



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 03:14 am GMT

PDB ID : 3WCJ
Title : The complex structure of HsSQS wtih ligand,E5700
Authors : Shang, N.; Li, Q.; Ko, T.P.; Chan, H.C.; Huang, C.H.; Ren, F.; Zheng, Y.;
Zhu, Z.; Chen, C.C.; Guo, R.T.
Deposited on : 2013-05-27
Resolution : 2.20 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

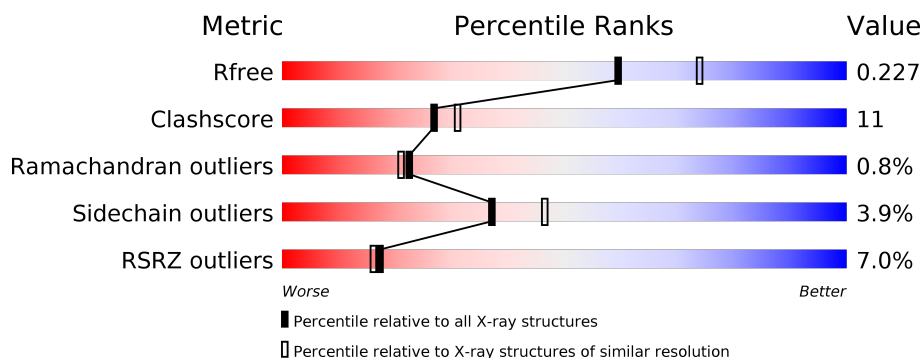
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	100719	4002 (2.20-2.20)
Clashscore	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)
RSRZ outliers	101464	4033 (2.20-2.20)

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	360	<div> <div>4%</div> <div> <div></div> <div>76%</div> <div>14%</div> <div>•</div> <div>7%</div> </div> </div>
1	B	360	<div> <div>4%</div> <div> <div></div> <div>75%</div> <div>15%</div> <div>•</div> <div>8%</div> </div> </div>
1	C	360	<div> <div>6%</div> <div> <div></div> <div>72%</div> <div>19%</div> <div>•</div> <div>7%</div> </div> </div>
1	D	360	<div> <div>6%</div> <div> <div></div> <div>67%</div> <div>24%</div> <div>•</div> <div>7%</div> </div> </div>
1	E	360	<div> <div>7%</div> <div> <div></div> <div>70%</div> <div>21%</div> <div>•</div> <div>7%</div> </div> </div>
1	F	360	<div> <div>13%</div> <div> <div></div> <div>63%</div> <div>27%</div> <div>•</div> <div>7%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 17199 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 Squalene synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	334	Total	C	N	O	S	0	0	0
			2696	1717	458	503	18			
1	B	332	Total	C	N	O	S	0	0	0
			2678	1705	453	502	18			
1	C	335	Total	C	N	O	S	0	0	0
			2704	1721	460	505	18			
1	D	335	Total	C	N	O	S	0	0	0
			2704	1721	460	505	18			
1	E	335	Total	C	N	O	S	0	0	0
			2704	1721	460	505	18			
1	F	334	Total	C	N	O	S	0	0	0
			2696	1717	458	503	18			

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	11	MET	-	EXPRESSION TAG	UNP P37268
A	12	GLY	-	EXPRESSION TAG	UNP P37268
A	13	SER	-	EXPRESSION TAG	UNP P37268
A	14	SER	-	EXPRESSION TAG	UNP P37268
A	15	HIS	-	EXPRESSION TAG	UNP P37268
A	16	HIS	-	EXPRESSION TAG	UNP P37268
A	17	HIS	-	EXPRESSION TAG	UNP P37268
A	18	HIS	-	EXPRESSION TAG	UNP P37268
A	19	HIS	-	EXPRESSION TAG	UNP P37268
A	20	HIS	-	EXPRESSION TAG	UNP P37268
A	21	SER	-	EXPRESSION TAG	UNP P37268
A	22	SER	-	EXPRESSION TAG	UNP P37268
A	23	GLY	-	EXPRESSION TAG	UNP P37268
A	24	LEU	-	EXPRESSION TAG	UNP P37268
A	25	VAL	-	EXPRESSION TAG	UNP P37268
A	26	PRO	-	EXPRESSION TAG	UNP P37268
A	27	ARG	-	EXPRESSION TAG	UNP P37268

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Chain	Residue	Modelled	Actual	Comment	Reference
A	28	GLY	-	EXPRESSION TAG	UNP P37268
A	29	SER	-	EXPRESSION TAG	UNP P37268
A	30	HIS	-	EXPRESSION TAG	UNP P37268
A	248	LEU	LYS	ENGINEERED MUTATION	UNP P37268
A	315	LEU	LYS	ENGINEERED MUTATION	UNP P37268
A	318	LEU	LYS	ENGINEERED MUTATION	UNP P37268
A	353	ASN	ASP	SEE REMARK 999	UNP P37268
B	11	MET	-	EXPRESSION TAG	UNP P37268
B	12	GLY	-	EXPRESSION TAG	UNP P37268
B	13	SER	-	EXPRESSION TAG	UNP P37268
B	14	SER	-	EXPRESSION TAG	UNP P37268
B	15	HIS	-	EXPRESSION TAG	UNP P37268
B	16	HIS	-	EXPRESSION TAG	UNP P37268
B	17	HIS	-	EXPRESSION TAG	UNP P37268
B	18	HIS	-	EXPRESSION TAG	UNP P37268
B	19	HIS	-	EXPRESSION TAG	UNP P37268
B	20	HIS	-	EXPRESSION TAG	UNP P37268
B	21	SER	-	EXPRESSION TAG	UNP P37268
B	22	SER	-	EXPRESSION TAG	UNP P37268
B	23	GLY	-	EXPRESSION TAG	UNP P37268
B	24	LEU	-	EXPRESSION TAG	UNP P37268
B	25	VAL	-	EXPRESSION TAG	UNP P37268
B	26	PRO	-	EXPRESSION TAG	UNP P37268
B	27	ARG	-	EXPRESSION TAG	UNP P37268
B	28	GLY	-	EXPRESSION TAG	UNP P37268
B	29	SER	-	EXPRESSION TAG	UNP P37268
B	30	HIS	-	EXPRESSION TAG	UNP P37268
B	248	LEU	LYS	ENGINEERED MUTATION	UNP P37268
B	315	LEU	LYS	ENGINEERED MUTATION	UNP P37268
B	318	LEU	LYS	ENGINEERED MUTATION	UNP P37268
B	353	ASN	ASP	SEE REMARK 999	UNP P37268
C	11	MET	-	EXPRESSION TAG	UNP P37268
C	12	GLY	-	EXPRESSION TAG	UNP P37268
C	13	SER	-	EXPRESSION TAG	UNP P37268
C	14	SER	-	EXPRESSION TAG	UNP P37268
C	15	HIS	-	EXPRESSION TAG	UNP P37268
C	16	HIS	-	EXPRESSION TAG	UNP P37268
C	17	HIS	-	EXPRESSION TAG	UNP P37268
C	18	HIS	-	EXPRESSION TAG	UNP P37268
C	19	HIS	-	EXPRESSION TAG	UNP P37268
C	20	HIS	-	EXPRESSION TAG	UNP P37268
C	21	SER	-	EXPRESSION TAG	UNP P37268

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Chain	Residue	Modelled	Actual	Comment	Reference
C	22	SER	-	EXPRESSION TAG	UNP P37268
C	23	GLY	-	EXPRESSION TAG	UNP P37268
C	24	LEU	-	EXPRESSION TAG	UNP P37268
C	25	VAL	-	EXPRESSION TAG	UNP P37268
C	26	PRO	-	EXPRESSION TAG	UNP P37268
C	27	ARG	-	EXPRESSION TAG	UNP P37268
C	28	GLY	-	EXPRESSION TAG	UNP P37268
C	29	SER	-	EXPRESSION TAG	UNP P37268
C	30	HIS	-	EXPRESSION TAG	UNP P37268
C	248	LEU	LYS	ENGINEERED MUTATION	UNP P37268
C	315	LEU	LYS	ENGINEERED MUTATION	UNP P37268
C	318	LEU	LYS	ENGINEERED MUTATION	UNP P37268
C	353	ASN	ASP	SEE REMARK 999	UNP P37268
D	11	MET	-	EXPRESSION TAG	UNP P37268
D	12	GLY	-	EXPRESSION TAG	UNP P37268
D	13	SER	-	EXPRESSION TAG	UNP P37268
D	14	SER	-	EXPRESSION TAG	UNP P37268
D	15	HIS	-	EXPRESSION TAG	UNP P37268
D	16	HIS	-	EXPRESSION TAG	UNP P37268
D	17	HIS	-	EXPRESSION TAG	UNP P37268
D	18	HIS	-	EXPRESSION TAG	UNP P37268
D	19	HIS	-	EXPRESSION TAG	UNP P37268
D	20	HIS	-	EXPRESSION TAG	UNP P37268
D	21	SER	-	EXPRESSION TAG	UNP P37268
D	22	SER	-	EXPRESSION TAG	UNP P37268
D	23	GLY	-	EXPRESSION TAG	UNP P37268
D	24	LEU	-	EXPRESSION TAG	UNP P37268
D	25	VAL	-	EXPRESSION TAG	UNP P37268
D	26	PRO	-	EXPRESSION TAG	UNP P37268
D	27	ARG	-	EXPRESSION TAG	UNP P37268
D	28	GLY	-	EXPRESSION TAG	UNP P37268
D	29	SER	-	EXPRESSION TAG	UNP P37268
D	30	HIS	-	EXPRESSION TAG	UNP P37268
D	248	LEU	LYS	ENGINEERED MUTATION	UNP P37268
D	315	LEU	LYS	ENGINEERED MUTATION	UNP P37268
D	318	LEU	LYS	ENGINEERED MUTATION	UNP P37268
D	353	ASN	ASP	SEE REMARK 999	UNP P37268
E	11	MET	-	EXPRESSION TAG	UNP P37268
E	12	GLY	-	EXPRESSION TAG	UNP P37268
E	13	SER	-	EXPRESSION TAG	UNP P37268
E	14	SER	-	EXPRESSION TAG	UNP P37268
E	15	HIS	-	EXPRESSION TAG	UNP P37268

