



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:00 AM GMT

PDB ID : 2VIG  
Title : CRYSTAL STRUCTURE OF HUMAN SHORT-CHAIN ACYL COA DEHYDROGENASE  
Authors : Pike, A.C.W.; Pantic, N.; Parizotto, E.; Gileadi, O.; Ugochukwu, E.; Von Delft, F.; Weigelt, J.; Arrowsmith, C.H.; Edwards, A.; Oppermann, U.  
Deposited on : 2007-11-30  
Resolution : 1.90 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](mailto: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.

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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

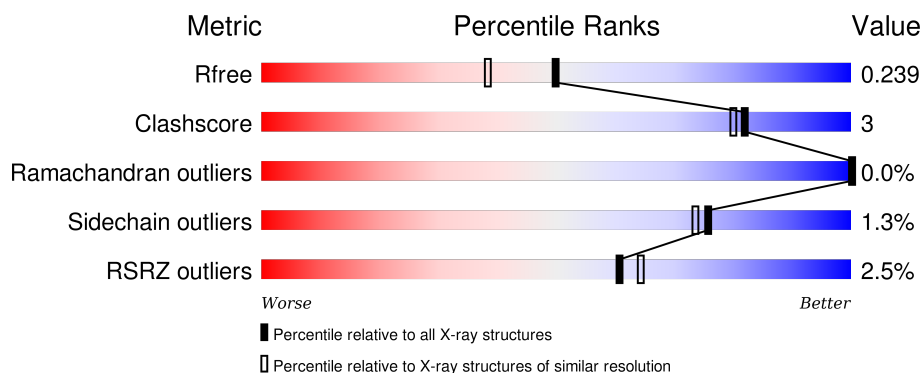
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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  $\geq 3$ , 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	391	<div> <div>2%</div> <div>90%</div> <div>7%</div> <div>.</div> </div>
1	B	391	<div> <div>4%</div> <div>86%</div> <div>8%</div> <div>5%</div> </div>
1	C	391	<div> <div>3%</div> <div>86%</div> <div>11%</div> <div>.</div> </div>
1	D	391	<div> <div>3%</div> <div>87%</div> <div>9%</div> <div>.</div> </div>
1	E	391	<div> <div>%</div> <div>88%</div> <div>9%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	391	
1	G	391	
1	H	391	

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
3	EDO	B	1412	-	-	-	X
3	EDO	D	1415	-	-	-	X
3	EDO	E	1414	-	-	-	X
3	EDO	E	1415	-	-	-	X
3	EDO	E	1416	-	-	-	X
3	EDO	F	1414	-	-	-	X
3	EDO	F	1415	-	-	-	X
3	EDO	F	1416	-	-	-	X
3	EDO	H	1414	-	-	-	X
4	COS	B	605	-	-	-	X
4	COS	C	605	-	-	-	X
4	COS	D	605	-	-	-	X
4	COS	F	605	-	-	-	X
4	COS	G	605	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 24035 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.

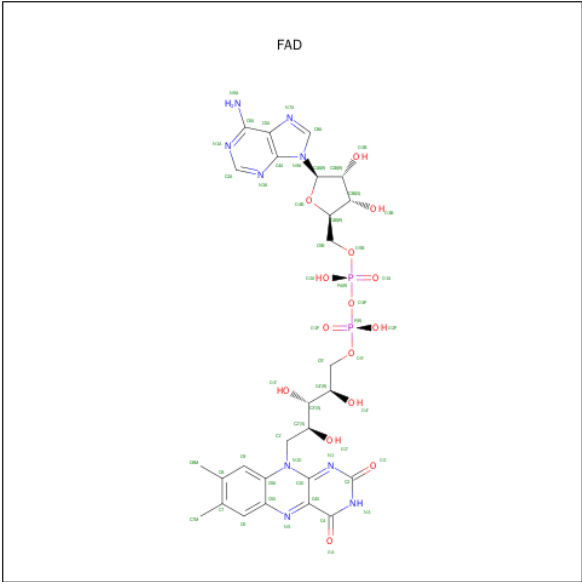
- Molecule 1 is a protein called SHORT-CHAIN SPECIFIC ACYL-COA DEHYDROGENASE,.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	379	Total	C	N	O	S	0	0	0
			2823	1790	482	532	19			
1	B	371	Total	C	N	O	S	0	0	0
			2748	1746	467	515	20			
1	C	379	Total	C	N	O	S	0	2	0
			2824	1795	482	528	19			
1	D	375	Total	C	N	O	S	0	0	0
			2781	1769	472	520	20			
1	E	380	Total	C	N	O	S	0	1	0
			2813	1785	482	527	19			
1	F	374	Total	C	N	O	S	0	1	0
			2776	1765	471	521	19			
1	G	375	Total	C	N	O	S	0	1	0
			2776	1762	475	520	19			
1	H	374	Total	C	N	O	S	0	0	0
			2760	1753	471	517	19			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	209	SER	GLY	CONFLICT SEE REMARK 9	UNP P16219
B	209	SER	GLY	CONFLICT SEE REMARK 9	UNP P16219
C	209	SER	GLY	CONFLICT SEE REMARK 9	UNP P16219
D	209	SER	GLY	CONFLICT SEE REMARK 9	UNP P16219
E	209	SER	GLY	CONFLICT SEE REMARK 9	UNP P16219
F	209	SER	GLY	CONFLICT SEE REMARK 9	UNP P16219
G	209	SER	GLY	CONFLICT SEE REMARK 9	UNP P16219
H	209	SER	GLY	CONFLICT SEE REMARK 9	UNP P16219

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



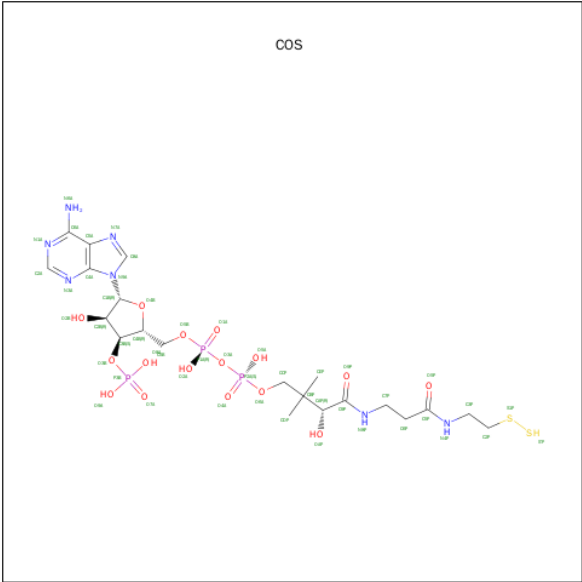
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	E	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	F	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	G	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	H	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

- Molecule 4 is COENZYME A PERSULFIDE (three-letter code: COS) (formula: C<sub>21</sub>H<sub>36</sub>N<sub>7</sub>O<sub>16</sub>P<sub>3</sub>S<sub>2</sub>).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	B	1	Total	C	N	O	P	S	0	0
			49	21	7	16	3	2		
4	C	1	Total	C	N	O	S		0	0
			10	5	2	1	2			
4	D	1	Total	C	N	O	S		0	0
			10	5	2	1	2			
4	F	1	Total	C	N	O	S		0	0
			10	5	2	1	2			
4	G	1	Total	C	N	O	P	S	0	0
			49	21	7	16	3	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	179	Total	O	0	0
			179	179		
5	B	122	Total	O	0	0
			122	122		
5	C	111	Total	O	0	0
			111	111		
5	D	122	Total	O	0	0
			122	122		
5	E	156	Total	O	0	5
			161	161		
5	F	160	Total	O	0	1
			161	161		
5	G	130	Total	O	0	0
			130	130		

