



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 11:28 AM GMT

PDB ID : 3OXO
Title : Succinyl-CoA:3-ketoacid CoA transferase from pig heart covalently bound to CoA
Authors : Fraser, M.E.
Deposited on : 2010-09-21
Resolution : 2.30 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

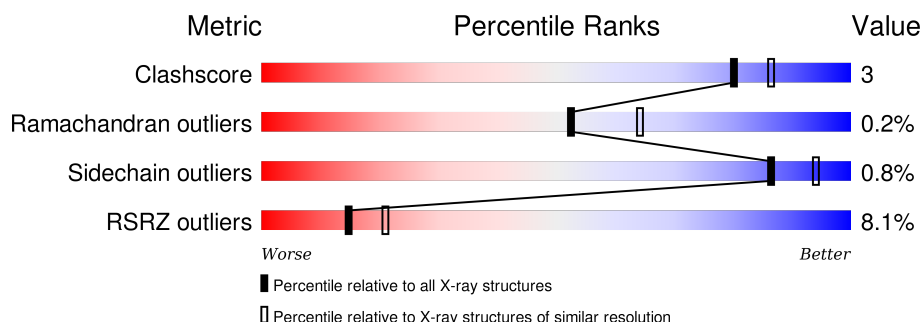
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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	488	<div> <div>4%</div> <div>92%</div> <div>• •</div> </div>
1	B	488	<div> <div>2%</div> <div>90%</div> <div>5% • 5%</div> </div>
1	C	488	<div> <div>2%</div> <div>89%</div> <div>6% 5%</div> </div>
1	D	488	<div> <div>3%</div> <div>90%</div> <div>6% •</div> </div>
1	E	488	<div> <div>9%</div> <div>84%</div> <div>10% 5%</div> </div>
1	F	488	<div> <div>7%</div> <div>82%</div> <div>13% 5%</div> </div>
1	G	488	<div> <div>11%</div> <div>85%</div> <div>8% 6%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	H	488	<div><div></div><div>24%</div><div>85%</div><div>9%</div><div>6%</div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 28904 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 Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	469	Total	C	N	O	S	0	0	0
			3576	2268	613	677	18			
1	B	466	Total	C	N	O	S	0	0	0
			3556	2258	609	671	18			
1	C	466	Total	C	N	O	S	0	0	0
			3555	2256	609	672	18			
1	D	467	Total	C	N	O	S	0	0	0
			3563	2260	610	675	18			
1	E	462	Total	C	N	O	S	0	0	0
			3519	2236	601	664	18			
1	F	463	Total	C	N	O	S	0	0	0
			3528	2241	602	667	18			
1	G	459	Total	C	N	O	S	0	0	0
			3489	2218	592	661	18			
1	H	458	Total	C	N	O	S	0	0	0
			3483	2212	593	660	18			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	479	LEU	-	EXPRESSION TAG	UNP Q29551
A	480	GLU	-	EXPRESSION TAG	UNP Q29551
A	481	HIS	-	EXPRESSION TAG	UNP Q29551
A	482	HIS	-	EXPRESSION TAG	UNP Q29551
A	483	HIS	-	EXPRESSION TAG	UNP Q29551
A	484	HIS	-	EXPRESSION TAG	UNP Q29551
A	485	HIS	-	EXPRESSION TAG	UNP Q29551
A	486	HIS	-	EXPRESSION TAG	UNP Q29551
A	487	HIS	-	EXPRESSION TAG	UNP Q29551
A	488	HIS	-	EXPRESSION TAG	UNP Q29551
B	479	LEU	-	EXPRESSION TAG	UNP Q29551
B	480	GLU	-	EXPRESSION TAG	UNP Q29551