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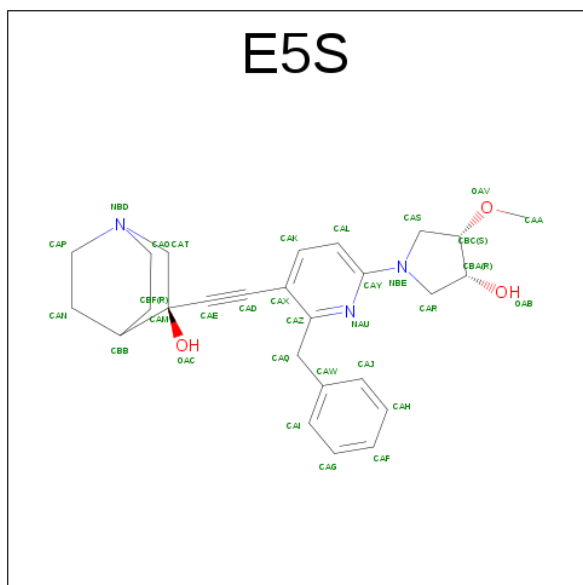
Chain	Residue	Modelled	Actual	Comment	Reference
E	16	HIS	-	EXPRESSION TAG	UNP P37268
E	17	HIS	-	EXPRESSION TAG	UNP P37268
E	18	HIS	-	EXPRESSION TAG	UNP P37268
E	19	HIS	-	EXPRESSION TAG	UNP P37268
E	20	HIS	-	EXPRESSION TAG	UNP P37268
E	21	SER	-	EXPRESSION TAG	UNP P37268
E	22	SER	-	EXPRESSION TAG	UNP P37268
E	23	GLY	-	EXPRESSION TAG	UNP P37268
E	24	LEU	-	EXPRESSION TAG	UNP P37268
E	25	VAL	-	EXPRESSION TAG	UNP P37268
E	26	PRO	-	EXPRESSION TAG	UNP P37268
E	27	ARG	-	EXPRESSION TAG	UNP P37268
E	28	GLY	-	EXPRESSION TAG	UNP P37268
E	29	SER	-	EXPRESSION TAG	UNP P37268
E	30	HIS	-	EXPRESSION TAG	UNP P37268
E	248	LEU	LYS	ENGINEERED MUTATION	UNP P37268
E	315	LEU	LYS	ENGINEERED MUTATION	UNP P37268
E	318	LEU	LYS	ENGINEERED MUTATION	UNP P37268
E	353	ASN	ASP	SEE REMARK 999	UNP P37268
F	11	MET	-	EXPRESSION TAG	UNP P37268
F	12	GLY	-	EXPRESSION TAG	UNP P37268
F	13	SER	-	EXPRESSION TAG	UNP P37268
F	14	SER	-	EXPRESSION TAG	UNP P37268
F	15	HIS	-	EXPRESSION TAG	UNP P37268
F	16	HIS	-	EXPRESSION TAG	UNP P37268
F	17	HIS	-	EXPRESSION TAG	UNP P37268
F	18	HIS	-	EXPRESSION TAG	UNP P37268
F	19	HIS	-	EXPRESSION TAG	UNP P37268
F	20	HIS	-	EXPRESSION TAG	UNP P37268
F	21	SER	-	EXPRESSION TAG	UNP P37268
F	22	SER	-	EXPRESSION TAG	UNP P37268
F	23	GLY	-	EXPRESSION TAG	UNP P37268
F	24	LEU	-	EXPRESSION TAG	UNP P37268
F	25	VAL	-	EXPRESSION TAG	UNP P37268
F	26	PRO	-	EXPRESSION TAG	UNP P37268
F	27	ARG	-	EXPRESSION TAG	UNP P37268
F	28	GLY	-	EXPRESSION TAG	UNP P37268
F	29	SER	-	EXPRESSION TAG	UNP P37268
F	30	HIS	-	EXPRESSION TAG	UNP P37268
F	248	LEU	LYS	ENGINEERED MUTATION	UNP P37268
F	315	LEU	LYS	ENGINEERED MUTATION	UNP P37268
F	318	LEU	LYS	ENGINEERED MUTATION	UNP P37268

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Chain	Residue	Modelled	Actual	Comment	Reference
F	353	ASN	ASP	SEE REMARK 999	UNP P37268

- Molecule 2 is (3R)-3-({2-BENZYL-6-[(3R,4S)-3-HYDROXY-4-METHOXPYRROLIDIN-1-YL]PYRIDIN-3-YL}ETHYNYL)-1-AZABICYCLO[2.2.2]OCTAN-3-OL (three-letter code: E5S) (formula: C₂₆H₃₁N₃O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			32	26	3	3		
2	B	1	Total	C	N	O	0	0
			32	26	3	3		
2	C	1	Total	C	N	O	0	0
			32	26	3	3		
2	D	1	Total	C	N	O	0	0
			32	26	3	3		
2	E	1	Total	C	N	O	0	0
			32	26	3	3		
2	F	1	Total	C	N	O	0	0
			32	26	3	3		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	178	Total	O	0	0
			178	178		
3	B	204	Total	O	0	0
			204	204		

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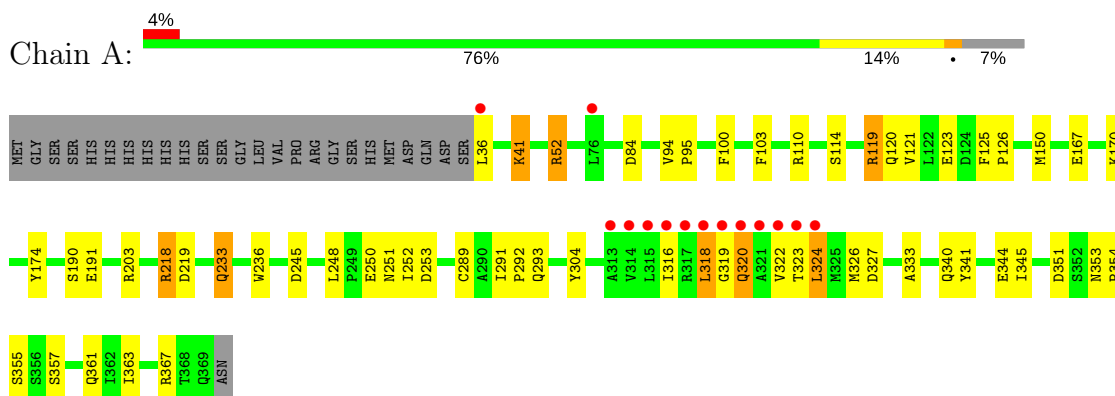
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	160	Total 160	O 160	0	0
3	D	131	Total 131	O 131	0	0
3	E	86	Total 86	O 86	0	0
3	F	66	Total 66	O 66	0	0