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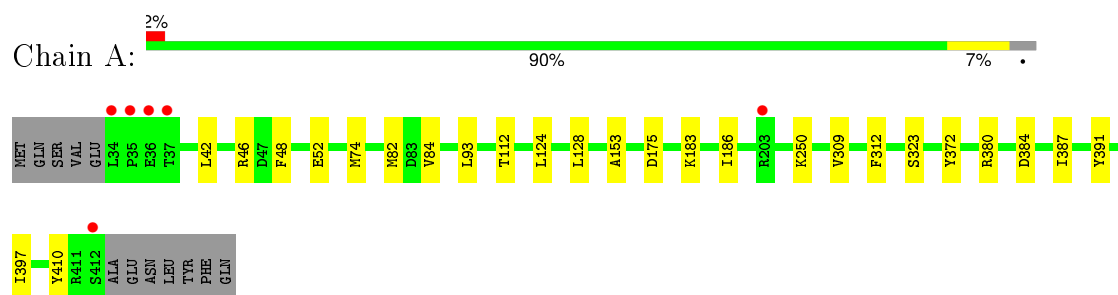
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	135	Total 135	O 135	0	0
5	L	13	Total 13	O 13	0	0

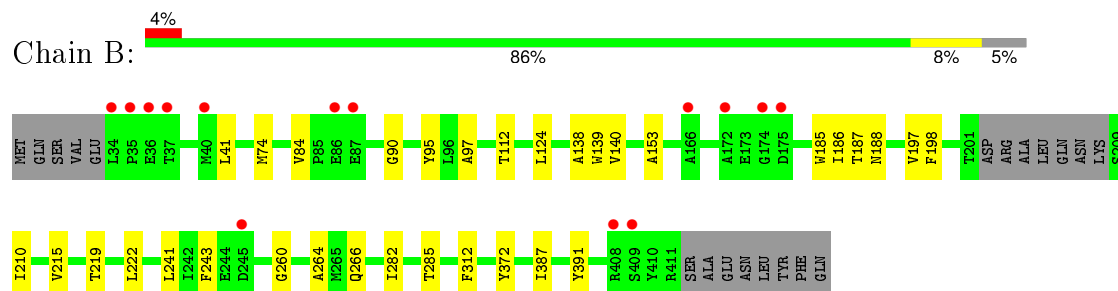
### 3 Residue-property plots [i](#)

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.

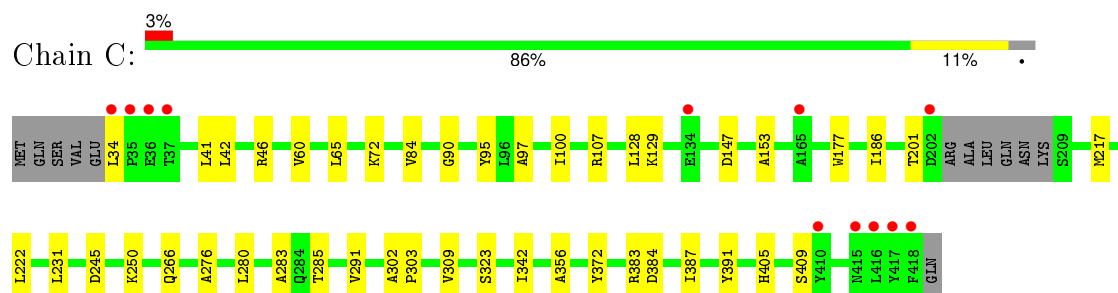
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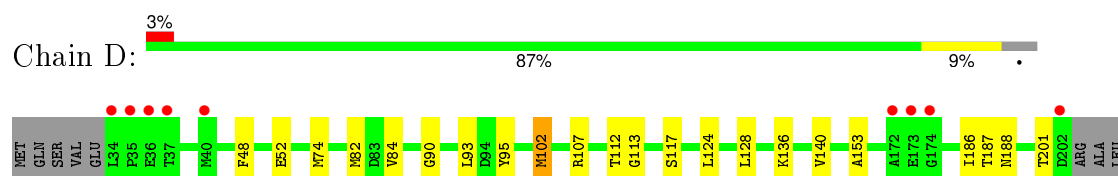
- Molecule 1: SHORT-CHAIN SPECIFIC ACYL-COA DEHYDROGENASE,



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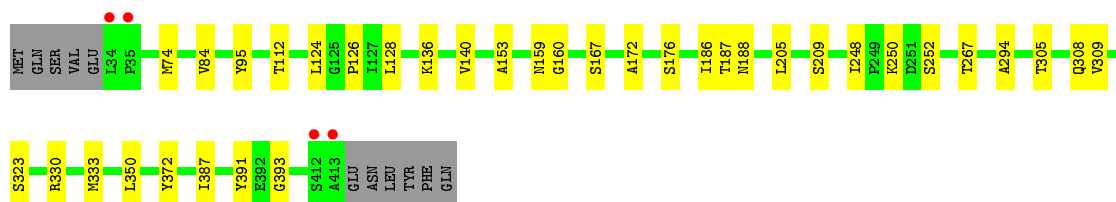
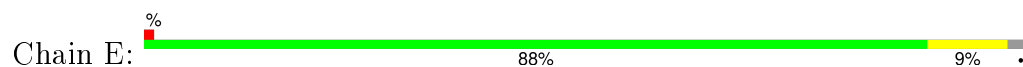


- Molecule 1: SHORT-CHAIN SPECIFIC ACYL-COA DEHYDROGENASE,

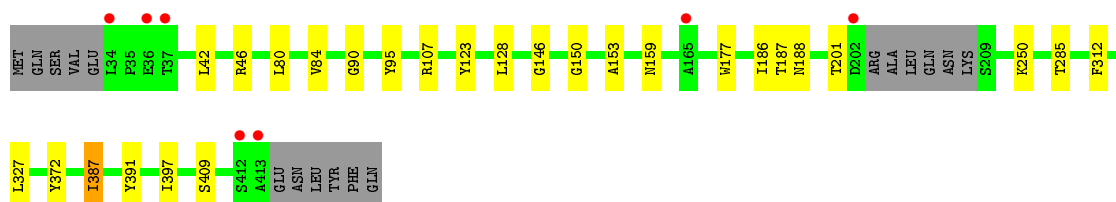
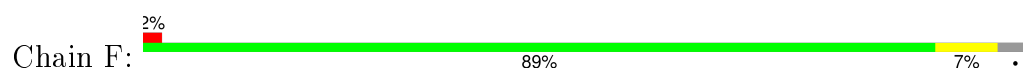




