1:H:364:HIS:HD2	1.99	0.46
1:E:17:PHE:CZ	1:F:129:ARG:HD3	2.51	0.46
1:F:206:GLN:O	1:F:207:ARG:HB2	2.16	0.46
1:G:44:LYS:H	1:G:47:GLN:NE2	2.13	0.46
1:G:216:THR:HG22	3:G:530:HOH:O	2.16	0.46
1:E:360:VAL:O	1:E:364:HIS:HD2	1.99	0.46
1:C:206:GLN:HG3	1:C:212:VAL:HG23	1.96	0.46
1:C:292:GLY:N	1:C:293:PRO:CD	2.78	0.45
1:E:216:THR:HG22	3:E:602:HOH:O	2.16	0.45
1:E:124:VAL:CG2	1:F:122:PRO:CG	2.95	0.45
1:A:122:PRO:HG2	1:B:124:VAL:CG2	2.46	0.45
1:G:140:VAL:CG1	1:G:145:VAL:HG21	2.47	0.45
1:H:313:LEU:O	1:H:374:GLY:HA2	2.17	0.45
1:A:125:LEU:HD21	1:E:139:LEU:CD1	2.46	0.44
1:C:200:VAL:HG22	3:C:602:HOH:O	2.06	0.44
1:C:125:LEU:HD21	1:H:139:LEU:CD1	2.47	0.44
1:D:138:LYS:HE2	1:G:136:ASP:OD2	2.18	0.44
1:B:216:THR:HG22	3:B:532:HOH:O	2.17	0.44
1:D:44:LYS:H	1:D:47:GLN:HE21	1.64	0.44
1:G:317:ASN:HB3	1:G:378:LEU:HB3	1.99	0.44
1:C:140:VAL:HG11	1:C:145:VAL:HG21	1.99	0.44
1:H:30:GLY:HA3	1:H:115:GLN:NE2	2.33	0.44
1:E:368:ARG:HB3	1:E:368:ARG:CZ	2.47	0.43
1:G:125:LEU:HD22	1:G:132:PHE:CZ	2.52	0.43
1:B:124:VAL:HG22	1:B:125:LEU:N	2.32	0.43
1:F:365:GLU:OE2	1:F:368:ARG:NH1	2.51	0.43
1:H:368:ARG:HB3	1:H:368:ARG:NH2	2.34	0.43
1:E:149:TRP:HE1	1:E:154:GLN:NE2	2.15	0.43
1:F:140:VAL:CG1	1:F:145:VAL:HG21	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:315:GLU:O	1:H:376:ALA:HA	2.17	0.43
1:G:129:ARG:HD3	1:H:17:PHE:CZ	2.54	0.43
1:B:26:ALA:HB3	1:B:27:PRO:HD3	2.00	0.43
1:D:355:GLY:HA2	1:D:378:LEU:HD11	2.01	0.43
1:H:368:ARG:HB3	1:H:368:ARG:CZ	2.49	0.43
1:E:30:GLY:HA3	1:E:115:GLN:NE2	2.34	0.43
1:A:355:GLY:HA2	1:A:378:LEU:HD11	2.00	0.42
1:G:46:GLU:HB2	1:G:78:MET:HE1	2.00	0.42
1:F:266:LYS:O	1:F:267:GLU:C	2.58	0.42
1:B:292:GLY:N	1:B:293:PRO:CD	2.82	0.42
1:H:216:THR:HG22	3:H:572:HOH:O	2.19	0.42
1:A:292:GLY:N	1:A:293:PRO:CD	2.82	0.42
1:C:7:VAL:CG1	1:C:7:VAL:O	2.67	0.42
1:E:180:VAL:HG21	1:E:226:LEU:HA	2.01	0.42
1:B:368:ARG:HD3	3:B:520:HOH:O	2.20	0.42
1:F:125:LEU:HD22	1:F:132:PHE:HZ	1.85	0.42
1:A:200:VAL:HG23	1:A:201:PRO:HD2	2.02	0.42
1:D:2:THR:CG2	3:D:470:HOH:O	2.66	0.42
1:D:140:VAL:CG1	1:D:145:VAL:HG21	2.50	0.42
1:G:125:LEU:HD22	1:G:132:PHE:HZ	1.84	0.41
1:D:7:VAL:HG11	1:D:270:LEU:HD13	2.02	0.41
1:G:140:VAL:HG13	1:G:145:VAL:HG21	2.02	0.41
1:F:9:ALA:HB1	1:F:360:VAL:HG22	2.03	0.41
1:D:360:VAL:O	1:D:364:HIS:HD2	2.04	0.41
1:G:368:ARG:HB3	1:G:368:ARG:CZ	2.49	0.41
1:F:325:LEU:HA	1:F:325:LEU:HD23	1.90	0.41
1:A:122:PRO:HG3	1:B:124:VAL:HG21	1.99	0.41
1:F:306:TRP:CE2	1:F:373:LYS:HD3	2.56	0.41
1:H:180:VAL:HG21	1:H:226:LEU:HA	2.02	0.41
1:A:140:VAL:HG11	1:A:145:VAL:HG21	2.03	0.41
1:H:233:LYS:HB3	1:H:233:LYS:HE3	1.76	0.41
1:D:149:TRP:HE1	1:D:154:GLN:NE2	2.19	0.40
1:B:355:GLY:HA2	1:B:378:LEU:HD11	2.03	0.40
1:F:44:LYS:H	1:F:47:GLN:NE2	2.17	0.40
1:E:124:VAL:HG21	1:F:122:PRO:CG	2.51	0.40
1:F:125:LEU:HD22	1:F:132:PHE:CZ	2.56	0.40
1:A:206:GLN:HG3	1:A:212:VAL:HG23	2.03	0.40
1:F:180:VAL:HG21	1:F:226:LEU:HA	2.02	0.40
1:C:191:LYS:HE3	1:C:222:GLN:OE1	2.22	0.40
1:F:194:LYS:HE2	1:F:368:ARG:CZ	2.51	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:368:ARG:NH2	1:F:269:GLY:O[2_556]	2.16	0.04