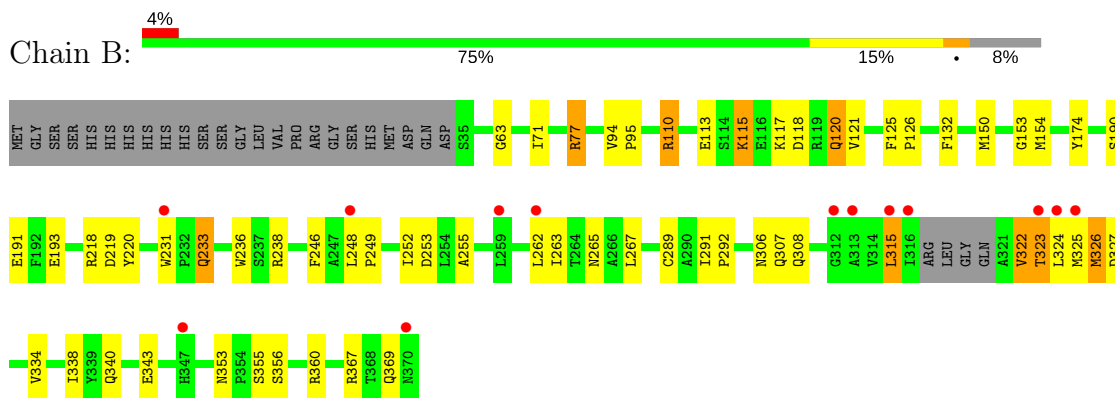
3 Residue-property plots

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

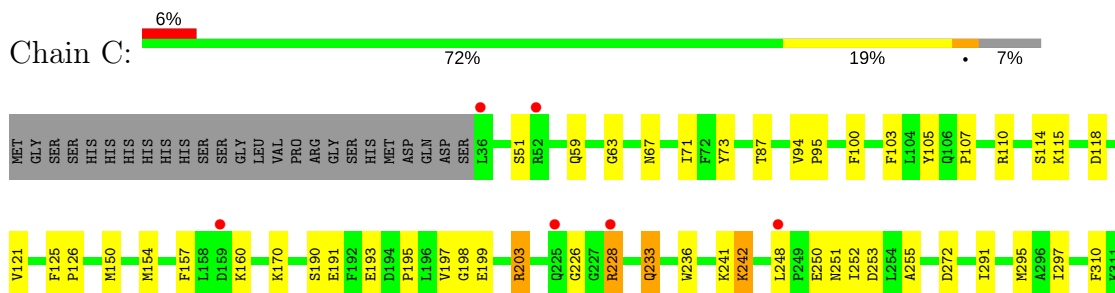
• Molecule 1: Squalene synthase

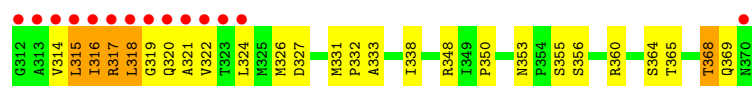


• Molecule 1: Squalene synthase

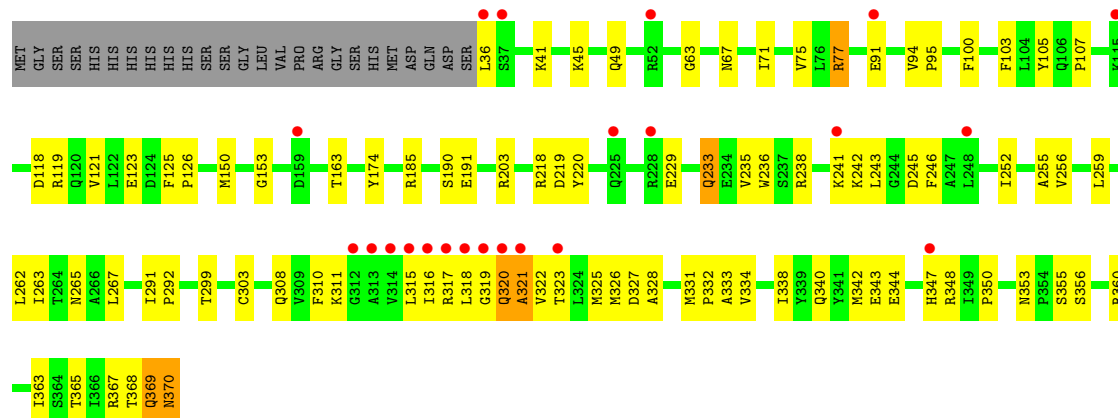


• Molecule 1: Squalene synthase

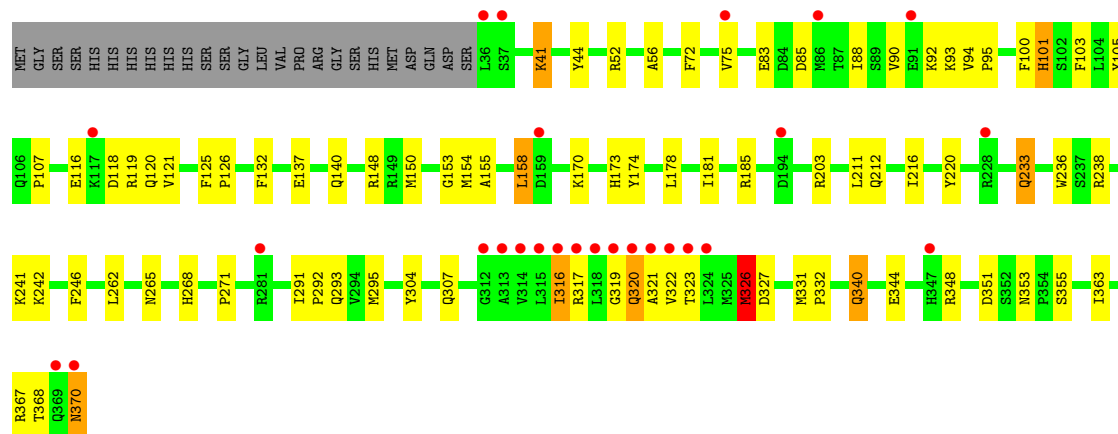




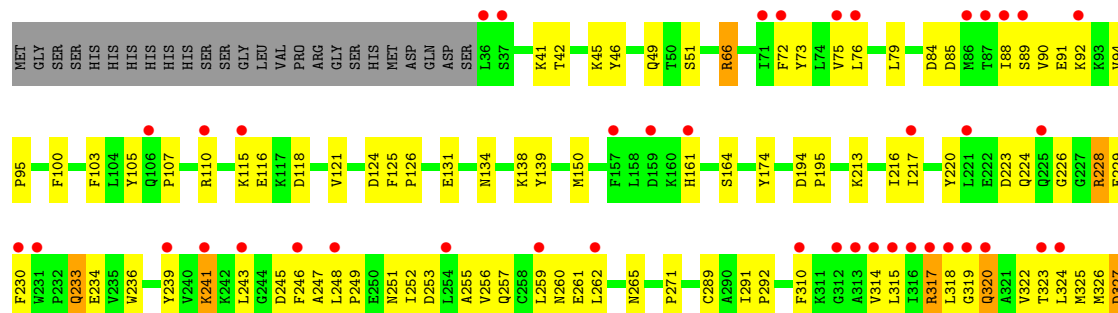
• Molecule 1: Squalene synthase

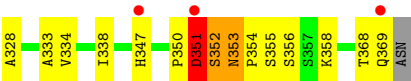


• Molecule 1: Squalene synthase



• Molecule 1: Squalene synthase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.33Å 153.62Å 92.11Å 90.00° 90.86° 90.00°	Depositor
Resolution (Å)	25.00 – 2.20 24.86 – 2.19	Depositor EDS
% Data completeness (in resolution range)	(Not available) (25.00-2.20) 93.8 (24.86-2.19)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.82 (at 2.19Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.198 , 0.225 0.198 , 0.227	Depositor DCC
R_{free} test set	5697 reflections (5.04%)	DCC
Wilson B-factor (Å ²)	27.7	Xtriage
Anisotropy	0.605	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 49.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.027 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	17199	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.10% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: E5S

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	0.39	0/2751	0.59	0/3724
1	B	0.37	0/2732	0.57	1/3698 (0.0%)
1	C	0.36	0/2759	0.57	0/3735
1	D	0.34	0/2759	0.54	0/3735
1	E	0.33	0/2759	0.53	0/3735
1	F	0.32	0/2751	0.52	0/3724
All	All	0.35	0/16511	0.55	1/22351 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	315	LEU	CA-CB-CG	6.63	130.56	115.30

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	2696	0	2676	51	0
1	B	2678	0	2651	56	0
1	C	2704	0	2682	72	0
1	D	2704	0	2682	66	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2704	0	2682	72	0
1	F	2696	0	2676	87	0
2	A	32	0	31	1	0
2	B	32	0	31	1	0
2	C	32	0	31	0	0
2	D	32	0	31	0	0
2	E	32	0	31	0	0
2	F	32	0	31	1	0
3	A	178	0	0	0	0
3	B	204	0	0	2	0
3	C	160	0	0	3	0
3	D	131	0	0	1	0
3	E	86	0	0	3	0
3	F	66	0	0	0	0
All	All	17199	0	16235	374	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 11.

