



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 08:41 AM GMT

PDB ID : 3WEF
Title : Crystal structure of the human squalene synthase in complex with farnesyl thiopyrophosphate
Authors : Liu, C.I.; Jeng, W.Y.; Wang, A.H.J.
Deposited on : 2013-07-07
Resolution : 2.35 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

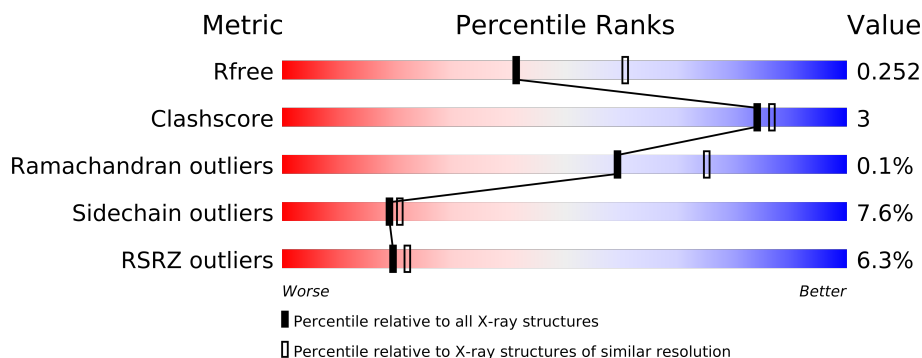
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.35 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}	66092	3327 (2.40-2.32)
Clashscore	79885	1064 (2.38-2.34)
Ramachandran outliers	78287	1048 (2.38-2.34)
Sidechain outliers	78261	1049 (2.38-2.34)
RSRZ outliers	66119	3330 (2.40-2.32)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	343	
1	B	343	
1	C	343	
1	D	343	
1	E	343	
1	F	343	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	FPS	A	401	-	X
2	FPS	A	402	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
2	FPS	B	402	-	X
2	FPS	C	401	-	X
2	FPS	D	401	-	X
2	FPS	E	402	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 16505 atoms, of which 0 are hydrogen and 0 are deuterium.

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	327	Total	C	N	O	S	0	0	0
			2650	1686	451	495	18			
1	B	333	Total	C	N	O	S	0	0	0
			2691	1711	459	503	18			
1	C	333	Total	C	N	O	S	0	0	0
			2690	1712	458	502	18			
1	D	329	Total	C	N	O	S	0	0	0
			2664	1695	453	498	18			
1	E	329	Total	C	N	O	S	0	0	0
			2658	1692	450	498	18			
1	F	322	Total	C	N	O	S	0	0	0
			2608	1659	442	489	18			

There are 18 discrepancies between the modelled and reference sequences:

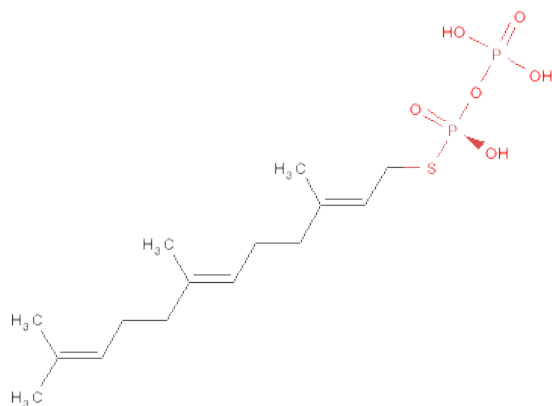
Chain	Residue	Modelled	Actual	Comment	Reference
A	28	GLY	-	EXPRESSION TAG	UNP P37268
A	29	SER	-	EXPRESSION TAG	UNP P37268
A	30	HIS	-	EXPRESSION TAG	UNP P37268
B	28	GLY	-	EXPRESSION TAG	UNP P37268
B	29	SER	-	EXPRESSION TAG	UNP P37268
B	30	HIS	-	EXPRESSION TAG	UNP P37268
C	28	GLY	-	EXPRESSION TAG	UNP P37268
C	29	SER	-	EXPRESSION TAG	UNP P37268
C	30	HIS	-	EXPRESSION TAG	UNP P37268
D	28	GLY	-	EXPRESSION TAG	UNP P37268
D	29	SER	-	EXPRESSION TAG	UNP P37268
D	30	HIS	-	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
F	28	GLY	-	EXPRESSION TAG	UNP P37268
F	29	SER	-	EXPRESSION TAG	UNP P37268