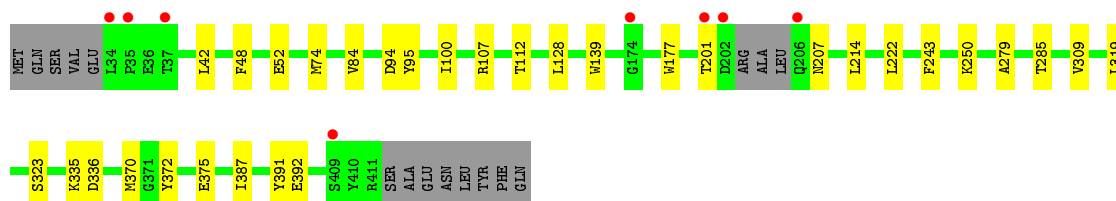
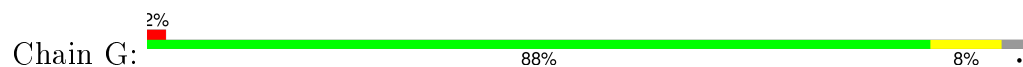
- Molecule 1: SHORT-CHAIN SPECIFIC ACYL-COA DEHYDROGENASE,



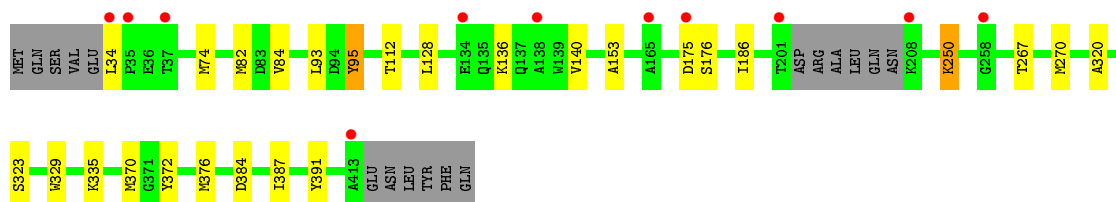
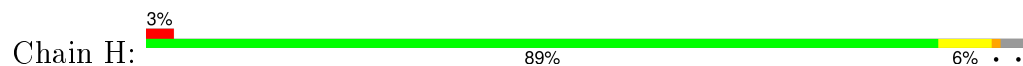
- Molecule 1: SHORT-CHAIN SPECIFIC ACYL-COA DEHYDROGENASE,



- Molecule 1: SHORT-CHAIN SPECIFIC ACYL-COA DEHYDROGENASE,



- Molecule 1: SHORT-CHAIN SPECIFIC ACYL-COA DEHYDROGENASE,



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	85.71Å 157.62Å 260.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	17.89 – 1.90 17.79 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.6 (17.89-1.90) 99.6 (17.79-1.90)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.40 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.3.0040	Depositor
R, $R_{free}$	0.198 , 0.231 0.205 , 0.239	Depositor DCC
$R_{free}$ test set	1730 reflections (0.63%)	DCC
Wilson B-factor (Å <sup>2</sup> )	27.5	Xtriage
Anisotropy	0.143	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 48.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 275747 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	24035	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.70% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: COS, EDO, FAD

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	0.61	0/2873	0.69	1/3887 (0.0%)
1	B	0.58	0/2797	0.64	0/3785
1	C	0.60	0/2888	0.65	0/3908
1	D	0.59	1/2830 (0.0%)	0.66	1/3827 (0.0%)
1	E	0.59	0/2868	0.65	0/3883
1	F	0.61	0/2830	0.68	0/3830
1	G	0.65	1/2830 (0.0%)	0.68	0/3832
1	H	0.61	1/2809 (0.0%)	0.66	0/3805
All	All	0.61	3/22725 (0.0%)	0.66	2/30757 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	246	CYS	CB-SG	-5.29	1.73	1.81
1	G	279	ALA	CA-CB	5.23	1.63	1.52
1	H	320	ALA	CA-CB	5.07	1.63	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	380	ARG	NE-CZ-NH1	-5.65	117.47	120.30
1	D	102	MET	CG-SD-CE	-5.48	91.43	100.20

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	2823	0	2833	17	0
1	B	2748	0	2748	18	0
1	C	2824	0	2823	25	0
1	D	2781	0	2792	20	0
1	E	2813	0	2815	25	0
1	F	2776	0	2780	15	0
1	G	2776	0	2763	19	0
1	H	2760	0	2745	16	0
2	A	53	0	31	0	0
2	B	53	0	31	2	0
2	C	53	0	31	0	0
2	D	53	0	31	2	0
2	E	53	0	31	0	0
2	F	53	0	31	2	0
2	G	53	0	31	1	0
2	H	53	0	31	0	0
3	A	4	0	6	0	0
3	B	4	0	6	0	0
3	D	8	0	12	0	0
3	E	12	0	18	1	0
3	F	12	0	18	0	0
3	H	8	0	12	0	0
4	B	49	0	32	6	0
4	C	10	0	10	0	0
4	D	10	0	10	0	0
4	F	10	0	10	1	0
4	G	49	0	32	6	0
5	A	179	0	0	0	0
5	B	122	0	0	0	0
5	C	111	0	0	0	0
5	D	122	0	0	0	0
5	E	161	0	0	3	0
5	F	161	0	0	2	0
5	G	130	0	0	0	0
5	H	135	0	0	0	0
5	L	13	0	0	0	0
All	All	24035	0	22713	148	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.