All (374) 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:C:315:LEU:HG	1:C:316:ILE:H	1.20	1.04
1:E:319:GLY:HA3	1:E:323:THR:HG21	1.40	1.01
1:B:323:THR:O	1:B:325:MET:N	1.98	0.96
1:F:260:ASN:HD22	1:F:353:ASN:ND2	1.65	0.94
1:C:317:ARG:HG3	1:C:317:ARG:HH21	1.32	0.92
1:C:317:ARG:HB2	3:C:578:HOH:O	1.69	0.92
1:C:315:LEU:HG	1:C:316:ILE:N	1.86	0.91
1:F:233:GLN:HA	1:F:236:TRP:NE1	1.86	0.90
1:E:319:GLY:CA	1:E:323:THR:HG21	2.03	0.89
1:E:326:MET:HA	1:F:327:ASP:OD2	1.75	0.86
1:C:226:GLY:HA3	1:C:228:ARG:HH11	1.40	0.86
1:C:317:ARG:CG	1:C:317:ARG:HH21	1.89	0.85
1:A:320:GLN:HG3	1:A:340:GLN:HB3	1.58	0.83
1:F:228:ARG:HB2	1:F:228:ARG:NH1	1.94	0.82
1:F:318:LEU:HD12	1:F:318:LEU:H	1.44	0.82
1:E:320:GLN:HG2	1:E:321:ALA:H	1.46	0.80
1:A:320:GLN:O	1:A:323:THR:HG22	1.81	0.79
1:D:368:THR:HG21	1:E:41:LYS:HA	1.64	0.78
1:A:326:MET:HA	1:B:327:ASP:HB2	1.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:260:ASN:HD22	1:F:353:ASN:HD21	1.31	0.77
1:B:233:GLN:HA	1:B:236:TRP:NE1	1.99	0.77
1:A:319:GLY:CA	1:A:323:THR:HG21	2.15	0.76
1:B:120:GLN:NE2	1:B:120:GLN:H	1.82	0.76
1:A:323:THR:HG23	1:A:324:LEU:N	2.00	0.75
1:E:326:MET:HA	1:F:327:ASP:CG	2.07	0.75
1:A:319:GLY:HA2	1:A:323:THR:HG21	1.69	0.74
1:A:320:GLN:NE2	1:A:344:GLU:HG3	2.02	0.74
1:F:233:GLN:HA	1:F:236:TRP:CD1	2.23	0.74
1:B:322:VAL:HG12	1:B:340:GLN:NE2	2.03	0.73
1:C:226:GLY:HA3	1:C:228:ARG:NH1	2.03	0.72
1:E:150:MET:HG3	1:E:174:TYR:O	1.90	0.72
1:D:233:GLN:HA	1:D:236:TRP:NE1	2.05	0.71
1:D:235:VAL:HA	1:D:238:ARG:HH21	1.53	0.71
1:E:105:TYR:O	1:E:107:PRO:HD3	1.91	0.70
1:E:90:VAL:O	1:E:94:VAL:HG23	1.91	0.70
1:D:327:ASP:CG	1:F:326:MET:HA	2.12	0.69
1:C:320:GLN:HG2	1:C:321:ALA:H	1.57	0.69
1:D:327:ASP:OD1	1:F:326:MET:HA	1.92	0.69
1:F:100:PHE:HA	1:F:103:PHE:CD2	2.27	0.69
1:F:319:GLY:HA3	1:F:323:THR:HG21	1.74	0.69
1:A:357:SER:O	1:A:361:GLN:HG3	1.93	0.68
1:F:229:GLU:HB2	1:F:243:LEU:HD13	1.76	0.68
1:B:326:MET:HE3	1:C:291:ILE:HD11	1.76	0.67
1:C:314:VAL:HG12	1:C:315:LEU:H	1.60	0.67
1:D:94:VAL:HB	1:D:95:PRO:HD3	1.77	0.66
1:D:365:THR:O	1:D:369:GLN:HB3	1.95	0.66
1:B:118:ASP:C	1:B:120:GLN:HE21	1.99	0.66
1:A:323:THR:HG23	1:A:324:LEU:H	1.61	0.66
1:E:93:LYS:HD2	1:E:158:LEU:HD11	1.76	0.65
1:A:322:VAL:HG12	1:A:326:MET:SD	2.36	0.65
1:E:155:ALA:O	1:E:158:LEU:HB2	1.96	0.65
1:A:327:ASP:OD1	1:C:327:ASP:HB3	1.97	0.65
1:F:105:TYR:O	1:F:107:PRO:HD3	1.96	0.65
1:F:320:GLN:O	1:F:324:LEU:HG	1.98	0.64
1:A:218:ARG:NH1	1:A:219:ASP:OD1	2.31	0.64
1:A:320:GLN:HB2	1:A:340:GLN:OE1	1.98	0.64
1:A:248:LEU:HD23	1:A:250:GLU:OE1	1.98	0.63
1:C:315:LEU:HG	1:C:316:ILE:HG12	1.81	0.63
1:C:315:LEU:CG	1:C:316:ILE:N	2.58	0.63
1:D:368:THR:HG22	1:E:44:TYR:HB2	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:118:ASP:O	1:E:121:VAL:HG22	1.99	0.63
1:A:326:MET:HE2	1:A:333:ALA:HA	1.80	0.63
1:C:365:THR:O	1:C:369:GLN:HG3	1.98	0.63
1:C:320:GLN:HG2	1:C:321:ALA:N	2.14	0.62
1:A:245:ASP:HA	1:A:248:LEU:HD13	1.81	0.62
1:C:317:ARG:NH2	1:C:317:ARG:HG3	2.05	0.62
1:E:132:PHE:CZ	1:E:140:GLN:HB2	2.34	0.62
1:E:353:ASN:ND2	1:E:355:SER:H	1.98	0.62
1:F:89:SER:HB2	1:F:91:GLU:OE1	2.00	0.62
1:C:118:ASP:O	1:C:121:VAL:HG22	2.00	0.61
1:C:203:ARG:HD2	1:C:272:ASP:OD1	2.00	0.61
1:D:322:VAL:HG13	1:E:291:ILE:HG21	1.81	0.61
1:A:318:LEU:HB3	1:A:341:TYR:HE1	1.65	0.61
1:C:314:VAL:HG12	1:C:315:LEU:N	2.16	0.60
1:E:317:ARG:NH1	1:E:348:ARG:NH1	2.49	0.60
1:C:320:GLN:CG	1:C:321:ALA:H	2.13	0.60
1:D:100:PHE:HA	1:D:103:PHE:CD2	2.37	0.60
1:C:233:GLN:HA	1:C:236:TRP:NE1	2.17	0.60
1:E:331:MET:HB3	1:E:332:PRO:HD3	1.84	0.60
1:F:236:TRP:CE2	1:F:243:LEU:HG	2.37	0.60
1:F:94:VAL:HB	1:F:95:PRO:HD3	1.83	0.60
1:B:353:ASN:ND2	1:B:355:SER:H	1.98	0.60
1:D:368:THR:HG21	1:E:41:LYS:HG3	1.84	0.60
1:B:323:THR:C	1:B:325:MET:H	1.99	0.59
1:F:322:VAL:O	1:F:325:MET:HB2	2.01	0.59
1:C:315:LEU:O	1:C:317:ARG:HD3	2.03	0.59
1:E:233:GLN:HA	1:E:236:TRP:NE1	2.17	0.59
1:A:323:THR:CG2	1:A:324:LEU:N	2.65	0.59
1:B:117:LYS:O	1:B:120:GLN:NE2	2.35	0.59
1:D:308:GLN:NE2	1:D:311:LYS:HD2	2.18	0.59
1:D:299:THR:HA	1:D:316:ILE:HD11	1.84	0.59
1:C:94:VAL:HB	1:C:95:PRO:HD3	1.85	0.58
1:B:322:VAL:HA	1:C:295:MET:CE	2.33	0.58
1:F:228:ARG:HB2	1:F:228:ARG:CZ	2.32	0.58
1:C:348:ARG:O	1:C:350:PRO:HD3	2.03	0.58
1:B:110:ARG:NH2	3:B:534:HOH:O	2.37	0.58
1:B:252:ILE:HG23	1:B:253:ASP:N	2.18	0.58
1:F:118:ASP:O	1:F:121:VAL:HG22	2.04	0.57
1:D:370:ASN:H	1:D:370:ASN:ND2	2.02	0.57
1:D:363:ILE:O	1:D:367:ARG:HG2	2.02	0.57
1:A:323:THR:CG2	1:A:324:LEU:H	2.18	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:320:GLN:O	1:C:324:LEU:HG	2.03	0.57
1:B:190:SER:O	1:B:191:GLU:HB2	2.03	0.57
1:F:90:VAL:O	1:F:94:VAL:HG23	2.05	0.57
1:D:308:GLN:NE2	1:D:308:GLN:HA	2.20	0.57
1:B:323:THR:O	1:B:326:MET:N	2.37	0.56
1:A:233:GLN:HA	1:A:236:TRP:NE1	2.20	0.56
1:C:248:LEU:HB2	1:C:251:ASN:HD22	1.70	0.56
1:A:363:ILE:O	1:A:367:ARG:HG2	2.05	0.56
1:D:308:GLN:HE21	1:D:308:GLN:HA	1.69	0.56
1:F:260:ASN:ND2	1:F:353:ASN:HD21	2.03	0.56
1:C:353:ASN:ND2	1:C:355:SER:H	2.02	0.56
1:D:150:MET:HG3	1:D:174:TYR:O	2.03	0.56
1:B:150:MET:HG3	1:B:174:TYR:O	2.06	0.56
1:D:353:ASN:ND2	1:D:355:SER:H	2.04	0.56
1:D:71:ILE:O	1:D:75:VAL:HG13	2.06	0.56
1:E:212:GLN:HE21	1:E:216:ILE:HG13	1.70	0.56
1:C:318:LEU:O	1:C:318:LEU:HD23	2.06	0.56
1:B:252:ILE:HD11	1:B:307:GLN:HB3	1.88	0.55
1:D:370:ASN:HD22	1:D:370:ASN:H	1.52	0.55
1:D:319:GLY:HA3	1:D:323:THR:HG21	1.88	0.55
1:E:125:PHE:N	1:E:126:PRO:CD	2.69	0.55
1:C:100:PHE:HA	1:C:103:PHE:CD2	2.42	0.55
1:A:36:LEU:N	1:A:36:LEU:HD12	2.22	0.55
1:F:220:TYR:OH	1:F:246:PHE:HB2	2.06	0.55
1:A:94:VAL:HB	1:A:95:PRO:HD3	1.89	0.55
1:C:195:PRO:O	1:C:199:GLU:HG3	2.07	0.55
1:B:325:MET:O	1:C:327:ASP:HB2	2.07	0.54
1:A:150:MET:HG3	1:A:174:TYR:O	2.07	0.54
1:A:326:MET:CE	1:A:333:ALA:HA	2.38	0.54
1:A:245:ASP:O	1:A:248:LEU:HB2	2.08	0.54
1:A:326:MET:HA	1:B:327:ASP:CB	2.33	0.54
1:D:348:ARG:O	1:D:350:PRO:HD3	2.08	0.54
1:C:105:TYR:O	1:C:107:PRO:HD3	2.07	0.54
1:A:41:LYS:HA	1:C:368:THR:HG21	1.89	0.54
1:D:327:ASP:OD2	1:D:328:ALA:N	2.40	0.54
1:F:325:MET:CE	1:F:325:MET:HA	2.38	0.54
1:A:353:ASN:ND2	1:A:355:SER:H	2.06	0.53
1:B:120:GLN:CD	1:B:120:GLN:H	2.09	0.53
1:E:320:GLN:CG	1:E:321:ALA:H	2.16	0.53
1:F:262:LEU:O	1:F:265:ASN:HB3	2.08	0.53
1:D:220:TYR:OH	1:D:246:PHE:HB2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:45:LYS:HG2	1:F:49:GLN:HE21	1.74	0.53
1:D:163:THR:HA	1:D:233:GLN:HB3	1.91	0.53
1:D:299:THR:HA	1:D:316:ILE:CD1	2.38	0.53
1:F:150:MET:HG3	1:F:174:TYR:O	2.09	0.53
1:F:85:ASP:OD2	1:F:88:ILE:HG13	2.09	0.53
1:C:248:LEU:HB3	1:C:250:GLU:OE1	2.10	0.52
1:F:255:ALA:HB1	1:F:310:PHE:CE2	2.44	0.52
1:F:239:TYR:HE2	1:F:261:GLU:OE1	1.93	0.52
1:F:350:PRO:C	1:F:352:SER:H	2.13	0.52
1:F:247:ALA:O	1:F:249:PRO:HD3	2.10	0.52
1:C:318:LEU:HD23	1:C:324:LEU:HD21	1.91	0.52
1:D:326:MET:HE2	1:D:333:ALA:HA	1.92	0.52
1:B:322:VAL:HA	1:C:295:MET:HE3	1.91	0.52
1:D:327:ASP:OD2	1:F:325:MET:O	2.28	0.52
1:B:289:CYS:HA	2:B:401:E5S:H20	1.92	0.51
1:D:153:GLY:HA3	1:D:174:TYR:CG	2.45	0.51
1:E:56:ALA:HB3	3:E:520:HOH:O	2.10	0.51
1:F:326:MET:HE2	1:F:333:ALA:HA	1.91	0.51
1:E:344:GLU:O	1:E:348:ARG:HD3	2.10	0.51
1:D:218:ARG:HD2	1:D:219:ASP:OD1	2.11	0.51
1:F:115:LYS:NZ	1:F:115:LYS:HB3	2.24	0.51
1:D:370:ASN:HD22	1:D:370:ASN:N	2.08	0.51
1:D:45:LYS:O	1:D:49:GLN:HG3	2.11	0.51
1:E:153:GLY:HA3	1:E:174:TYR:CG	2.45	0.51
1:F:260:ASN:ND2	1:F:353:ASN:ND2	2.48	0.51
1:B:218:ARG:HD2	1:B:219:ASP:OD1	2.11	0.51
1:B:369:GLN:HB2	3:B:679:HOH:O	2.10	0.51
1:C:51:SER:HB2	1:C:73:TYR:CZ	2.46	0.51
1:C:316:ILE:C	1:C:318:LEU:H	2.14	0.51
1:D:125:PHE:N	1:D:126:PRO:CD	2.73	0.50
1:F:320:GLN:O	1:F:323:THR:HG22	2.12	0.50
1:B:343:GLU:OE1	1:B:367:ARG:NH2	2.43	0.50
1:E:236:TRP:CZ3	1:E:242:LYS:HA	2.46	0.50
1:F:138:LYS:HE3	1:F:139:TYR:CZ	2.47	0.50
1:E:323:THR:HB	1:E:340:GLN:NE2	2.26	0.50
1:F:89:SER:OG	1:F:92:LYS:HB2	2.12	0.50
1:C:326:MET:HE2	1:C:333:ALA:HA	1.94	0.50
1:E:295:MET:CE	1:E:295:MET:HA	2.42	0.50
1:F:228:ARG:HB2	1:F:228:ARG:HH11	1.71	0.50
1:E:323:THR:HA	1:E:326:MET:CG	2.42	0.50
1:F:79:LEU:HB2	1:F:100:PHE:CE2	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:291:ILE:HB	1:F:292:PRO:HD3	1.94	0.50
1:E:322:VAL:HB	1:E:340:GLN:OE1	2.12	0.49
1:F:236:TRP:HZ3	1:F:241:LYS:C	2.16	0.49
1:A:170:LYS:HE2	1:A:174:TYR:OH	2.12	0.49
1:E:100:PHE:HA	1:E:103:PHE:CD2	2.47	0.49
1:F:75:VAL:HG23	1:F:76:LEU:N	2.27	0.49
1:E:320:GLN:HG2	1:E:321:ALA:N	2.21	0.49