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	391/393 (100%)	378 (97%)	11 (3%)	2 (0%)	34	26
1	B	391/393 (100%)	381 (97%)	9 (2%)	1 (0%)	46	41
1	C	391/393 (100%)	380 (97%)	9 (2%)	2 (0%)	34	26
1	D	391/393 (100%)	381 (97%)	9 (2%)	1 (0%)	46	41
1	E	391/393 (100%)	380 (97%)	10 (3%)	1 (0%)	46	41
1	F	391/393 (100%)	380 (97%)	10 (3%)	1 (0%)	46	41
1	G	391/393 (100%)	379 (97%)	11 (3%)	1 (0%)	46	41
1	H	391/393 (100%)	382 (98%)	8 (2%)	1 (0%)	46	41
All	All	3128/3144 (100%)	3041 (97%)	77 (2%)	10 (0%)	46	41

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	207	ARG
1	A	87	VAL
1	B	87	VAL
1	C	87	VAL
1	D	87	VAL
1	E	87	VAL
1	F	87	VAL
1	G	87	VAL
1	H	87	VAL
1	A	207	ARG

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	285/285 (100%)	268 (94%)	17 (6%)	24	17
1	B	285/285 (100%)	274 (96%)	11 (4%)	39	35
1	C	285/285 (100%)	270 (95%)	15 (5%)	28	22
1	D	285/285 (100%)	271 (95%)	14 (5%)	31	25
1	E	285/285 (100%)	265 (93%)	20 (7%)	19	12
1	F	285/285 (100%)	269 (94%)	16 (6%)	26	20
1	G	285/285 (100%)	271 (95%)	14 (5%)	31	25
1	H	285/285 (100%)	267 (94%)	18 (6%)	22	16
All	All	2280/2280 (100%)	2155 (94%)	125 (6%)	27	21