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	481	HIS	-	EXPRESSION TAG	UNP Q29551
B	482	HIS	-	EXPRESSION TAG	UNP Q29551
B	483	HIS	-	EXPRESSION TAG	UNP Q29551
B	484	HIS	-	EXPRESSION TAG	UNP Q29551
B	485	HIS	-	EXPRESSION TAG	UNP Q29551
B	486	HIS	-	EXPRESSION TAG	UNP Q29551
B	487	HIS	-	EXPRESSION TAG	UNP Q29551
B	488	HIS	-	EXPRESSION TAG	UNP Q29551
C	479	LEU	-	EXPRESSION TAG	UNP Q29551
C	480	GLU	-	EXPRESSION TAG	UNP Q29551
C	481	HIS	-	EXPRESSION TAG	UNP Q29551
C	482	HIS	-	EXPRESSION TAG	UNP Q29551
C	483	HIS	-	EXPRESSION TAG	UNP Q29551
C	484	HIS	-	EXPRESSION TAG	UNP Q29551
C	485	HIS	-	EXPRESSION TAG	UNP Q29551
C	486	HIS	-	EXPRESSION TAG	UNP Q29551
C	487	HIS	-	EXPRESSION TAG	UNP Q29551
C	488	HIS	-	EXPRESSION TAG	UNP Q29551
D	479	LEU	-	EXPRESSION TAG	UNP Q29551
D	480	GLU	-	EXPRESSION TAG	UNP Q29551
D	481	HIS	-	EXPRESSION TAG	UNP Q29551
D	482	HIS	-	EXPRESSION TAG	UNP Q29551
D	483	HIS	-	EXPRESSION TAG	UNP Q29551
D	484	HIS	-	EXPRESSION TAG	UNP Q29551
D	485	HIS	-	EXPRESSION TAG	UNP Q29551
D	486	HIS	-	EXPRESSION TAG	UNP Q29551
D	487	HIS	-	EXPRESSION TAG	UNP Q29551
D	488	HIS	-	EXPRESSION TAG	UNP Q29551
E	479	LEU	-	EXPRESSION TAG	UNP Q29551
E	480	GLU	-	EXPRESSION TAG	UNP Q29551
E	481	HIS	-	EXPRESSION TAG	UNP Q29551
E	482	HIS	-	EXPRESSION TAG	UNP Q29551
E	483	HIS	-	EXPRESSION TAG	UNP Q29551
E	484	HIS	-	EXPRESSION TAG	UNP Q29551
E	485	HIS	-	EXPRESSION TAG	UNP Q29551
E	486	HIS	-	EXPRESSION TAG	UNP Q29551
E	487	HIS	-	EXPRESSION TAG	UNP Q29551
E	488	HIS	-	EXPRESSION TAG	UNP Q29551
F	479	LEU	-	EXPRESSION TAG	UNP Q29551
F	480	GLU	-	EXPRESSION TAG	UNP Q29551
F	481	HIS	-	EXPRESSION TAG	UNP Q29551
F	482	HIS	-	EXPRESSION TAG	UNP Q29551

Continued on next page...

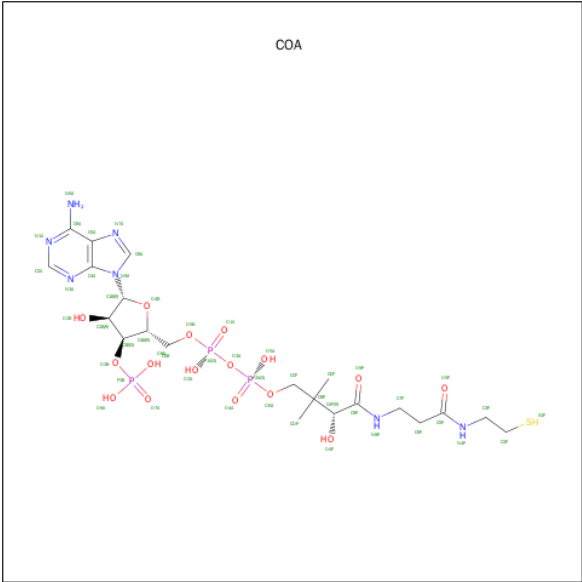
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	483	HIS	-	EXPRESSION TAG	UNP Q29551
F	484	HIS	-	EXPRESSION TAG	UNP Q29551
F	485	HIS	-	EXPRESSION TAG	UNP Q29551
F	486	HIS	-	EXPRESSION TAG	UNP Q29551
F	487	HIS	-	EXPRESSION TAG	UNP Q29551
F	488	HIS	-	EXPRESSION TAG	UNP Q29551
G	479	LEU	-	EXPRESSION TAG	UNP Q29551
G	480	GLU	-	EXPRESSION TAG	UNP Q29551
G	481	HIS	-	EXPRESSION TAG	UNP Q29551
G	482	HIS	-	EXPRESSION TAG	UNP Q29551
G	483	HIS	-	EXPRESSION TAG	UNP Q29551
G	484	HIS	-	EXPRESSION TAG	UNP Q29551
G	485	HIS	-	EXPRESSION TAG	UNP Q29551
G	486	HIS	-	EXPRESSION TAG	UNP Q29551
G	487	HIS	-	EXPRESSION TAG	UNP Q29551
G	488	HIS	-	EXPRESSION TAG	UNP Q29551
H	479	LEU	-	EXPRESSION TAG	UNP Q29551
H	480	GLU	-	EXPRESSION TAG	UNP Q29551
H	481	HIS	-	EXPRESSION TAG	UNP Q29551
H	482	HIS	-	EXPRESSION TAG	UNP Q29551
H	483	HIS	-	EXPRESSION TAG	UNP Q29551
H	484	HIS	-	EXPRESSION TAG	UNP Q29551
H	485	HIS	-	EXPRESSION TAG	UNP Q29551
H	486	HIS	-	EXPRESSION TAG	UNP Q29551
H	487	HIS	-	EXPRESSION TAG	UNP Q29551
H	488	HIS	-	EXPRESSION TAG	UNP Q29551