1:D:242:LYS:HB2	1:D:245:ASP:OD2	2.13	0.49
1:E:92:LYS:O	1:E:95:PRO:HD2	2.11	0.49
1:A:248:LEU:HB2	1:A:251:ASN:HD22	1.78	0.49
1:A:291:ILE:HG21	1:C:322:VAL:HG13	1.94	0.49
1:C:317:ARG:O	1:C:319:GLY:N	2.45	0.49
1:D:252:ILE:O	1:D:256:VAL:HG23	2.12	0.49
1:E:233:GLN:HA	1:E:236:TRP:CD1	2.48	0.49
1:F:115:LYS:HB3	1:F:115:LYS:HZ2	1.77	0.49
1:C:170:LYS:HA	3:C:585:HOH:O	2.11	0.49
1:D:259:LEU:HB2	1:D:310:PHE:HZ	1.76	0.49
1:C:190:SER:O	1:C:191:GLU:HB2	2.13	0.49
1:E:233:GLN:HA	1:E:236:TRP:CE2	2.48	0.49
1:D:319:GLY:C	1:D:323:THR:HB	2.33	0.49
1:E:170:LYS:O	1:E:173:HIS:HB3	2.13	0.48
1:B:353:ASN:HD21	1:B:355:SER:HB2	1.77	0.48
1:C:250:GLU:CD	1:C:250:GLU:H	2.17	0.48
1:E:320:GLN:HB3	1:E:340:GLN:OE1	2.14	0.48
1:B:322:VAL:HA	1:C:295:MET:HE1	1.96	0.48
1:E:307:GLN:HG3	3:E:513:HOH:O	2.13	0.48
1:B:233:GLN:HA	1:B:236:TRP:CD1	2.49	0.48
1:D:291:ILE:HB	1:D:292:PRO:HD3	1.95	0.48
1:A:326:MET:CA	1:B:327:ASP:HB2	2.40	0.47
1:A:289:CYS:HA	2:A:901:E5S:H20	1.95	0.47
1:C:364:SER:O	1:C:368:THR:HG23	2.14	0.47
1:A:114:SER:O	1:A:119:ARG:HD3	2.14	0.47
1:F:125:PHE:N	1:F:126:PRO:CD	2.77	0.47
1:B:125:PHE:N	1:B:126:PRO:CD	2.77	0.47
1:D:233:GLN:HA	1:D:236:TRP:CE2	2.50	0.47
1:C:150:MET:O	1:C:154:MET:HG3	2.14	0.47
1:D:67:ASN:O	1:D:71:ILE:HG12	2.15	0.47
1:C:320:GLN:CG	1:C:321:ALA:N	2.77	0.47
1:B:323:THR:HG22	1:B:340:GLN:OE1	2.14	0.47
1:B:94:VAL:HB	1:B:95:PRO:HD3	1.96	0.47
1:E:326:MET:HE3	1:F:291:ILE:HD11	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:304:TYR:O	1:E:348:ARG:NH2	2.47	0.47
1:E:72:PHE:O	1:E:75:VAL:HG22	2.15	0.47
1:D:316:ILE:O	1:D:316:ILE:HG22	2.16	0.46
1:F:325:MET:HA	1:F:325:MET:HE2	1.97	0.46
1:E:319:GLY:CA	1:E:323:THR:CG2	2.87	0.46
1:C:193:GLU:HB3	1:C:197:VAL:HG21	1.98	0.46
1:D:77:ARG:HG2	1:D:77:ARG:NH1	2.29	0.46
1:A:119:ARG:O	1:A:123:GLU:HG3	2.15	0.46
1:C:228:ARG:H	1:C:228:ARG:HD3	1.80	0.46
1:E:291:ILE:HB	1:E:292:PRO:HD3	1.98	0.46
1:E:92:LYS:C	1:E:95:PRO:HD2	2.35	0.46
1:D:185:ARG:HD2	3:D:512:HOH:O	2.16	0.46
1:D:338:ILE:O	1:D:342:MET:HG2	2.16	0.46
1:E:116:GLU:O	1:E:119:ARG:HG3	2.15	0.46
1:E:85:ASP:HB3	1:E:88:ILE:HD12	1.98	0.46
1:A:125:PHE:N	1:A:126:PRO:CD	2.79	0.45
1:C:250:GLU:N	1:C:250:GLU:OE2	2.49	0.45
1:D:119:ARG:O	1:D:123:GLU:HG3	2.15	0.45
1:D:246:PHE:CD1	1:D:255:ALA:HA	2.51	0.45
1:A:100:PHE:HA	1:A:103:PHE:CD2	2.52	0.45
1:E:368:THR:OG1	1:F:41:LYS:HA	2.16	0.45
1:F:72:PHE:CZ	1:F:76:LEU:HD11	2.52	0.45
1:E:94:VAL:N	1:E:95:PRO:CD	2.80	0.45
1:F:51:SER:HB2	1:F:73:TYR:CZ	2.51	0.45
1:D:325:MET:O	1:E:327:ASP:HB2	2.17	0.45
1:B:306:ASN:OD1	1:B:308:GLN:HB2	2.17	0.44
1:C:87:THR:OG1	1:C:115:LYS:HG2	2.17	0.44
1:F:245:ASP:O	1:F:248:LEU:HB2	2.17	0.44
1:F:246:PHE:CD1	1:F:255:ALA:HA	2.52	0.44
1:C:157:PHE:CE2	1:C:160:LYS:HE3	2.52	0.44
1:E:370:ASN:HB3	1:F:66:ARG:CD	2.47	0.44
1:F:334:VAL:O	1:F:338:ILE:HG13	2.18	0.44
1:B:153:GLY:HA3	1:B:174:TYR:CG	2.52	0.44
1:D:105:TYR:O	1:D:107:PRO:HD3	2.18	0.44
1:D:308:GLN:HE22	1:D:311:LYS:HD2	1.83	0.44
1:E:268:HIS:O	1:E:271:PRO:HD2	2.17	0.44
1:B:262:LEU:O	1:B:265:ASN:HB3	2.18	0.44
1:D:153:GLY:HA3	1:D:174:TYR:CD1	2.53	0.44
1:F:131:GLU:HA	1:F:134:ASN:HD22	1.83	0.44
1:F:248:LEU:HB2	1:F:251:ASN:HD22	1.82	0.44
1:F:318:LEU:H	1:F:318:LEU:CD1	2.21	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:ARG:CG	1:A:52:ARG:HH11	2.29	0.43
1:E:93:LYS:CD	1:E:158:LEU:HD11	2.47	0.43
1:C:233:GLN:HA	1:C:236:TRP:CD1	2.53	0.43
1:F:194:ASP:OD1	1:F:195:PRO:HD2	2.18	0.43
1:D:41:LYS:HA	1:F:368:THR:HG21	1.99	0.43
1:A:289:CYS:O	1:A:293:GLN:HG2	2.18	0.43
1:D:320:GLN:O	1:D:321:ALA:C	2.56	0.43
1:B:291:ILE:HB	1:B:292:PRO:HD3	1.99	0.43
1:C:317:ARG:HD2	1:C:317:ARG:HA	1.89	0.43
1:A:327:ASP:HB3	1:C:326:MET:HA	2.00	0.43
1:D:190:SER:O	1:D:191:GLU:HB2	2.18	0.43
1:D:77:ARG:CG	1:D:77:ARG:HH11	2.32	0.43
1:F:124:ASP:O	1:F:124:ASP:CG	2.57	0.43
1:F:85:ASP:HA	1:F:116:GLU:OE2	2.17	0.43
1:B:246:PHE:CD1	1:B:255:ALA:HA	2.53	0.43
1:B:248:LEU:HA	1:B:249:PRO:HD3	1.87	0.43
1:B:353:ASN:ND2	1:B:355:SER:HB2	2.34	0.43
1:C:67:ASN:O	1:C:71:ILE:HG12	2.18	0.43
1:F:353:ASN:HA	1:F:354:PRO:HD3	1.79	0.43
1:F:92:LYS:C	1:F:95:PRO:HD2	2.39	0.43
1:A:316:ILE:N	1:A:316:ILE:HD12	2.33	0.43
1:E:181:ILE:O	1:E:185:ARG:HG3	2.19	0.43
1:F:239:TYR:HE1	1:F:257:GLN:HE21	1.67	0.43
1:C:297:ILE:CD1	1:C:338:ILE:HG12	2.49	0.43
1:E:137:GLU:HA	1:E:140:GLN:HG2	2.00	0.43
1:E:211:LEU:HG	1:E:293:GLN:HE22	1.83	0.43
1:E:83:GLU:HB2	1:E:154:MET:HE2	2.00	0.43
1:A:252:ILE:HG23	1:A:253:ASP:N	2.33	0.42
1:B:263:ILE:O	1:B:267:LEU:HG	2.18	0.42
1:F:213:LYS:O	1:F:217:ILE:HG13	2.19	0.42
1:A:233:GLN:HA	1:A:236:TRP:CD1	2.54	0.42
1:C:114:SER:C	1:C:115:LYS:HD2	2.39	0.42
1:D:229:GLU:HG2	1:D:243:LEU:HD23	2.02	0.42
1:E:320:GLN:O	1:E:323:THR:HG22	2.19	0.42
1:F:317:ARG:HG3	1:F:318:LEU:O	2.20	0.42
1:B:326:MET:HA	1:C:327:ASP:HB2	2.02	0.42
1:E:101:HIS:ND1	1:E:148:ARG:HB2	2.34	0.42
1:D:343:GLU:OE1	1:D:367:ARG:NH2	2.52	0.42
1:F:355:SER:O	1:F:358:LYS:N	2.52	0.42
1:B:326:MET:HE3	1:C:291:ILE:CD1	2.44	0.42
1:F:271:PRO:HA	1:F:369:GLN:HE22	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:323:THR:O	1:B:326:MET:HG3	2.19	0.42
1:B:71:ILE:HG21	1:B:132:PHE:HA	2.02	0.42
1:C:331:MET:HB3	1:C:332:PRO:HD3	2.02	0.42
1:E:320:GLN:CG	1:E:321:ALA:N	2.81	0.42
1:F:256:VAL:O	1:F:259:LEU:HB3	2.19	0.42
1:A:233:GLN:HE21	1:A:233:GLN:HB3	1.62	0.42
1:B:113:GLU:O	1:B:115:LYS:HD2	2.20	0.42
1:B:193:GLU:OE1	1:B:193:GLU:HA	2.19	0.42
1:E:295:MET:HE2	1:E:295:MET:HA	2.02	0.42
1:F:42:THR:HG22	1:F:46:TYR:CE2	2.55	0.42
1:B:220:TYR:HB2	1:B:231:TRP:CZ2	2.54	0.42
1:C:241:LYS:HE3	1:C:241:LYS:HB3	1.85	0.42
1:D:344:GLU:HG2	1:D:348:ARG:HH12	1.85	0.42
1:D:356:SER:O	1:D:360:ARG:HG3	2.18	0.42
1:E:317:ARG:HB2	3:E:507:HOH:O	2.19	0.42
1:F:92:LYS:O	1:F:95:PRO:HD2	2.20	0.42
1:D:331:MET:HB3	1:D:332:PRO:HD3	2.02	0.42
1:D:320:GLN:HB3	1:D:340:GLN:OE1	2.19	0.42
1:E:353:ASN:HD21	1:E:355:SER:HB2	1.85	0.42
1:F:223:ASP:O	1:F:228:ARG:O	2.37	0.42
1:F:220:TYR:CZ	1:F:246:PHE:HB2	2.54	0.42
1:F:355:SER:O	1:F:356:SER:C	2.58	0.42
1:F:216:ILE:HG23	1:F:230:PHE:HB2	2.02	0.41
1:F:241:LYS:NZ	1:F:241:LYS:HB2	2.35	0.41
1:C:252:ILE:HG23	1:C:253:ASP:N	2.34	0.41
1:D:262:LEU:O	1:D:265:ASN:HB3	2.21	0.41
1:F:224:GLN:C	1:F:226:GLY:H	2.23	0.41
1:F:252:ILE:HG23	1:F:253:ASP:N	2.36	0.41
1:F:318:LEU:N	1:F:318:LEU:HD12	2.22	0.41
1:E:363:ILE:O	1:E:367:ARG:HG3	2.20	0.41
1:F:289:CYS:HA	2:F:401:E5S:H20	2.02	0.41
1:F:164:SER:HB3	1:F:234:GLU:OE1	2.20	0.41
1:A:353:ASN:HA	1:A:354:PRO:HD3	1.83	0.41
1:B:118:ASP:O	1:B:121:VAL:HG22	2.21	0.41
1:B:233:GLN:HE21	1:B:233:GLN:HB3	1.57	0.41
1:B:252:ILE:CG2	1:B:253:ASP:N	2.84	0.41
1:E:326:MET:N	1:F:327:ASP:HB2	2.35	0.41
1:B:150:MET:O	1:B:154:MET:HG3	2.19	0.41
1:B:334:VAL:O	1:B:338:ILE:HG13	2.21	0.41
1:B:356:SER:O	1:B:360:ARG:HG3	2.20	0.41
1:E:370:ASN:HB3	1:F:66:ARG:HD3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:120:GLN:HG2	1:A:121:VAL:N	2.36	0.41
1:A:291:ILE:HB	1:A:292:PRO:HD3	2.02	0.41
1:A:304:TYR:CD2	1:A:345:ILE:HG23	2.56	0.41
1:B:77:ARG:HD3	1:B:77:ARG:HA	1.90	0.41
1:E:150:MET:HG2	1:E:154:MET:SD	2.61	0.41
1:E:233:GLN:HB3	1:E:233:GLN:HE21	1.71	0.41
1:E:94:VAL:HB	1:E:95:PRO:HD3	2.02	0.41
1:A:322:VAL:CG1	1:A:326:MET:SD	3.07	0.41
1:D:263:ILE:O	1:D:267:LEU:HG	2.21	0.41
1:D:334:VAL:O	1:D:338:ILE:HG13	2.20	0.41
1:C:59:GLN:HE21	1:C:59:GLN:HB2	1.75	0.41
1:D:259:LEU:HD21	1:D:303:CYS:O	2.20	0.40
1:B:233:GLN:HA	1:B:236:TRP:CE2	2.55	0.40
1:F:351:ASP:OD1	1:F:351:ASP:N	2.45	0.40
1:A:190:SER:O	1:A:191:GLU:HB2	2.20	0.40
1:C:198:GLY:HA3	3:C:592:HOH:O	2.21	0.40
1:C:236:TRP:CZ3	1:C:242:LYS:HA	2.57	0.40
1:C:255:ALA:HB1	1:C:310:PHE:CZ	2.56	0.40
1:C:356:SER:O	1:C:360:ARG:HG3	2.20	0.40
1:B:353:ASN:HD22	1:B:355:SER:H	1.66	0.40
1:C:125:PHE:N	1:C:126:PRO:CD	2.85	0.40
1:C:248:LEU:HB2	1:C:251:ASN:ND2	2.34	0.40
1:D:118:ASP:O	1:D:121:VAL:HG22	2.22	0.40
1:E:220:TYR:CZ	1:E:246:PHE:HB2	2.56	0.40
1:E:262:LEU:O	1:E:265:ASN:HB3	2.21	0.40
1:F:72:PHE:CE1	1:F:76:LEU:HD11	2.56	0.40
1:E:178:LEU:HD23	1:E:181:ILE:HD12	2.02	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	332/360 (92%)	318 (96%)	13 (4%)	1 (0%)	44	49
1	B	328/360 (91%)	314 (96%)	12 (4%)	2 (1%)	28	29
1	C	333/360 (92%)	320 (96%)	10 (3%)	3 (1%)	20	18
1	D	333/360 (92%)	315 (95%)	14 (4%)	4 (1%)	15	12
1	E	333/360 (92%)	315 (95%)	15 (4%)	3 (1%)	20	18
1	F	332/360 (92%)	305 (92%)	24 (7%)	3 (1%)	20	18
All	All	1991/2160 (92%)	1887 (95%)	88 (4%)	16 (1%)	22	21