All (148) 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:E:84:VAL:HG22	1:E:128:LEU:HD11	1.50	0.93
1:H:84:VAL:HG22	1:H:128:LEU:HD11	1.59	0.83
1:G:84:VAL:HG22	1:G:128:LEU:HD11	1.66	0.77
1:C:129:LYS:NZ	1:C:266:GLN:OE1	2.18	0.77
1:A:84:VAL:HG22	1:A:128:LEU:HD11	1.66	0.76
1:C:42:LEU:HD21	1:C:46:ARG:HH21	1.53	0.72
1:D:84:VAL:HG22	1:D:128:LEU:HD11	1.71	0.72
1:A:323:SER:OG	1:C:323:SER:OG	2.09	0.71
1:H:153:ALA:HA	1:H:186:ILE:HD12	1.72	0.70
1:F:84:VAL:HG22	1:F:128:LEU:HD11	1.76	0.68
1:E:309:VAL:HG21	2:F:600:FAD:H2A	1.78	0.66
4:G:605:COS:H141	4:G:605:COS:N8P	2.09	0.65
1:E:205:LEU:O	1:E:209:SER:HB3	1.95	0.65
4:F:605:COS:H22	5:F:2055:HOH:O	1.99	0.61
1:B:266:GLN:HE21	4:B:605:COS:H2A	1.66	0.60
1:C:309:VAL:HG21	2:D:600:FAD:H2A	1.83	0.60
1:B:153:ALA:HA	1:B:186:ILE:HD12	1.84	0.59
1:B:312:PHE:CZ	1:C:309:VAL:HG11	2.36	0.59
4:G:605:COS:N8P	4:G:605:COS:CEP	2.65	0.59
4:B:605:COS:N8P	4:B:605:COS:CEP	2.66	0.58
1:E:308:GLN:HG2	5:E:2113:HOH:O	2.03	0.58
1:C:84:VAL:HG22	1:C:128:LEU:HD11	1.87	0.57
1:E:159:ASN:ND2	5:E:2046:HOH:O	2.37	0.57
1:F:153:ALA:HA	1:F:186:ILE:HD12	1.86	0.56
1:G:392:GLU:HA	4:G:605:COS:H31	1.88	0.56
1:C:72:LYS:NZ	1:C:147:ASP:OD1	2.31	0.56
1:C:84:VAL:HB	1:C:90:GLY:HA3	1.87	0.55
1:G:74:MET:SD	1:G:112:THR:CG2	2.95	0.55
1:E:172:ALA:HB1	1:E:250:LYS:HE2	1.88	0.55
1:E:309:VAL:CG2	2:F:600:FAD:H2A	2.38	0.54
1:E:172:ALA:HB1	1:E:250:LYS:CE	2.37	0.54
4:B:605:COS:N8P	4:B:605:COS:H141	2.23	0.54
1:D:84:VAL:HB	1:D:90:GLY:HA3	1.90	0.54
1:D:102:MET:HE1	1:D:117:SER:HB2	1.90	0.53
1:A:372:TYR:CZ	1:B:387:ILE:HB	2.43	0.53
4:G:605:COS:H141	4:G:605:COS:HN8	1.72	0.53
1:E:74:MET:SD	1:E:112:THR:CG2	2.96	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:MET:HE1	1:A:93:LEU:HD12	1.89	0.53
1:A:384:ASP:O	1:A:387:ILE:HG22	2.09	0.52
1:E:167:SER:OG	3:E:1416:EDO:H11	2.10	0.52
1:A:312:PHE:CZ	1:D:309:VAL:HG21	2.44	0.52
1:C:384:ASP:O	1:C:387:ILE:HG22	2.11	0.51
1:D:102:MET:HE1	1:D:113:GLY:O	2.10	0.51
1:C:387:ILE:HB	1:D:372:TYR:CZ	2.45	0.51
1:B:124:LEU:HD22	1:B:140:VAL:HG13	1.92	0.51
1:D:153:ALA:HA	1:D:186:ILE:HD12	1.93	0.51
1:E:330:ARG:HA	1:E:333:MET:HE3	1.90	0.51
1:A:175:ASP:O	1:A:250:LYS:HB3	2.10	0.51
1:G:372:TYR:CZ	1:H:387:ILE:HB	2.46	0.50
1:G:139:TRP:CD1	1:G:214:LEU:HD13	2.47	0.50
1:E:248:ILE:HD12	1:E:252:SER:CB	2.42	0.50
1:H:370:MET:CE	1:H:376:MET:HG2	2.42	0.50
1:A:82:MET:CE	1:A:93:LEU:HD12	2.41	0.49
1:D:107:ARG:HG3	1:D:285:THR:HB	1.94	0.49
1:B:198:PHE:CE1	1:B:264:ALA:HB2	2.46	0.49
1:E:153:ALA:HA	1:E:186:ILE:HD12	1.94	0.49
1:G:48:PHE:CE1	1:G:52:GLU:HG3	2.47	0.49
1:E:248:ILE:HD12	1:E:252:SER:HB3	1.94	0.49
1:H:74:MET:SD	1:H:112:THR:CG2	3.00	0.49
1:G:74:MET:SD	1:G:112:THR:HG21	2.53	0.49
1:F:187:THR:O	1:F:188:ASN:HB2	2.12	0.49
1:H:82:MET:HE3	1:H:93:LEU:HD12	1.94	0.49
1:B:41:LEU:CD2	1:B:97:ALA:HB1	2.43	0.48
1:A:153:ALA:HA	1:A:186:ILE:HD12	1.95	0.48
1:B:74:MET:SD	1:B:112:THR:CG2	3.01	0.48
1:G:207:ASN:HD22	4:G:605:COS:H52A	1.78	0.48
1:E:126:PRO:HD3	1:E:267:THR:HG23	1.96	0.48
1:A:48:PHE:CE1	1:A:52:GLU:HG3	2.49	0.48
1:E:350:LEU:HD23	1:G:319:LEU:HD22	1.96	0.48
1:E:387:ILE:HB	1:F:372:TYR:CZ	2.49	0.47
1:A:387:ILE:HB	1:B:372:TYR:CZ	2.49	0.47
1:E:323:SER:OG	1:G:323:SER:HB2	2.15	0.47
1:C:217:MET:HG2	1:C:222:LEU:HD21	1.97	0.47
2:G:600:FAD:O2'	4:G:605:COS:H32	2.12	0.47
1:A:74:MET:SD	1:A:112:THR:CG2	3.03	0.47
1:G:94:ASP:HB2	1:G:336:ASP:OD1	2.14	0.47
1:A:309:VAL:HG11	1:D:312:PHE:CE2	2.50	0.47
1:H:384:ASP:O	1:H:387:ILE:HG22	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:95:TYR:CD2	1:G:335:LYS:HE3	2.50	0.47
1:D:136:LYS:O	1:D:140:VAL:HB	2.15	0.47
1:G:222:LEU:HD13	1:G:243:PHE:CE1	2.50	0.46
1:B:282:ILE:O	1:B:285:THR:HG22	2.16	0.46
1:H:95:TYR:CD2	1:H:335:LYS:HE3	2.49	0.46
1:C:372:TYR:CZ	1:D:387:ILE:HB	2.50	0.46
1:B:222:LEU:HD13	1:B:243:PHE:CE1	2.51	0.46
1:B:187:THR:O	1:B:188:ASN:HB2	2.16	0.46
1:G:370:MET:HE1	1:G:375:GLU:HG2	1.97	0.46
1:F:159:ASN:ND2	5:F:2054:HOH:O	2.48	0.45
1:C:276:ALA:O	1:C:280:LEU:HG	2.17	0.45
1:E:74:MET:SD	1:E:112:THR:HG21	2.55	0.45
1:D:48:PHE:CE1	1:D:52:GLU:HG3	2.50	0.45
1:F:80[B]:LEU:CD2	1:F:146:GLY:HA2	2.47	0.45
1:G:177:TRP:CD1	1:G:250:LYS:HA	2.52	0.45
1:E:187:THR:O	1:E:188:ASN:HB2	2.18	0.44
4:B:605:COS:HN8	4:B:605:COS:H141	1.83	0.44
1:D:384:ASP:O	1:D:387:ILE:HG22	2.18	0.44
1:E:372:TYR:CZ	1:F:387:ILE:HB	2.52	0.44
2:B:600:FAD:O2'	4:B:605:COS:H32	2.17	0.44
1:F:312:PHE:CZ	1:G:309:VAL:HG21	2.53	0.44
1:D:124:LEU:HD22	1:D:140:VAL:HG13	1.98	0.43
1:C:153:ALA:HA	1:C:186:ILE:HD12	1.99	0.43
1:D:187:THR:O	1:D:188:ASN:HB2	2.19	0.43
1:A:410:TYR:CG	1:C:291:VAL:HG11	2.54	0.43
1:C:107:ARG:HG3	1:C:285:THR:HB	1.99	0.43
1:H:176:SER:O	1:H:250:LYS:NZ	2.52	0.43
1:D:82:MET:HE2	1:D:93:LEU:HD12	2.00	0.43
1:H:34:LEU:HD21	1:H:329:TRP:CZ3	2.53	0.43
1:H:34:LEU:HD21	1:H:329:TRP:CH2	2.53	0.43
1:B:84:VAL:HB	1:B:90:GLY:HA3	2.01	0.43
1:C:231:LEU:HD11	1:C:383:ARG:HG2	2.01	0.43
1:F:107:ARG:HG3	1:F:285:THR:HB	2.01	0.43
1:H:370:MET:HE2	1:H:376:MET:CG	2.49	0.42
1:B:138:ALA:HB3	1:B:139:TRP:CD1	2.54	0.42
1:C:309:VAL:CG2	2:D:600:FAD:H2A	2.47	0.42
1:D:262:LYS:CG	1:D:266:GLN:HE21	2.33	0.42
1:A:42:LEU:HD21	1:A:46:ARG:HH21	1.85	0.42
1:C:302:ALA:HB1	1:C:303:PRO:HD2	2.02	0.42
1:A:153:ALA:HB1	1:A:183:LYS:HG3	2.02	0.42
1:D:270:MET:SD	1:D:335:LYS:NZ	2.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:60:VAL:HG13	1:C:65:LEU:O	2.20	0.42
1:F:84:VAL:HG22	1:F:128:LEU:CD1	2.46	0.41
1:B:210:ILE:HG22	1:B:260:GLY:HA3	2.01	0.41
1:F:123:TYR:CG	1:F:150:GLY:HA3	2.55	0.41
1:G:107:ARG:HG3	1:G:285:THR:HB	2.01	0.41
1:G:42:LEU:HD12	1:G:100:ILE:HG23	2.01	0.41
1:B:185:TRP:O	2:B:600:FAD:C4X	2.69	0.41
1:C:41:LEU:HD22	1:C:97:ALA:HB1	2.01	0.41
1:G:387:ILE:HB	1:H:372:TYR:CZ	2.56	0.41
1:A:84:VAL:HG21	1:A:124:LEU:HD13	2.03	0.41
1:B:197:VAL:HG21	1:B:215:VAL:HG21	2.03	0.41
1:F:177:TRP:CD1	1:F:250:LYS:HA	2.56	0.41
1:F:42:LEU:HD21	1:F:46:ARG:HH11	1.86	0.41
1:F:327:LEU:HD11	1:H:323:SER:OG	2.21	0.41
1:C:342:ILE:HG21	1:C:405:HIS:CE1	2.56	0.41
1:C:177:TRP:CD1	1:C:250:LYS:HA	2.56	0.41
1:E:124:LEU:HD22	1:E:140:VAL:HG13	2.03	0.41
4:B:605:COS:O5A	4:B:605:COS:H133	2.21	0.41
1:D:82:MET:CE	1:D:93:LEU:HD12	2.51	0.41
1:B:186:ILE:HG13	1:B:241:LEU:HG	2.03	0.40
1:D:74:MET:SD	1:D:112:THR:CG2	3.09	0.40
1:H:267:THR:HA	1:H:270:MET:HE2	2.03	0.40
1:H:136:LYS:O	1:H:140:VAL:HB	2.21	0.40
1:F:84:VAL:HB	1:F:90:GLY:HA3	2.03	0.40
1:C:283:ALA:HB2	1:C:356:ALA:HA	2.04	0.40
1:E:136:LYS:O	1:E:140:VAL:HB	2.21	0.40
1:C:34:LEU:HD21	1:C:100:ILE:HD11	2.03	0.40
1:E:294:ALA:HB1	1:E:305:THR:HG23	2.03	0.40
1:E:393:GLY:HA2	5:E:2150:HOH:O	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	377/391 (96%)	366 (97%)	11 (3%)	0	100	100
1	B	367/391 (94%)	356 (97%)	11 (3%)	0	100	100
1	C	377/391 (96%)	366 (97%)	11 (3%)	0	100	100
1	D	371/391 (95%)	361 (97%)	10 (3%)	0	100	100
1	E	379/391 (97%)	367 (97%)	11 (3%)	1 (0%)	46	35
1	F	371/391 (95%)	362 (98%)	9 (2%)	0	100	100
1	G	372/391 (95%)	363 (98%)	9 (2%)	0	100	100
1	H	370/391 (95%)	361 (98%)	9 (2%)	0	100	100
All	All	2984/3128 (95%)	2902 (97%)	81 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	160	GLY