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Chain	Residue	Modelled	Actual	Comment	Reference
F	30	HIS	-	EXPRESSION TAG	UNP P37268

- Molecule 2 is S-[(2E,6E)-3,7,11-TRIMETHYLDODECA-2,6,10-TRIENYL]TRIHYDROGEN THIODIPHOSPHATE (three-letter code: FPS) (formula: C₁₅H₂₈O₆P₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	O	P	S	0	0
			24	15	6	2	1		
2	A	1	Total	C	O	P	S	0	0
			24	15	6	2	1		
2	B	1	Total	C	O	P	S	0	0
			24	15	6	2	1		
2	B	1	Total	C	O	P	S	0	0
			24	15	6	2	1		
2	C	1	Total	C	O	P	S	0	0
			24	15	6	2	1		
2	D	1	Total	C	O	P	S	0	0
			24	15	6	2	1		
2	E	1	Total	C	O	P	S	0	0
			24	15	6	2	1		
2	E	1	Total	C	O	P	S	0	0
			24	15	6	2	1		

- Molecule 3 is water.

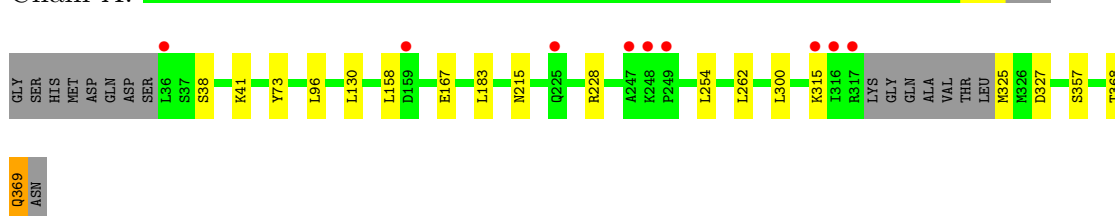
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	111	Total 111	O 111	0	0
3	B	75	Total 75	O 75	0	0
3	C	94	Total 94	O 94	0	0
3	D	22	Total 22	O 22	0	0
3	E	42	Total 42	O 42	0	0
3	F	8	Total 8	O 8	0	0

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 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.

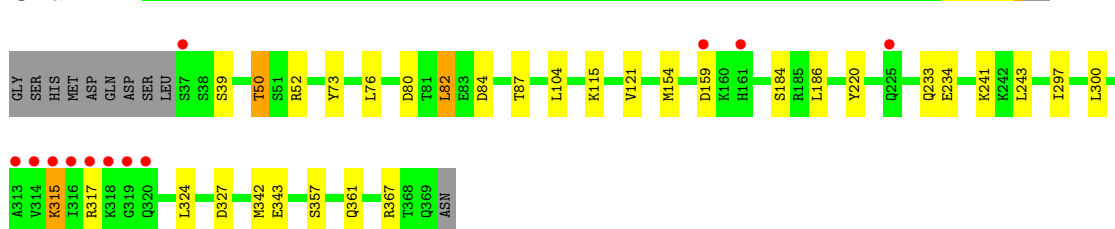
- Molecule 1: Squalene synthase

Chain A:



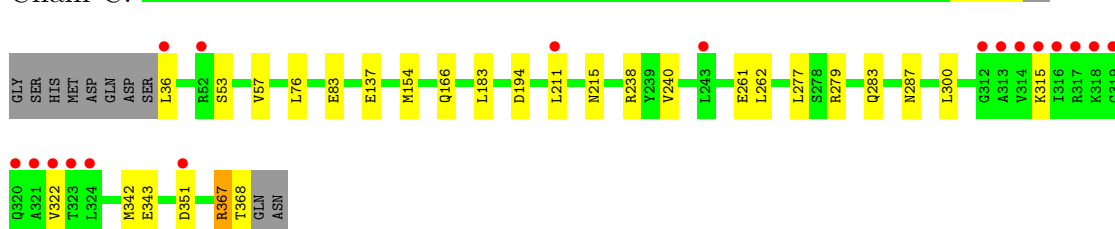
- Molecule 1: Squalene synthase

Chain B:



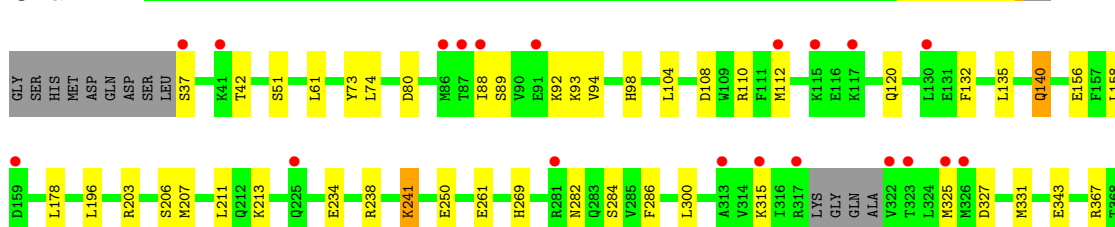
- Molecule 1: Squalene synthase

Chain C:



- Molecule 1: Squalene synthase

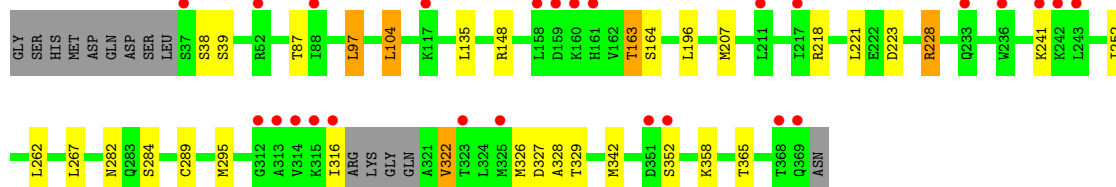
Chain D:





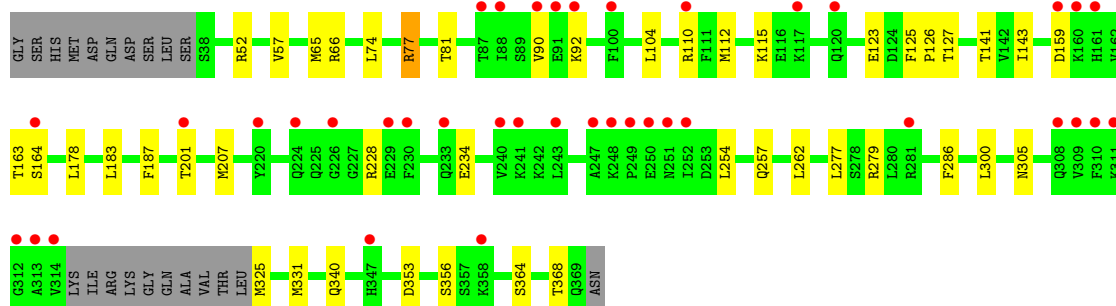
• Molecule 1: Squalene synthase

Chain E:



• Molecule 1: Squalene synthase

Chain F:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.89Å 153.75Å 91.61Å 90.00° 91.06° 90.00°	Depositor
Resolution (Å)	30.00 – 2.35 29.95 – 2.35	Depositor EDS
% Data completeness (in resolution range)	98.7 (30.00-2.35) 98.7 (29.95-2.35)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.18 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.190 , 0.257 0.185 , 0.252	Depositor DCC
R_{free} test set	4876 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	37.4	Xtriage
Anisotropy	0.450	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 33.5	EDS
Estimated twinning fraction	0.034 for h,-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	1 of 97751 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	16505	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.60% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