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	318	LEU
1	B	324	LEU
1	C	316	ILE
1	C	318	LEU
1	D	320	GLN
1	E	316	ILE
1	F	328	ALA
1	D	318	LEU
1	E	320	GLN
1	D	321	ALA
1	C	63	GLY
1	D	63	GLY
1	E	326	MET
1	F	66	ARG
1	F	351	ASP
1	B	63	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	297/320 (93%)	285 (96%)	12 (4%)	36	45
1	B	296/320 (92%)	286 (97%)	10 (3%)	42	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	C	298/320 (93%)	290 (97%)	8 (3%)	50 62
1	D	298/320 (93%)	287 (96%)	11 (4%)	39 49
1	E	298/320 (93%)	284 (95%)	14 (5%)	30 37
1	F	297/320 (93%)	282 (95%)	15 (5%)	28 33
All	All	1784/1920 (93%)	1714 (96%)	70 (4%)	37 46

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	LYS
1	A	52	ARG
1	A	84	ASP
1	A	110	ARG
1	A	119	ARG
1	A	167	GLU
1	A	203	ARG
1	A	218	ARG
1	A	233	GLN
1	A	320	GLN
1	A	324	LEU
1	A	351	ASP
1	B	77	ARG
1	B	110	ARG
1	B	115	LYS
1	B	120	GLN
1	B	233	GLN
1	B	238	ARG
1	B	315	LEU
1	B	322	VAL
1	B	323	THR
1	B	326	MET
1	C	110	ARG
1	C	203	ARG
1	C	228	ARG
1	C	233	GLN
1	C	242	LYS
1	C	315	LEU
1	C	317	ARG
1	C	368	THR
1	D	36	LEU
1	D	77	ARG