### 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	284/303 (94%)	282 (99%)	2 (1%)	88	88
1	B	274/303 (90%)	271 (99%)	3 (1%)	80	79
1	C	283/303 (93%)	278 (98%)	5 (2%)	66	61
1	D	277/303 (91%)	273 (99%)	4 (1%)	74	71
1	E	280/303 (92%)	277 (99%)	3 (1%)	80	79
1	F	277/303 (91%)	271 (98%)	6 (2%)	60	53
1	G	275/303 (91%)	273 (99%)	2 (1%)	88	88
1	H	272/303 (90%)	268 (98%)	4 (2%)	72	69
All	All	2222/2424 (92%)	2193 (99%)	29 (1%)	76	73

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	391	TYR
1	A	397	ILE
1	B	95	TYR
1	B	219	THR
1	B	391	TYR
1	C	95	TYR
1	C	201	THR
1	C	245	ASP
1	C	391	TYR
1	C	409	SER
1	D	95	TYR
1	D	201	THR
1	D	391	TYR
1	D	412	SER
1	E	95	TYR
1	E	176	SER
1	E	391	TYR
1	F	95	TYR
1	F	201	THR
1	F	387	ILE
1	F	391	TYR
1	F	397	ILE
1	F	409	SER
1	G	201	THR
1	G	391	TYR
1	H	95	TYR
1	H	175	ASP
1	H	250	LYS
1	H	391	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	159	ASN
1	A	405	HIS
1	D	266	GLN
1	G	207	ASN

### 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](#)

25 ligands 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	$\# Z  > 2$
3	EDO	A	1413	-	3,3,3	0.45	0	2,2,2	0.32	0
2	FAD	A	600	-	48,58,58	1.17	3 (6%)	54,89,89	2.09	11 (20%)
3	EDO	B	1412	-	3,3,3	0.57	0	2,2,2	0.18	0
2	FAD	B	600	-	48,58,58	1.35	5 (10%)	54,89,89	2.22	13 (24%)
4	COS	B	605	-	40,51,51	1.17	5 (12%)	52,76,76	2.05	10 (19%)
2	FAD	C	600	-	48,58,58	1.49	6 (12%)	54,89,89	2.30	15 (27%)
4	COS	C	605	-	7,9,51	0.50	0	8,9,76	1.01	1 (12%)
3	EDO	D	1414	-	3,3,3	0.66	0	2,2,2	0.07	0
3	EDO	D	1415	-	3,3,3	0.53	0	2,2,2	0.43	0
2	FAD	D	600	-	48,58,58	1.18	2 (4%)	54,89,89	2.14	10 (18%)
4	COS	D	605	-	7,9,51	0.65	0	8,9,76	0.58	0
3	EDO	E	1414	-	3,3,3	0.62	0	2,2,2	0.23	0
3	EDO	E	1415	-	3,3,3	0.53	0	2,2,2	0.52	0
3	EDO	E	1416	-	3,3,3	0.57	0	2,2,2	0.31	0
2	FAD	E	600	-	48,58,58	1.47	7 (14%)	54,89,89	2.08	13 (24%)
3	EDO	F	1414	-	3,3,3	0.62	0	2,2,2	0.21	0
3	EDO	F	1415	-	3,3,3	0.39	0	2,2,2	0.79	0
3	EDO	F	1416	-	3,3,3	0.63	0	2,2,2	0.18	0
2	FAD	F	600	-	48,58,58	1.22	6 (12%)	54,89,89	2.05	9 (16%)
4	COS	F	605	-	7,9,51	0.45	0	8,9,76	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	FAD	G	600	-	48,58,58	1.25	6 (12%)	54,89,89	2.19	11 (20%)
4	COS	G	605	-	40,51,51	1.31	4 (10%)	52,76,76	1.75	7 (13%)
3	EDO	H	1414	-	3,3,3	0.57	0	2,2,2	0.09	0
3	EDO	H	1415	-	3,3,3	0.55	0	2,2,2	0.27	0
2	FAD	H	600	-	48,58,58	1.30	6 (12%)	54,89,89	2.28	13 (24%)