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 3 is COENZYME A (three-letter code: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	E	1	Total 48	C 21	N 7	O 16	P 3	S 1	0	0
3	F	1	Total 48	C 21	N 7	O 16	P 3	S 1	0	0
3	G	1	Total 48	C 21	N 7	O 16	P 3	S 1	0	0
3	H	1	Total 48	C 21	N 7	O 16	P 3	S 1	0	0

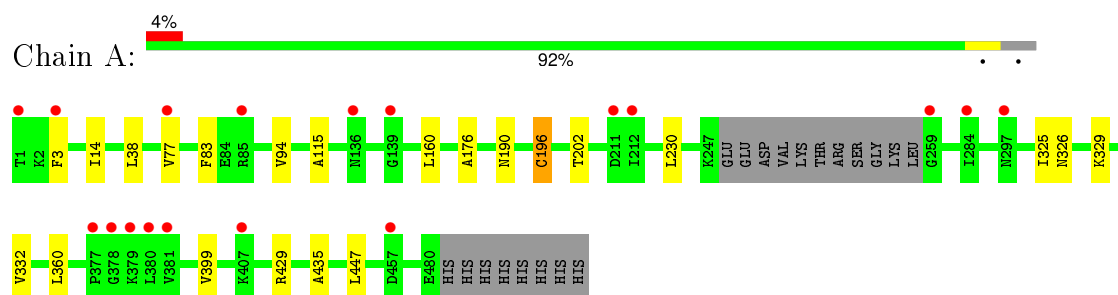
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	91	Total	O	0	0
			91	91		
4	B	60	Total	O	0	0
			60	60		
4	C	65	Total	O	0	0
			65	65		
4	D	58	Total	O	0	0
			58	58		
4	E	53	Total	O	0	0
			53	53		
4	F	44	Total	O	0	0
			44	44		
4	G	43	Total	O	0	0
			43	43		
4	H	26	Total	O	0	0
			26	26		

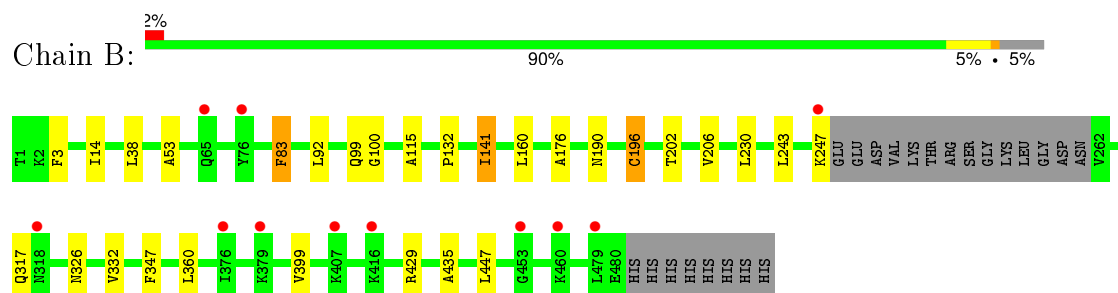
3 Residue-property plots [i](#)

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.