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	0.40	0/2704	0.72	0/3655
1	B	0.37	0/2746	0.68	1/3713 (0.0%)
1	C	0.36	0/2745	0.68	1/3712 (0.0%)
1	D	0.33	0/2718	0.65	1/3675 (0.0%)
1	E	0.33	0/2712	0.66	3/3668 (0.1%)
1	F	0.31	0/2662	0.63	1/3600 (0.0%)
All	All	0.35	0/16287	0.67	7/22023 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	97	LEU	CA-CB-CG	6.58	130.44	115.30
1	E	207	MET	CG-SD-CE	-6.17	90.33	100.20
1	E	104	LEU	CA-CB-CG	5.31	127.52	115.30
1	F	207	MET	CG-SD-CE	-5.23	91.83	100.20
1	B	82	LEU	CA-CB-CG	5.16	127.17	115.30
1	D	207	MET	CG-SD-CE	-5.11	92.03	100.20
1	C	367	ARG	NE-CZ-NH2	-5.01	117.80	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the

chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2650	0	0	5	0
1	B	2691	0	0	8	0
1	C	2690	0	0	7	0
1	D	2664	0	0	11	0
1	E	2658	0	0	8	0
1	F	2608	0	0	9	0
2	A	48	0	0	0	0
2	B	48	0	0	1	0
2	C	24	0	0	1	0
2	D	24	0	0	0	0
2	E	48	0	0	2	0
3	A	111	0	0	1	0
3	B	75	0	0	0	0
3	C	94	0	0	1	0
3	D	22	0	0	0	0
3	E	42	0	0	1	0
3	F	8	0	0	0	0
All	All	16505	0	0	47	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 3.

All (47) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:286:PHE:CE1	1:D:331:MET:CE	2.50	0.95
1:D:132:PHE:O	1:D:140:GLN:NE2	2.13	0.81
1:B:297:ILE:CD1	1:B:342:MET:CE	2.63	0.76
1:F:286:PHE:CE1	1:F:331:MET:CE	2.71	0.74
1:B:154:MET:CE	2:B:402:FPS:C4	2.66	0.73
1:E:163:THR:CG2	1:E:164:SER:N	2.55	0.69
1:F:65:MET:CE	1:F:187:PHE:CD1	2.76	0.68
1:E:282:ASN:ND2	1:E:284:SER:CB	2.61	0.64
1:E:322:VAL:CG1	1:E:326:MET:CE	2.75	0.64
1:F:163:THR:CG2	1:F:164:SER:N	2.64	0.61
1:C:83:GLU:CB	1:C:154:MET:CE	2.79	0.60
1:E:223:ASP:OD1	1:E:228:ARG:NH1	2.36	0.59
1:A:215:ASN:ND2	3:A:579:HOH:O	2.37	0.56
1:F:77:ARG:O	1:F:81:THR:OG1	2.22	0.56
1:D:241:LYS:CA	1:D:241:LYS:CE	2.84	0.55
1:B:343:GLU:OE2	1:B:367:ARG:NH1	2.40	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:353:ASP:O	1:F:356:SER:OG	2.26	0.54
1:C:343:GLU:OE1	1:C:367:ARG:NH2	2.41	0.54
1:D:213:LYS:NZ	1:D:269:HIS:NE2	2.56	0.54
1:F:110:ARG:NH1	1:F:123:GLU:O	2.42	0.53
1:B:220:TYR:OH	1:B:243:LEU:O	2.28	0.51
1:B:50:THR:CG2	1:B:73:TYR:CE1	2.94	0.51
1:A:73:TYR:CD1	1:A:73:TYR:C	2.84	0.51
1:E:327:ASP:OD1	1:E:328:ALA:N	2.45	0.49
1:D:238:ARG:NH2	1:D:261:GLU:OE2	2.47	0.48
2:E:402:FPS:C7	2:E:402:FPS:C4	2.92	0.48
1:D:327:ASP:OD2	1:E:327:ASP:N	2.48	0.47
1:E:148:ARG:NE	3:E:501:HOH:O	2.48	0.46
1:D:73:TYR:CD1	1:D:73:TYR:C	2.89	0.46
1:D:343:GLU:OE2	1:D:367:ARG:NE	2.48	0.46
1:C:215:ASN:ND2	2:C:401:FPS:C4	2.79	0.46
1:A:368:THR:O	1:A:369:GLN:C	2.55	0.45
1:B:315:LYS:N	1:B:315:LYS:CD	2.78	0.45
1:C:283:GLN:NE2	1:C:287:ASN:ND2	2.65	0.45
1:C:194:ASP:OD2	1:F:279:ARG:NE	2.50	0.45
1:F:125:PHE:N	1:F:126:PRO:CD	2.81	0.44
1:E:289:CYS:SG	2:E:401:FPS:C14	3.06	0.43
1:D:51:SER:CB	1:D:73:TYR:CZ	3.02	0.43
1:A:228:ARG:CG	1:A:228:ARG:NH1	2.81	0.42
1:B:73:TYR:CD1	1:B:73:TYR:C	2.92	0.42
1:C:279:ARG:NH1	3:C:557:HOH:O	2.51	0.42
1:D:343:GLU:OE1	1:D:367:ARG:NH2	2.53	0.41
1:C:238:ARG:NH2	1:C:261:GLU:OE2	2.54	0.41
1:D:282:ASN:ND2	1:D:284:SER:OG	2.54	0.41
1:F:277:LEU:C	1:F:331:MET:CE	2.89	0.41
1:B:80:ASP:O	1:B:84:ASP:CB	2.69	0.41
1:A:369:GLN:OE1	1:A:369:GLN:CA	2.69	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	323/343 (94%)	316 (98%)	7 (2%)	0	100	100
1	B	331/343 (96%)	326 (98%)	5 (2%)	0	100	100
1	C	331/343 (96%)	321 (97%)	9 (3%)	1 (0%)	50	62
1	D	325/343 (95%)	312 (96%)	13 (4%)	0	100	100
1	E	325/343 (95%)	314 (97%)	11 (3%)	0	100	100
1	F	318/343 (93%)	298 (94%)	19 (6%)	1 (0%)	50	62
All	All	1953/2058 (95%)	1887 (97%)	64 (3%)	2 (0%)	59	75