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	EDO	A	1413	-	-	0/1/1/1	0/0/0/0
2	FAD	A	600	-	-	0/30/50/50	0/6/6/6
3	EDO	B	1412	-	-	0/1/1/1	0/0/0/0
2	FAD	B	600	-	-	0/30/50/50	0/6/6/6
4	COS	B	605	-	-	0/44/65/65	0/3/3/3
2	FAD	C	600	-	-	0/30/50/50	0/6/6/6
4	COS	C	605	-	-	0/7/8/65	0/0/0/3
3	EDO	D	1414	-	-	0/1/1/1	0/0/0/0
3	EDO	D	1415	-	-	0/1/1/1	0/0/0/0
2	FAD	D	600	-	-	0/30/50/50	0/6/6/6
4	COS	D	605	-	-	0/7/8/65	0/0/0/3
3	EDO	E	1414	-	-	0/1/1/1	0/0/0/0
3	EDO	E	1415	-	-	0/1/1/1	0/0/0/0
3	EDO	E	1416	-	-	0/1/1/1	0/0/0/0
2	FAD	E	600	-	-	0/30/50/50	0/6/6/6
3	EDO	F	1414	-	-	0/1/1/1	0/0/0/0
3	EDO	F	1415	-	-	0/1/1/1	0/0/0/0
3	EDO	F	1416	-	-	0/1/1/1	0/0/0/0
2	FAD	F	600	-	-	0/30/50/50	0/6/6/6
4	COS	F	605	-	-	0/7/8/65	0/0/0/3
2	FAD	G	600	-	-	0/30/50/50	0/6/6/6
4	COS	G	605	-	-	0/44/65/65	0/3/3/3
3	EDO	H	1414	-	-	0/1/1/1	0/0/0/0
3	EDO	H	1415	-	-	0/1/1/1	0/0/0/0
2	FAD	H	600	-	-	0/30/50/50	0/6/6/6

All (50) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	600	FAD	C6-C5X	-2.31	1.38	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	600	FAD	P-O2P	-2.20	1.45	1.54
2	G	600	FAD	C5A-N7A	-2.11	1.32	1.39
2	F	600	FAD	O5'-C5'	-2.09	1.36	1.44
2	E	600	FAD	O5'-C5'	-2.07	1.36	1.44
2	B	600	FAD	C9A-C5X	-2.02	1.38	1.42
2	A	600	FAD	C10-N1	2.00	1.39	1.35
4	B	605	COS	C5B-C4B	2.00	1.58	1.51
2	F	600	FAD	PA-O1A	2.01	1.58	1.51
2	C	600	FAD	PA-O1A	2.01	1.58	1.51
2	D	600	FAD	P-O1P	2.01	1.58	1.51
2	E	600	FAD	C10-N1	2.04	1.39	1.35
2	G	600	FAD	P-O1P	2.04	1.58	1.51
2	E	600	FAD	C4'-C3'	2.11	1.57	1.53
2	C	600	FAD	O3'-C3'	2.15	1.48	1.43
2	C	600	FAD	P-O1P	2.15	1.59	1.51
4	B	605	COS	P3B-O8A	2.21	1.62	1.54
2	G	600	FAD	C5'-C4'	2.24	1.55	1.51
2	H	600	FAD	C7M-C7	2.34	1.55	1.51
4	G	605	COS	P3B-O8A	2.35	1.63	1.54
2	H	600	FAD	C5'-C4'	2.37	1.55	1.51
2	F	600	FAD	C9A-N10	2.41	1.42	1.38
2	B	600	FAD	C8M-C8	2.42	1.55	1.51
2	F	600	FAD	C5'-C4'	2.49	1.55	1.51
2	G	600	FAD	C1'-N10	2.49	1.51	1.48
2	F	600	FAD	O4B-C1B	2.59	1.44	1.41
2	E	600	FAD	PA-O1A	2.59	1.60	1.51
2	H	600	FAD	PA-O1A	2.66	1.60	1.51
2	G	600	FAD	PA-O1A	2.72	1.61	1.51
4	B	605	COS	O4B-C1B	2.78	1.44	1.41
2	F	600	FAD	C4-N3	2.78	1.38	1.33
2	H	600	FAD	C10-N1	2.84	1.40	1.35
2	H	600	FAD	O4B-C1B	2.94	1.44	1.41
2	B	600	FAD	C10-N1	2.95	1.40	1.35
2	E	600	FAD	C4-N3	2.98	1.38	1.33
2	C	600	FAD	C10-N1	3.10	1.40	1.35
4	B	605	COS	P1A-O1A	3.11	1.62	1.51
2	C	600	FAD	C4-N3	3.29	1.39	1.33
4	B	605	COS	P3B-O7A	3.34	1.62	1.51
4	G	605	COS	P1A-O1A	3.40	1.63	1.51
2	A	600	FAD	C4-N3	3.62	1.39	1.33
2	B	600	FAD	C4-N3	3.74	1.40	1.33
4	G	605	COS	P3B-O7A	3.75	1.63	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	600	FAD	C4-N3	3.83	1.40	1.33
2	D	600	FAD	C4-N3	3.92	1.40	1.33
2	G	600	FAD	C4-N3	4.18	1.40	1.33
4	G	605	COS	O4B-C1B	4.42	1.46	1.41
2	B	600	FAD	O4B-C1B	4.85	1.47	1.41
2	C	600	FAD	O4B-C1B	5.77	1.48	1.41
2	E	600	FAD	O4B-C1B	5.92	1.48	1.41