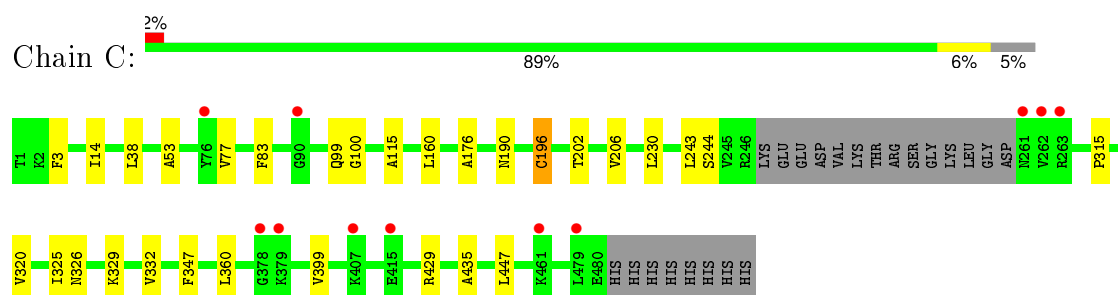
- Molecule 1: Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial



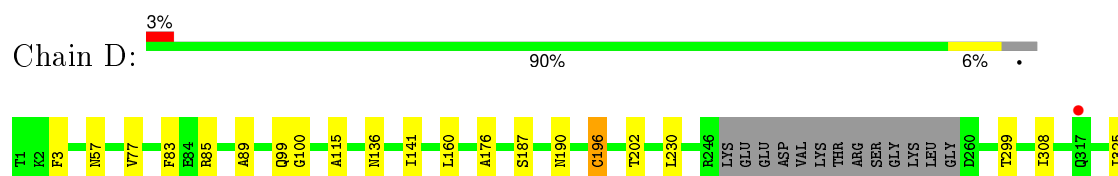
- Molecule 1: Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial



- Molecule 1: Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial

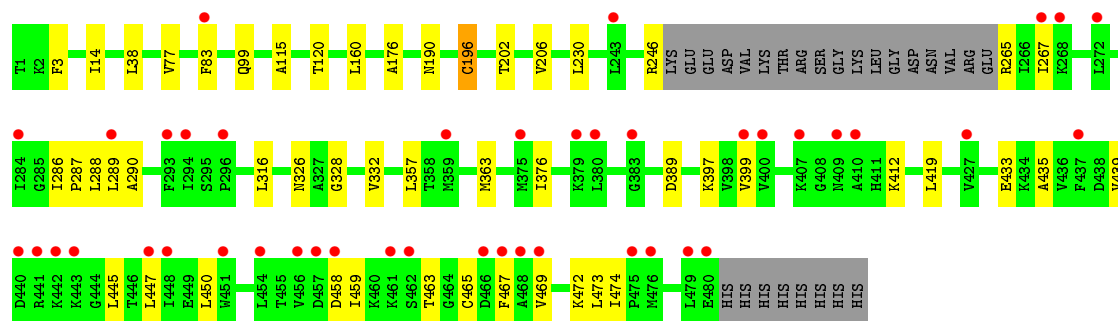
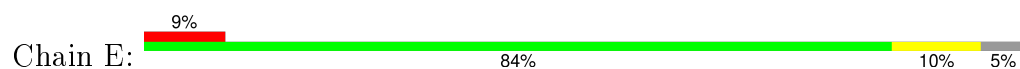