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	315	LYS
1	F	66	ARG

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	292/305 (96%)	277 (95%)	15 (5%)	33	41
1	B	296/305 (97%)	274 (93%)	22 (7%)	20	22
1	C	296/305 (97%)	280 (95%)	16 (5%)	31	38
1	D	294/305 (96%)	263 (90%)	31 (10%)	10	10
1	E	293/305 (96%)	270 (92%)	23 (8%)	18	19
1	F	287/305 (94%)	260 (91%)	27 (9%)	13	12
All	All	1758/1830 (96%)	1624 (92%)	134 (8%)	19	21

All (134) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	SER
1	A	41	LYS
1	A	96	LEU
1	A	130	LEU
1	A	158	LEU

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Mol	Chain	Res	Type
1	A	167	GLU
1	A	183	LEU
1	A	254	LEU
1	A	262	LEU
1	A	300	LEU
1	A	315	LYS
1	A	325	MET
1	A	327	ASP
1	A	357	SER
1	A	369	GLN
1	B	39	SER
1	B	50	THR
1	B	52	ARG
1	B	76	LEU
1	B	82	LEU
1	B	87	THR
1	B	104	LEU
1	B	115	LYS
1	B	121	VAL
1	B	159	ASP
1	B	184	SER
1	B	186	LEU
1	B	233	GLN
1	B	234	GLU
1	B	241	LYS
1	B	300	LEU
1	B	315	LYS
1	B	317	ARG
1	B	324	LEU
1	B	327	ASP
1	B	357	SER
1	B	361	GLN
1	C	36	LEU
1	C	53	SER
1	C	57	VAL
1	C	76	LEU
1	C	137	GLU
1	C	166	GLN
1	C	183	LEU
1	C	211	LEU
1	C	240	VAL
1	C	262	LEU

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Mol	Chain	Res	Type
1	C	277	LEU
1	C	300	LEU
1	C	322	VAL
1	C	342	MET
1	C	351	ASP
1	C	368	THR
1	D	37	SER
1	D	42	THR
1	D	61	LEU
1	D	74	LEU
1	D	80	ASP
1	D	88	ILE
1	D	89	SER
1	D	92	LYS
1	D	93	LYS
1	D	94	VAL
1	D	98	HIS
1	D	104	LEU
1	D	108	ASP
1	D	110	ARG
1	D	112	MET
1	D	120	GLN
1	D	135	LEU
1	D	140	GLN
1	D	156	GLU
1	D	158	LEU
1	D	178	LEU
1	D	196	LEU
1	D	203	ARG
1	D	206	SER
1	D	211	LEU
1	D	234	GLU
1	D	241	LYS
1	D	250	GLU
1	D	300	LEU
1	D	315	LYS
1	D	325	MET
1	E	38	SER
1	E	39	SER
1	E	87	THR
1	E	97	LEU
1	E	104	LEU