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Mol	Chain	Res	Type
1	D	91	GLU
1	D	203	ARG
1	D	233	GLN
1	D	241	LYS
1	D	315	LEU
1	D	317	ARG
1	D	347	HIS
1	D	369	GLN
1	D	370	ASN
1	E	41	LYS
1	E	52	ARG
1	E	101	HIS
1	E	120	GLN
1	E	158	LEU
1	E	203	ARG
1	E	233	GLN
1	E	238	ARG
1	E	241	LYS
1	E	316	ILE
1	E	326	MET
1	E	340	GLN
1	E	351	ASP
1	E	370	ASN
1	F	84	ASP
1	F	110	ARG
1	F	161	HIS
1	F	228	ARG
1	F	233	GLN
1	F	241	LYS
1	F	314	VAL
1	F	315	LEU
1	F	317	ARG
1	F	320	GLN
1	F	327	ASP
1	F	347	HIS
1	F	351	ASP
1	F	352	SER
1	F	353	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	225	GLN
1	A	233	GLN
1	A	251	ASN
1	A	257	GLN
1	A	308	GLN
1	A	320	GLN
1	A	361	GLN
1	B	120	GLN
1	B	225	GLN
1	B	233	GLN
1	B	251	ASN
1	B	257	GLN
1	B	308	GLN
1	B	340	GLN
1	C	49	GLN
1	C	225	GLN
1	C	251	ASN
1	C	257	GLN
1	D	225	GLN
1	D	233	GLN
1	D	257	GLN
1	D	308	GLN
1	D	353	ASN
1	D	370	ASN
1	E	49	GLN
1	E	212	GLN
1	E	225	GLN
1	E	233	GLN
1	E	257	GLN
1	E	293	GLN
1	E	353	ASN
1	F	134	ASN
1	F	161	HIS
1	F	225	GLN
1	F	233	GLN
1	F	251	ASN
1	F	257	GLN
1	F	308	GLN
1	F	353	ASN
1	F	369	GLN

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](#)

6 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$
2	E5S	A	901	-	34,36,36	2.77	4 (11%)	42,52,52	1.28	2 (4%)
2	E5S	B	401	-	34,36,36	2.73	4 (11%)	42,52,52	1.24	1 (2%)
2	E5S	C	401	-	34,36,36	2.76	4 (11%)	42,52,52	1.23	3 (7%)
2	E5S	D	401	-	34,36,36	2.78	4 (11%)	42,52,52	1.33	4 (9%)
2	E5S	E	401	-	34,36,36	2.78	4 (11%)	42,52,52	1.22	3 (7%)
2	E5S	F	401	-	34,36,36	2.79	4 (11%)	42,52,52	1.25	2 (4%)

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	E5S	A	901	-	-	0/14/49/49	0/3/5/5
2	E5S	B	401	-	-	0/14/49/49	0/3/5/5
2	E5S	C	401	-	-	0/14/49/49	0/3/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	E5S	D	401	-	-	0/14/49/49	0/3/5/5
2	E5S	E	401	-	-	0/14/49/49	0/3/5/5
2	E5S	F	401	-	-	0/14/49/49	0/3/5/5