- Molecule 1: Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial

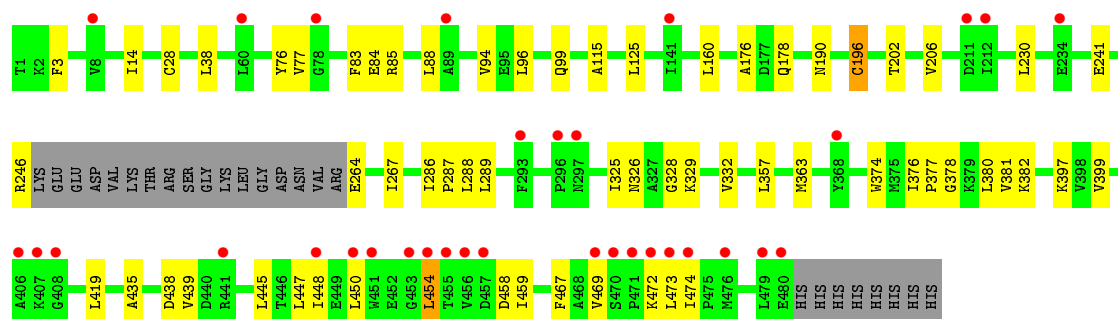
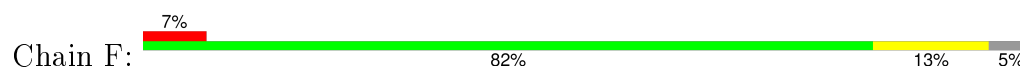




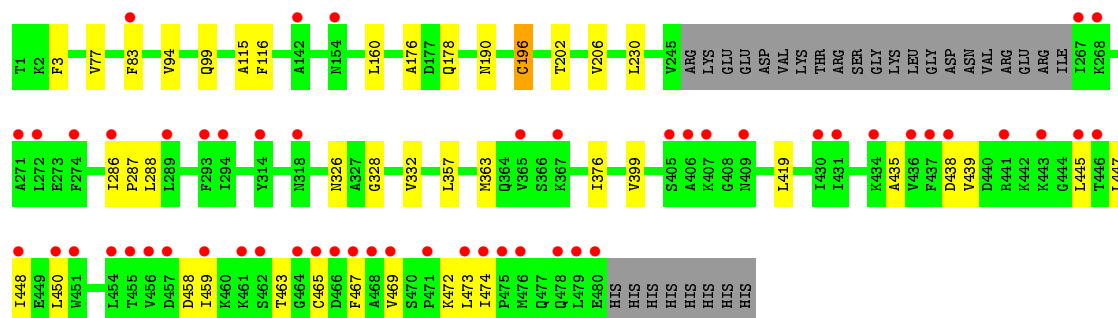
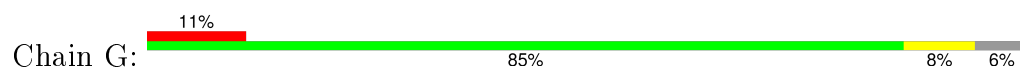
- Molecule 1: Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial



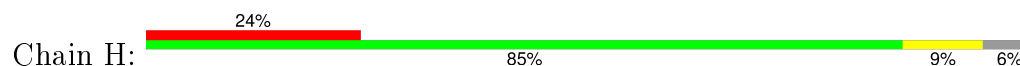
- Molecule 1: Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial



- Molecule 1: Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial



- Molecule 1: Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial



HIS	T418	Q317	G213	T1
HIS	L419	V320	S214	K2
HIS	K424	N326	F215	F3
HIS	V427	A327	L230	I14
	I430	G328	L243	I30
	I431	T331	S244	L34
	T432	V332	V245	L38
	E433	P336	R246	A53
	K434	S342	LYS	F58
	A435	S343	GLU	L62
	V436	D344	GLU	L63
	F437	V439	ASP	L62
	D438	L357	VAL	V77
	V439	T358	LYS	E79
	D440	M359	THR	F83
	R441	L360	ARG	A89
	K442	M363	SER	G90
	K443	G444	GLY	V94
	G444	L445	LYS	A115
	L446	Q364	LEU	G123
	I447	V365	GLY	T124
	I448	V366	ASP	L125
	E449	S367	ASN	G139
	L450	K367	VAL	S140
	W451	Y368	ARG	I141
	G452	G369	GLU	A142
	G453	D370	ARG	I143
	L454	L371	ARG	A144
	T455	M375	I1E	V150
	V456	I376	LYS	L160
	D457	P377	L272	K174
	D458	G378	E273	K175
	I459	V381	F274	A176
	K460	K382	L282	N190
	S462	G383	G283	C196
	T463	M384	I284	T202
	G464	K397	G285	V206
	C465	V398	L286	L209
	D465	V399	F287	
	F467	V400	L288	
	A468	E403	L289	
	V469	H404	A290	
	S470	S405	S291	
	P471	S406	N292	
	K472	A406	F293	
	L473	K407	I294	
	L474	G408	S295	
	P475	N409	P296	
	M476	A410	N297	
	L479	H411	P313	
	E480	K412	Y314	
	HIS	I413	P315	
	HIS	C417	L316	
	HIS			