All (125) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	16	LYS
1	A	87	VAL
1	A	125	LEU
1	A	130	ASP
1	A	133	ARG
1	A	155	TYR
1	A	232	LEU
1	A	238	LYS
1	A	289	MET
1	A	314	MET
1	A	323	GLN
1	A	333	TRP
1	A	362	LEU
1	A	368	ARG
1	A	369	ARG
1	A	393	LYS
1	B	125	LEU
1	B	155	TYR

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Mol	Chain	Res	Type
1	B	167	GLU
1	B	232	LEU
1	B	238	LYS
1	B	289	MET
1	B	314	MET
1	B	323	GLN
1	B	333	TRP
1	B	362	LEU
1	B	368	ARG
1	C	1	MET
1	C	125	LEU
1	C	130	ASP
1	C	133	ARG
1	C	155	TYR
1	C	167	GLU
1	C	232	LEU
1	C	238	LYS
1	C	289	MET
1	C	314	MET
1	C	323	GLN
1	C	333	TRP
1	C	362	LEU
1	C	368	ARG
1	C	393	LYS
1	D	2	THR
1	D	124	VAL
1	D	125	LEU
1	D	155	TYR
1	D	166	LYS
1	D	167	GLU
1	D	207	ARG
1	D	232	LEU
1	D	238	LYS
1	D	289	MET
1	D	314	MET
1	D	323	GLN
1	D	333	TRP
1	D	362	LEU
1	E	1	MET
1	E	2	THR
1	E	49	SER
1	E	125	LEU

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Mol	Chain	Res	Type
1	E	133	ARG
1	E	155	TYR
1	E	167	GLU
1	E	177	GLU
1	E	200	VAL
1	E	232	LEU
1	E	238	LYS
1	E	248	SER
1	E	266	LYS
1	E	289	MET
1	E	314	MET
1	E	323	GLN
1	E	333	TRP
1	E	362	LEU
1	E	367	LYS
1	E	368	ARG
1	F	1	MET
1	F	23	LYS
1	F	125	LEU
1	F	155	TYR
1	F	200	VAL
1	F	232	LEU
1	F	238	LYS
1	F	248	SER
1	F	266	LYS
1	F	289	MET
1	F	314	MET
1	F	323	GLN
1	F	333	TRP
1	F	362	LEU
1	F	375	LEU
1	F	378	LEU
1	G	125	LEU
1	G	130	ASP
1	G	155	TYR
1	G	200	VAL
1	G	208	LYS
1	G	232	LEU
1	G	233	LYS
1	G	238	LYS
1	G	266	LYS
1	G	289	MET

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Mol	Chain	Res	Type
1	G	323	GLN
1	G	333	TRP
1	G	362	LEU
1	G	378	LEU
1	H	2	THR
1	H	49	SER
1	H	87	VAL
1	H	125	LEU
1	H	133	ARG
1	H	155	TYR
1	H	167	GLU
1	H	208	LYS
1	H	232	LEU
1	H	238	LYS
1	H	248	SER
1	H	266	LYS
1	H	289	MET
1	H	314	MET
1	H	323	GLN
1	H	333	TRP
1	H	362	LEU
1	H	367	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (38) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	GLN
1	A	115	GLN
1	A	154	GLN
1	A	364	HIS
1	B	47	GLN
1	B	115	GLN
1	B	154	GLN
1	B	184	ASN
1	B	364	HIS
1	C	47	GLN
1	C	115	GLN
1	C	154	GLN
1	C	364	HIS
1	D	47	GLN
1	D	115	GLN
1	D	154	GLN

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Mol	Chain	Res	Type
1	D	184	ASN
1	D	364	HIS
1	E	47	GLN
1	E	115	GLN
1	E	154	GLN
1	E	184	ASN
1	E	364	HIS
1	F	47	GLN
1	F	115	GLN
1	F	154	GLN
1	F	184	ASN
1	F	364	HIS
1	G	47	GLN
1	G	115	GLN
1	G	154	GLN
1	G	184	ASN
1	G	364	HIS
1	H	47	GLN
1	H	115	GLN
1	H	154	GLN
1	H	184	ASN
1	H	364	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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
2	COA	C	401	-	40,50,50	1.53	5 (12%)	50,75,75	2.31	13 (26%)