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	401	E5S	CAQ-CAZ	-15.09	1.39	1.51
2	E	401	E5S	CAQ-CAZ	-15.08	1.39	1.51
2	D	401	E5S	CAQ-CAZ	-15.07	1.39	1.51
2	A	901	E5S	CAQ-CAZ	-14.98	1.39	1.51
2	C	401	E5S	CAQ-CAZ	-14.84	1.39	1.51
2	B	401	E5S	CAQ-CAZ	-14.80	1.39	1.51
2	A	901	E5S	CAQ-CAW	-3.68	1.39	1.52
2	E	401	E5S	CAQ-CAW	-3.68	1.39	1.52
2	D	401	E5S	CAQ-CAW	-3.68	1.39	1.52
2	F	401	E5S	CAQ-CAW	-3.67	1.39	1.52
2	C	401	E5S	CAQ-CAW	-3.65	1.39	1.52
2	B	401	E5S	CAQ-CAW	-3.61	1.39	1.52
2	E	401	E5S	CAY-NBE	-2.17	1.33	1.37
2	F	401	E5S	CAY-NBE	-2.12	1.33	1.37
2	C	401	E5S	CAY-NBE	-2.12	1.33	1.37
2	A	901	E5S	CAY-NBE	-2.10	1.33	1.37
2	D	401	E5S	CAY-NBE	-2.03	1.33	1.37
2	B	401	E5S	CAY-NBE	-2.01	1.33	1.37
2	A	901	E5S	CAD-CAE	2.38	1.22	1.19
2	B	401	E5S	CAD-CAE	2.42	1.22	1.19
2	D	401	E5S	CAD-CAE	2.44	1.22	1.19
2	E	401	E5S	CAD-CAE	2.56	1.22	1.19
2	F	401	E5S	CAD-CAE	2.57	1.22	1.19
2	C	401	E5S	CAD-CAE	2.84	1.23	1.19

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	401	E5S	CAR-CBA-CBC	-5.90	98.52	104.18
2	C	401	E5S	CAR-CBA-CBC	-5.44	98.96	104.18
2	B	401	E5S	CAR-CBA-CBC	-5.43	98.97	104.18
2	F	401	E5S	CAR-CBA-CBC	-5.43	98.97	104.18
2	E	401	E5S	CAR-CBA-CBC	-5.36	99.03	104.18
2	A	901	E5S	CAR-CBA-CBC	-5.13	99.25	104.18
2	F	401	E5S	CAN-CBB-CBF	-2.71	108.04	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	401	E5S	CAN-CBB-CBF	-2.43	108.19	109.50
2	C	401	E5S	CAL-CAY-NAU	-2.20	119.96	123.55
2	C	401	E5S	CAN-CBB-CBF	-2.16	108.34	109.50
2	E	401	E5S	CAM-CBB-CBF	-2.06	108.39	109.50
2	D	401	E5S	CAT-CBF-CAE	-2.02	108.21	112.36
2	D	401	E5S	CAL-CAY-NAU	-2.00	120.29	123.55
2	E	401	E5S	CAL-CAY-NAU	-2.00	120.29	123.55
2	A	901	E5S	NAU-CAY-NBE	2.94	119.91	116.61

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
2	A	901	E5S	1	0
2	B	401	E5S	1	0
2	F	401	E5S	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	334/360 (92%)	-0.25	14 (4%)	37	35	16, 27, 57, 101	0
1	B	332/360 (92%)	-0.12	13 (3%)	40	38	16, 30, 68, 95	0
1	C	335/360 (93%)	0.03	20 (5%)	23	22	20, 32, 64, 107	0
1	D	335/360 (93%)	0.14	22 (6%)	19	18	22, 38, 79, 112	0
1	E	335/360 (93%)	0.33	26 (7%)	14	13	29, 48, 82, 113	0
1	F	334/360 (92%)	0.69	45 (13%)	3	3	25, 59, 91, 112	0
All	All	2005/2160 (92%)	0.14	140 (6%)	17	16	16, 39, 84, 113	0

All (140) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	318	LEU	9.1
1	A	318	LEU	8.4
1	F	318	LEU	8.1
1	C	318	LEU	8.1
1	D	36	LEU	7.9
1	C	313	ALA	7.0
1	F	315	LEU	7.0
1	F	320	GLN	6.9
1	C	319	GLY	6.6
1	F	324	LEU	6.4
1	D	317	ARG	6.4
1	F	319	GLY	6.2
1	F	323	THR	6.1
1	A	315	LEU	6.0
1	D	319	GLY	5.9
1	C	321	ALA	5.8
1	D	313	ALA	5.7
1	C	315	LEU	5.6
1	E	317	ARG	5.6

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Mol	Chain	Res	Type	RSRZ
1	E	320	GLN	5.5
1	D	323	THR	5.4
1	A	319	GLY	5.3
1	C	316	ILE	5.3
1	D	316	ILE	5.2
1	F	316	ILE	5.2
1	C	320	GLN	5.1
1	E	319	GLY	5.1
1	E	318	LEU	5.0
1	F	317	ARG	5.0
1	D	315	LEU	5.0
1	C	36	LEU	4.9
1	B	313	ALA	4.8
1	F	36	LEU	4.8
1	B	315	LEU	4.8
1	A	320	GLN	4.8
1	D	312	GLY	4.7
1	A	324	LEU	4.7
1	E	36	LEU	4.7
1	B	312	GLY	4.6
1	E	313	ALA	4.5
1	F	313	ALA	4.5
1	D	320	GLN	4.4
1	E	321	ALA	4.3
1	F	159	ASP	4.3
1	D	321	ALA	4.2
1	E	323	THR	4.2
1	B	370	ASN	4.0
1	D	37	SER	3.9
1	F	312	GLY	3.9
1	A	36	LEU	3.8
1	E	370	ASN	3.8
1	F	241	LYS	3.7
1	E	91	GLU	3.7
1	B	316	ILE	3.6
1	A	321	ALA	3.5
1	A	323	THR	3.4
1	C	312	GLY	3.4
1	F	248	LEU	3.4
1	F	351	ASP	3.3
1	F	92	LYS	3.3
1	F	89	SER	3.3

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Mol	Chain	Res	Type	RSRZ
1	F	225	GLN	3.3
1	F	87	THR	3.3
1	A	317	ARG	3.2
1	E	37	SER	3.2
1	C	248	LEU	3.2
1	D	347	HIS	3.2
1	E	86	MET	3.2
1	F	231	TRP	3.1
1	B	323	THR	3.1
1	E	315	LEU	3.1
1	F	217	ILE	3.1
1	A	313	ALA	3.1
1	F	37	SER	3.1
1	D	115	LYS	3.0
1	D	159	ASP	3.0
1	C	314	VAL	3.0
1	D	314	VAL	2.9
1	F	115	LYS	2.9
1	F	230	PHE	2.8
1	C	317	ARG	2.8
1	E	159	ASP	2.7
1	F	314	VAL	2.7
1	F	75	VAL	2.7
1	A	322	VAL	2.7
1	D	248	LEU	2.6
1	E	75	VAL	2.6
1	D	228	ARG	2.6
1	E	281	ARG	2.6
1	F	239	TYR	2.6
1	C	323	THR	2.6
1	F	106	GLN	2.6
1	F	221	LEU	2.5
1	F	254	LEU	2.5
1	E	117	LYS	2.4
1	E	194	ASP	2.4
1	D	225	GLN	2.4
1	C	228	ARG	2.4
1	E	322	VAL	2.4
1	E	312	GLY	2.4
1	F	161	HIS	2.4
1	F	71	ILE	2.4
1	B	231	TRP	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	259	LEU	2.4
1	F	243	LEU	2.4
1	D	91	GLU	2.4
1	B	324	LEU	2.3
1	F	86	MET	2.3
1	C	159	ASP	2.3
1	F	369	GLN	2.3
1	E	347	HIS	2.3
1	F	72	PHE	2.3
1	A	316	ILE	2.3
1	C	52	ARG	2.2
1	E	316	ILE	2.2
1	F	76	LEU	2.2
1	E	369	GLN	2.2
1	D	241	LYS	2.2
1	B	325	MET	2.2
1	C	324	LEU	2.2
1	F	246	PHE	2.2
1	F	259	LEU	2.2
1	D	52	ARG	2.1
1	E	228	ARG	2.1
1	F	310	PHE	2.1
1	F	88	ILE	2.1
1	B	248	LEU	2.1
1	F	157	PHE	2.1
1	F	110	ARG	2.1
1	E	314	VAL	2.1
1	A	76	LEU	2.1
1	B	347	HIS	2.1
1	F	347	HIS	2.1
1	C	370	ASN	2.1
1	C	322	VAL	2.1
1	F	262	LEU	2.0
1	A	314	VAL	2.0
1	B	262	LEU	2.0
1	C	225	GLN	2.0
1	E	324	LEU	2.0

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 [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	E5S	F	401	32/32	0.85	0.20	0.86	44,53,63,63	0
2	E5S	C	401	32/32	0.93	0.17	0.80	25,37,48,48	0
2	E5S	A	901	32/32	0.94	0.15	0.53	18,36,44,45	0
2	E5S	E	401	32/32	0.91	0.17	0.43	38,42,51,51	0
2	E5S	D	401	32/32	0.93	0.13	0.41	25,37,50,51	0
2	E5S	B	401	32/32	0.95	0.13	0.20	22,27,36,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.