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	69.12Å 107.13Å 134.56Å 89.60° 80.21° 75.13°	Depositor
Resolution (Å)	21.20 – 2.30 21.21 – 2.30	Depositor EDS
% Data completeness (in resolution range)	91.4 (21.20-2.30) 72.9 (21.21-2.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.55 (at 2.30Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.245 , 0.273 0.252 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	31.9	Xtriage
Anisotropy	0.247	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 18.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 149071 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	28904	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.34% 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, CL

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	0.37	0/3634	0.51	0/4903
1	B	0.35	0/3614	0.51	0/4876
1	C	0.35	0/3613	0.50	0/4876
1	D	0.34	0/3621	0.49	0/4887
1	E	0.33	0/3577	0.49	0/4827
1	F	0.32	0/3586	0.49	0/4839
1	G	0.32	0/3547	0.49	0/4788
1	H	0.32	0/3541	0.48	0/4780
All	All	0.34	0/28733	0.49	0/38776

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	F	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	454	LEU	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	3576	0	3644	13	0
1	B	3556	0	3631	20	0
1	C	3555	0	3624	17	0
1	D	3563	0	3628	18	0
1	E	3519	0	3590	33	0
1	F	3528	0	3596	46	0
1	G	3489	0	3553	30	0
1	H	3483	0	3542	28	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	E	48	0	31	1	0
3	F	48	0	31	1	0
3	G	48	0	31	1	0
3	H	48	0	31	0	0
4	A	91	0	0	0	0
4	B	60	0	0	2	0
4	C	65	0	0	1	0
4	D	58	0	0	2	0
4	E	53	0	0	2	0
4	F	44	0	0	1	0
4	G	43	0	0	1	0
4	H	26	0	0	0	0
All	All	28904	0	28932	197	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 197 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:D:85:ARG:HB2	1:H:243:LEU:HD22	1.46	0.96
1:B:99:GLN:NE2	4:B:549:HOH:O	2.01	0.90
1:B:53:ALA:CB	1:B:83:PHE:CD1	2.66	0.78
1:D:136:ASN:HB3	1:F:125:LEU:HD21	1.66	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:53:ALA:HB2	1:B:83:PHE:CE1	2.24	0.73

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	465/488 (95%)	456 (98%)	8 (2%)	1 (0%)	52	64
1	B	462/488 (95%)	451 (98%)	10 (2%)	1 (0%)	52	64
1	C	462/488 (95%)	451 (98%)	10 (2%)	1 (0%)	52	64
1	D	463/488 (95%)	453 (98%)	9 (2%)	1 (0%)	52	64
1	E	458/488 (94%)	447 (98%)	10 (2%)	1 (0%)	52	64
1	F	459/488 (94%)	447 (97%)	11 (2%)	1 (0%)	52	64
1	G	455/488 (93%)	444 (98%)	10 (2%)	1 (0%)	52	64
1	H	454/488 (93%)	443 (98%)	10 (2%)	1 (0%)	52	64
All	All	3678/3904 (94%)	3592 (98%)	78 (2%)	8 (0%)	52	64

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	190	ASN
1	B	190	ASN
1	C	190	ASN
1	E	190	ASN
1	F	190	ASN