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
2	COA	C	401	-	-	0/44/64/64	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	401	COA	C2A-N3A	2.59	1.36	1.32
2	C	401	COA	O4B-C1B	2.76	1.44	1.41
2	C	401	COA	C5A-C4A	3.33	1.48	1.40
2	C	401	COA	C2P-S1P	3.99	1.94	1.80
2	C	401	COA	C3P-N4P	5.34	1.58	1.46

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	COA	N3A-C2A-N1A	-8.31	122.53	128.89
2	C	401	COA	CDP-CBP-CCP	-5.61	101.23	108.50
2	C	401	COA	O5P-C5P-C6P	-5.37	112.72	121.98
2	C	401	COA	C7P-C6P-C5P	-4.00	105.72	112.31
2	C	401	COA	C3B-C2B-C1B	2.00	104.78	99.98
2	C	401	COA	N6A-C6A-N1A	2.09	123.69	119.20
2	C	401	COA	O9A-P3B-O8A	2.14	115.51	107.38
2	C	401	COA	CAP-C9P-N8P	2.37	121.72	116.47
2	C	401	COA	P3B-O3B-C3B	2.51	127.58	121.56
2	C	401	COA	O4B-C1B-N9A	2.56	113.46	108.10
2	C	401	COA	C6P-C5P-N4P	3.30	122.19	116.46
2	C	401	COA	CEP-CBP-CDP	3.54	116.38	109.28
2	C	401	COA	C2P-C3P-N4P	5.69	123.62	112.37

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	393/393 (100%)	-0.21	3 (0%) 87 88	12, 19, 32, 83	0
1	B	393/393 (100%)	-0.28	1 (0%) 94 94	12, 19, 32, 70	0
1	C	393/393 (100%)	-0.26	3 (0%) 87 88	12, 19, 33, 77	0
1	D	393/393 (100%)	-0.23	3 (0%) 87 88	12, 19, 32, 71	0
1	E	393/393 (100%)	-0.12	4 (1%) 84 84	12, 20, 36, 77	0
1	F	393/393 (100%)	-0.05	6 (1%) 76 77	13, 22, 41, 80	0
1	G	393/393 (100%)	-0.05	6 (1%) 76 77	13, 22, 42, 82	0
1	H	393/393 (100%)	-0.13	5 (1%) 79 80	12, 20, 37, 81	0
All	All	3144/3144 (100%)	-0.17	31 (0%) 84 84	12, 20, 36, 83	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	MET	7.7
1	E	207	ARG	6.0
1	C	1	MET	5.5
1	F	2	THR	4.9
1	F	209	GLY	4.8
1	F	207	ARG	4.6
1	G	208	LYS	4.5
1	G	209	GLY	4.1
1	F	210	ASP	4.0
1	B	1	MET	4.0
1	E	1	MET	4.0
1	H	1	MET	3.9
1	H	207	ARG	3.7
1	G	207	ARG	3.6
1	D	2	THR	3.3
1	F	208	LYS	3.3

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Mol	Chain	Res	Type	RSRZ
1	D	1	MET	3.2
1	E	208	LYS	3.2
1	C	238	LYS	2.9
1	A	207	ARG	2.8
1	H	209	GLY	2.7
1	G	1	MET	2.7
1	G	210	ASP	2.6
1	A	2	THR	2.6
1	F	212	VAL	2.6
1	C	207	ARG	2.5
1	E	210	ASP	2.5
1	D	393	LYS	2.3
1	H	210	ASP	2.3
1	H	208	LYS	2.2
1	G	2	THR	2.2

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 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(Å ²)	Q<0.9
2	COA	C	401	48/48	0.76	0.43	17.46	24,125,158,164	0

6.5 Other polymers [i](#)

There are no such residues in this entry.