All (113) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	600	FAD	N3A-C2A-N1A	-10.72	120.68	128.89
2	F	600	FAD	N3A-C2A-N1A	-10.41	120.92	128.89
2	A	600	FAD	N3A-C2A-N1A	-10.14	121.13	128.89
2	C	600	FAD	N3A-C2A-N1A	-9.70	121.47	128.89
2	D	600	FAD	N3A-C2A-N1A	-9.55	121.58	128.89
4	B	605	COS	N3A-C2A-N1A	-9.54	121.59	128.89
2	B	600	FAD	N3A-C2A-N1A	-9.36	121.73	128.89
4	G	605	COS	N3A-C2A-N1A	-9.15	121.89	128.89
2	H	600	FAD	N3A-C2A-N1A	-9.11	121.92	128.89
2	E	600	FAD	N3A-C2A-N1A	-8.97	122.03	128.89
2	H	600	FAD	C2B-C1B-N9A	-5.65	105.66	114.29
4	B	605	COS	C2B-C1B-N9A	-5.03	106.60	114.29
2	H	600	FAD	P-O3P-PA	-4.74	119.42	132.73
2	B	600	FAD	P-O3P-PA	-4.61	119.78	132.73
2	D	600	FAD	C2B-C1B-N9A	-4.41	107.56	114.29
2	H	600	FAD	C4X-C10-N10	-3.65	118.37	120.52
2	C	600	FAD	C4B-O4B-C1B	-3.60	105.77	109.72
2	D	600	FAD	P-O3P-PA	-3.51	122.87	132.73
2	A	600	FAD	P-O3P-PA	-3.46	123.01	132.73
2	G	600	FAD	P-O3P-PA	-3.43	123.10	132.73
2	D	600	FAD	C4X-C4-N3	-3.41	118.93	123.59
4	B	605	COS	P2A-O3A-P1A	-3.37	123.26	132.73
4	B	605	COS	C7P-C6P-C5P	-3.33	106.82	112.31
2	F	600	FAD	C1B-N9A-C4A	-3.25	122.04	126.94
2	B	600	FAD	C4X-C10-N10	-3.22	118.62	120.52
4	B	605	COS	C4B-O4B-C1B	-3.22	106.19	109.72
2	D	600	FAD	C4B-O4B-C1B	-3.20	106.20	109.72
2	B	600	FAD	C2B-C1B-N9A	-3.17	109.44	114.29
4	G	605	COS	C7P-C6P-C5P	-3.15	107.11	112.31
2	G	600	FAD	C4A-C5A-N7A	-3.14	106.59	109.48
2	B	600	FAD	C4X-C4-N3	-3.08	119.38	123.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	600	FAD	C4-C4X-C10	-3.07	117.98	119.94
2	C	600	FAD	C4A-C5A-N7A	-3.04	106.69	109.48
2	E	600	FAD	C4-C4X-C10	-2.97	118.04	119.94
2	H	600	FAD	C4X-C4-N3	-2.95	119.56	123.59
2	H	600	FAD	C4B-O4B-C1B	-2.91	106.52	109.72
2	F	600	FAD	C4X-C4-N3	-2.91	119.61	123.59
4	G	605	COS	P2A-O3A-P1A	-2.89	124.61	132.73
2	H	600	FAD	C4A-C5A-N7A	-2.79	106.92	109.48
2	F	600	FAD	C4A-C5A-N7A	-2.79	106.92	109.48
2	B	600	FAD	C1B-N9A-C4A	-2.77	122.76	126.94
2	G	600	FAD	C4X-C4-N3	-2.74	119.84	123.59
2	F	600	FAD	P-O3P-PA	-2.71	125.12	132.73
2	A	600	FAD	C4X-C4-N3	-2.71	119.89	123.59
2	C	600	FAD	C4X-C4-N3	-2.67	119.94	123.59
2	E	600	FAD	C4B-O4B-C1B	-2.66	106.79	109.72
2	A	600	FAD	O4'-C4'-C5'	-2.65	104.42	110.19
2	E	600	FAD	C4X-C10-N10	-2.62	118.97	120.52
2	A	600	FAD	C4B-O4B-C1B	-2.57	106.89	109.72
2	A	600	FAD	C1B-N9A-C4A	-2.55	123.09	126.94
2	G	600	FAD	C4B-O4B-C1B	-2.53	106.94	109.72
4	C	605	COS	C2P-C3P-N4P	-2.51	107.33	112.36
2	E	600	FAD	C2B-C1B-N9A	-2.51	110.46	114.29
2	B	600	FAD	C4B-O4B-C1B	-2.49	106.98	109.72
2	C	600	FAD	P-O3P-PA	-2.45	125.85	132.73
2	B	600	FAD	C4A-C5A-N7A	-2.44	107.23	109.48
2	A	600	FAD	C5B-C4B-C3B	-2.40	105.68	115.21
2	E	600	FAD	C9A-C5X-N5	-2.37	118.85	122.36
2	C	600	FAD	C1B-N9A-C4A	-2.33	123.43	126.94
2	D	600	FAD	C1B-N9A-C4A	-2.33	123.43	126.94
2	B	600	FAD	O5B-PA-O1A	-2.31	100.66	109.62
2	D	600	FAD	C4A-C5A-N7A	-2.21	107.45	109.48
2	E	600	FAD	C4X-C4-N3	-2.20	120.58	123.59
4	G	605	COS	C4B-O4B-C1B	-2.13	107.37	109.72
4	B	605	COS	C2P-C3P-N4P	-2.09	108.18	112.36
2	E	600	FAD	O4'-C4'-C5'	-2.07	105.69	110.19
4	G	605	COS	C2B-C1B-N9A	-2.06	111.15	114.29
4	B	605	COS	C6P-C7P-N8P	-2.04	107.41	111.88
2	C	600	FAD	C9A-C5X-N5	-2.03	119.35	122.36
2	C	600	FAD	O5B-PA-O1A	-2.02	101.78	109.62
2	E	600	FAD	C4A-C5A-N7A	-2.01	107.63	109.48
4	G	605	COS	C6P-C7P-N8P	-2.00	107.48	111.88
4	B	605	COS	O2A-P1A-O3A	2.01	114.19	105.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	605	COS	O2A-P1A-O3A	2.09	114.56	105.09
2	C	600	FAD	C1'-N10-C9A	2.15	121.27	118.86
2	B	600	FAD	C4X-N5-C5X	2.15	119.23	116.76
2	D	600	FAD	O2'-C2'-C3'	2.15	114.41	109.02
2	B	600	FAD	O2P-P-O3P	2.16	114.90	105.09
2	G	600	FAD	C4X-N5-C5X	2.18	119.27	116.76
2	C	600	FAD	O4B-C1B-N9A	2.21	112.72	108.10
2	H	600	FAD	C5X-C9A-N10	2.23	119.31	117.62
2	F	600	FAD	C2A-N1A-C6A	2.25	122.78	118.77
2	H	600	FAD	O2A-PA-O3P	2.29	115.49	105.09
2	H	600	FAD	O2P-P-O3P	2.33	115.64	105.09
2	G	600	FAD	O3'-C3'-C4'	2.33	114.61	108.75
2	C	600	FAD	C6-C5X-N5	2.34	121.98	118.96
2	H	600	FAD	C4-C4X-N5	2.37	121.59	118.72
4	B	605	COS	O4B-C1B-N9A	2.42	113.17	108.10
2	E	600	FAD	C6-C5X-N5	2.44	122.10	118.96
2	F	600	FAD	O2'-C2'-C1'	2.55	116.21	109.94
2	A	600	FAD	C4-C4X-N5	2.60	121.87	118.72
2	G	600	FAD	O3P-PA-O5B	2.60	109.83	102.94
2	G	600	FAD	C4-C4X-N5	2.67	121.96	118.72
2	D	600	FAD	C4-C4X-N5	2.71	122.01	118.72
2	E	600	FAD	C4X-N5-C5X	2.74	119.91	116.76
2	C	600	FAD	C4X-N5-C5X	2.80	119.98	116.76
2	A	600	FAD	O2P-P-O3P	2.87	118.12	105.09
2	A	600	FAD	O2'-C2'-C3'	2.93	116.39	109.02
4	B	605	COS	CDP-CBP-CCP	2.94	112.32	108.50
2	H	600	FAD	C6-C5X-N5	3.02	122.85	118.96
2	B	600	FAD	C4-C4X-N5	3.07	122.45	118.72
2	F	600	FAD	C4-C4X-N5	3.25	122.66	118.72
2	G	600	FAD	O2A-PA-O3P	3.37	120.37	105.09
2	E	600	FAD	C4-C4X-N5	3.82	123.36	118.72
2	C	600	FAD	C4-C4X-N5	4.41	124.08	118.72
2	G	600	FAD	C4-N3-C2	4.93	119.51	115.25
2	A	600	FAD	C4-N3-C2	5.51	120.01	115.25
2	F	600	FAD	C4-N3-C2	5.74	120.20	115.25
2	H	600	FAD	C4-N3-C2	6.47	120.84	115.25
2	E	600	FAD	C4-N3-C2	6.64	120.98	115.25
2	B	600	FAD	C4-N3-C2	6.97	121.27	115.25
2	D	600	FAD	C4-N3-C2	7.03	121.32	115.25
2	C	600	FAD	C4-N3-C2	7.49	121.72	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	600	FAD	2	0
4	B	605	COS	6	0
2	D	600	FAD	2	0
3	E	1416	EDO	1	0
2	F	600	FAD	2	0
4	F	605	COS	1	0
2	G	600	FAD	1	0
4	G	605	COS	6	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	379/391 (96%)	-0.04	6 (1%) 74 78	18, 27, 42, 53	0
1	B	371/391 (94%)	0.00	14 (3%) 44 48	20, 29, 42, 59	0
1	C	379/391 (96%)	0.07	12 (3%) 51 54	19, 29, 44, 72	1 (0%)
1	D	375/391 (95%)	-0.01	12 (3%) 51 54	20, 29, 43, 58	0
1	E	380/391 (97%)	-0.05	4 (1%) 82 84	17, 28, 42, 64	0
1	F	374/391 (95%)	-0.02	7 (1%) 70 73	18, 27, 43, 57	0
1	G	375/391 (95%)	0.08	8 (2%) 67 70	18, 29, 43, 66	0
1	H	374/391 (95%)	0.07	11 (2%) 55 59	18, 29, 42, 60	0
All	All	3007/3128 (96%)	0.01	74 (2%) 61 64	17, 28, 43, 72	1 (0%)