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	382/400 (96%)	380 (100%)	2 (0%)	92	97
1	B	380/400 (95%)	375 (99%)	5 (1%)	76	87
1	C	380/400 (95%)	378 (100%)	2 (0%)	92	97
1	D	381/400 (95%)	378 (99%)	3 (1%)	86	94
1	E	376/400 (94%)	374 (100%)	2 (0%)	92	97
1	F	377/400 (94%)	373 (99%)	4 (1%)	80	90
1	G	373/400 (93%)	370 (99%)	3 (1%)	86	94
1	H	372/400 (93%)	370 (100%)	2 (0%)	92	97
All	All	3021/3200 (94%)	2998 (99%)	23 (1%)	86	94

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	196	CYS
1	E	196	CYS
1	H	196	CYS
1	D	360	LEU
1	E	458	ASP

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

Mol	Chain	Res	Type
1	F	157	HIS
1	H	317	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 3 are monoatomic - leaving 4 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	COA	E	1305	1	40,50,50	1.75	3 (7%)	50,75,75	1.88	4 (8%)
3	COA	F	1305	1	40,50,50	1.71	3 (7%)	50,75,75	1.91	5 (10%)
3	COA	G	1305	1	40,50,50	1.70	3 (7%)	50,75,75	1.92	5 (10%)
3	COA	H	1305	1	40,50,50	1.73	3 (7%)	50,75,75	1.88	4 (8%)

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	COA	E	1305	1	-	0/44/64/64	0/3/3/3
3	COA	F	1305	1	-	0/44/64/64	0/3/3/3
3	COA	G	1305	1	-	0/44/64/64	0/3/3/3
3	COA	H	1305	1	-	0/44/64/64	0/3/3/3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	1305	COA	C2A-N1A	2.56	1.38	1.33
3	F	1305	COA	C2A-N1A	2.59	1.38	1.33

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	1305	COA	C2A-N1A	2.61	1.38	1.33
3	E	1305	COA	C2A-N1A	2.72	1.39	1.33
3	F	1305	COA	C2A-N3A	3.71	1.38	1.32

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	1305	COA	N3A-C2A-N1A	-11.49	120.09	128.89
3	F	1305	COA	N3A-C2A-N1A	-11.34	120.21	128.89
3	H	1305	COA	N3A-C2A-N1A	-11.28	120.26	128.89
3	E	1305	COA	N3A-C2A-N1A	-11.24	120.28	128.89
3	G	1305	COA	C2P-C3P-N4P	-3.68	105.10	112.37

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	1305	COA	1	0
3	F	1305	COA	1	0
3	G	1305	COA	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 ⓘ

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	469/488 (96%)	0.16	18 (3%) 44 53	6, 28, 50, 61	0
1	B	466/488 (95%)	0.15	11 (2%) 62 71	9, 33, 52, 63	0
1	C	466/488 (95%)	0.24	11 (2%) 62 71	10, 35, 51, 60	0
1	D	467/488 (95%)	0.28	14 (2%) 54 63	10, 37, 56, 67	0
1	E	462/488 (94%)	0.55	43 (9%) 11 16	12, 37, 78, 89	0
1	F	463/488 (94%)	0.59	33 (7%) 19 26	16, 41, 75, 87	0
1	G	459/488 (94%)	0.64	54 (11%) 6 10	17, 40, 83, 93	0
1	H	458/488 (93%)	1.44	118 (25%) 1 1	25, 50, 84, 91	0
All	All	3710/3904 (95%)	0.50	302 (8%) 15 21	6, 37, 72, 93	0

The worst 5 of 302 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	469	VAL	9.9
1	H	454	LEU	9.2
1	H	479	LEU	7.4
1	H	293	PHE	7.0
1	H	448	ILE	6.8

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

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

6.3 Carbohydrates ⓘ

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
3	COA	F	1305	48/48	0.85	0.18	0.11	40,51,68,72	0
3	COA	G	1305	48/48	0.88	0.15	-0.33	29,45,57,59	0
3	COA	H	1305	48/48	0.83	0.22	-0.34	55,67,77,80	0
3	COA	E	1305	48/48	0.89	0.15	-0.65	39,48,65,70	0
2	CL	C	489	1/1	0.99	0.10	-1.26	39,39,39,39	0
2	CL	B	489	1/1	0.98	0.07	-1.66	37,37,37,37	0
2	CL	D	489	1/1	0.98	0.06	-4.00	36,36,36,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.