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	413	ALA	6.3
1	D	413	ALA	6.2
1	E	34	LEU	5.3
1	F	413	ALA	5.3
1	C	417	TYR	4.8
1	A	35	PRO	4.7
1	G	34	LEU	4.6
1	E	412	SER	4.5
1	D	412	SER	4.4
1	B	175	ASP	4.3
1	C	35	PRO	4.3
1	D	35	PRO	4.2
1	F	412	SER	3.9
1	H	413	ALA	3.9
1	D	36	GLU	3.8
1	H	35	PRO	3.8

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Mol	Chain	Res	Type	RSRZ
1	E	35	PRO	3.7
1	H	34	LEU	3.6
1	D	40	MET	3.4
1	H	175	ASP	3.4
1	H	37	THR	3.3
1	C	416	LEU	3.3
1	F	36	GLU	3.2
1	C	36	GLU	3.1
1	G	37	THR	3.0
1	G	35	PRO	3.0
1	C	202	ASP	3.0
1	B	172	ALA	3.0
1	A	412	SER	3.0
1	G	206	GLN	3.0
1	B	35	PRO	3.0
1	H	208	LYS	3.0
1	C	165	ALA	3.0
1	F	202	ASP	2.9
1	C	418	PHE	2.8
1	D	202	ASP	2.8
1	A	36	GLU	2.8
1	D	34	LEU	2.8
1	A	37	THR	2.7
1	F	34	LEU	2.7
1	G	201	THR	2.7
1	D	37	THR	2.6
1	C	410	TYR	2.6
1	H	165	ALA	2.5
1	C	37	THR	2.5
1	B	174	GLY	2.5
1	F	165	ALA	2.5
1	B	34	LEU	2.5
1	H	201	THR	2.5
1	B	87	GLU	2.4
1	B	40	MET	2.4
1	B	409	SER	2.4
1	B	37	THR	2.3
1	C	415	ASN	2.3
1	B	86	GLU	2.3
1	D	208	LYS	2.3
1	G	174	GLY	2.3
1	H	134	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	172	ALA	2.2
1	C	34	LEU	2.2
1	B	36	GLU	2.2
1	B	166	ALA	2.2
1	H	258	GLY	2.2
1	A	34	LEU	2.2
1	G	202	ASP	2.2
1	D	173	GLU	2.2
1	B	245	ASP	2.1
1	A	203	ARG	2.1
1	H	138	ALA	2.1
1	F	37	THR	2.1
1	G	409	SER	2.0
1	B	408	ARG	2.0
1	C	134	GLU	2.0
1	D	174	GLY	2.0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
4	COS	B	605	49/49	0.66	0.39	11.65	56,114,131,134	0
3	EDO	E	1416	4/4	0.93	0.33	9.29	31,31,34,36	0
4	COS	D	605	10/49	0.70	0.28	8.57	44,74,102,105	0
4	COS	G	605	49/49	0.82	0.28	7.05	26,70,88,92	0
3	EDO	F	1416	4/4	0.89	0.26	6.89	35,37,40,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	EDO	E	1414	4/4	0.89	0.19	5.20	37,41,45,49	0
4	COS	C	605	10/49	0.82	0.21	4.95	51,65,78,109	0
3	EDO	H	1414	4/4	0.92	0.21	4.87	32,40,47,48	0
3	EDO	D	1415	4/4	0.91	0.16	4.78	29,34,39,57	0
4	COS	F	605	10/49	0.82	0.19	4.66	41,69,75,97	0
3	EDO	F	1415	4/4	0.92	0.21	3.73	34,36,43,50	0
3	EDO	E	1415	4/4	0.96	0.13	2.59	21,28,38,43	0
3	EDO	F	1414	4/4	0.92	0.14	2.47	35,36,36,36	0
3	EDO	B	1412	4/4	0.85	0.14	2.12	47,51,54,57	0
3	EDO	A	1413	4/4	0.94	0.11	1.71	29,48,52,58	0
3	EDO	D	1414	4/4	0.87	0.12	1.06	44,44,50,53	0
2	FAD	C	600	53/53	0.97	0.10	0.25	18,26,35,39	0
2	FAD	A	600	53/53	0.97	0.10	-0.22	14,22,29,33	0
2	FAD	D	600	53/53	0.97	0.09	-0.28	17,26,38,46	0
2	FAD	G	600	53/53	0.97	0.10	-0.30	15,21,30,35	0
2	FAD	H	600	53/53	0.97	0.09	-0.40	17,25,31,31	0
2	FAD	F	600	53/53	0.98	0.10	-0.42	14,22,30,33	0
2	FAD	B	600	53/53	0.97	0.08	-0.59	18,26,33,42	0
2	FAD	E	600	53/53	0.97	0.09	-0.66	14,22,30,37	0
3	EDO	H	1415	4/4	0.95	0.14	-	32,39,44,45	0

## 6.5 Other polymers

There are no such residues in this entry.