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Mol	Chain	Res	Type
1	E	135	LEU
1	E	163	THR
1	E	196	LEU
1	E	218	ARG
1	E	221	LEU
1	E	228	ARG
1	E	241	LYS
1	E	252	ILE
1	E	262	LEU
1	E	267	LEU
1	E	295	MET
1	E	316	ILE
1	E	322	VAL
1	E	329	THR
1	E	342	MET
1	E	352	SER
1	E	358	LYS
1	E	365	THR
1	F	52	ARG
1	F	57	VAL
1	F	74	LEU
1	F	77	ARG
1	F	90	VAL
1	F	92	LYS
1	F	104	LEU
1	F	112	MET
1	F	115	LYS
1	F	127	THR
1	F	141	THR
1	F	143	ILE
1	F	159	ASP
1	F	178	LEU
1	F	183	LEU
1	F	201	THR
1	F	228	ARG
1	F	234	GLU
1	F	254	LEU
1	F	257	GLN
1	F	262	LEU
1	F	300	LEU
1	F	305	ASN
1	F	325	MET

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Mol	Chain	Res	Type
1	F	340	GLN
1	F	364	SER
1	F	368	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

8 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	FPS	A	401	-	23,23,23	2.75	10 (43%)	29,31,31	1.91	9 (31%)
2	FPS	A	402	-	23,23,23	2.75	11 (47%)	29,31,31	1.56	5 (17%)
2	FPS	B	401	-	23,23,23	2.71	10 (43%)	29,31,31	2.40	12 (41%)
2	FPS	B	402	-	23,23,23	2.76	10 (43%)	29,31,31	1.84	10 (34%)
2	FPS	C	401	-	23,23,23	2.69	9 (39%)	29,31,31	2.73	13 (44%)
2	FPS	D	401	-	23,23,23	2.75	10 (43%)	29,31,31	2.04	9 (31%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	FPS	E	401	-	23,23,23	2.74	10 (43%)	29,31,31	1.92	7 (24%)
2	FPS	E	402	-	23,23,23	3.10	11 (47%)	29,31,31	2.19	10 (34%)

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	FPS	A	401	-	-	0/23/25/25	0/0/0/0
2	FPS	A	402	-	-	0/23/25/25	0/0/0/0
2	FPS	B	401	-	-	1/23/25/25	0/0/0/0
2	FPS	B	402	-	-	2/23/25/25	0/0/0/0
2	FPS	C	401	-	-	1/23/25/25	0/0/0/0
2	FPS	D	401	-	-	1/23/25/25	0/0/0/0
2	FPS	E	401	-	-	1/23/25/25	0/0/0/0
2	FPS	E	402	-	-	0/23/25/25	0/0/0/0

All (81) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	402	FPS	PA-S1	-7.22	1.89	2.08
2	B	402	FPS	C1-C2	-6.88	1.39	1.49
2	A	401	FPS	C1-C2	-6.67	1.39	1.49
2	E	401	FPS	C1-C2	-6.60	1.39	1.49
2	E	402	FPS	C1-C2	-6.54	1.39	1.49
2	B	401	FPS	C1-C2	-6.37	1.39	1.49
2	D	401	FPS	C1-C2	-6.37	1.39	1.49
2	A	402	FPS	C1-C2	-6.36	1.40	1.49
2	E	401	FPS	PA-O1A	6.15	1.62	1.47
2	A	401	FPS	PA-O1A	6.08	1.62	1.47
2	E	402	FPS	PA-O1A	6.05	1.62	1.47
2	B	402	FPS	PA-O1A	5.97	1.62	1.47
2	D	401	FPS	PA-O1A	5.96	1.62	1.47
2	C	401	FPS	PA-O1A	5.96	1.62	1.47
2	A	402	FPS	PA-O1A	5.93	1.61	1.47
2	C	401	FPS	C1-C2	-5.79	1.40	1.49
2	B	401	FPS	PA-O1A	5.77	1.61	1.47
2	E	402	FPS	C11-C12	-4.03	1.38	1.50
2	C	401	FPS	C6-C7	-3.93	1.39	1.50
2	A	402	FPS	C6-C7	-3.90	1.39	1.50
2	A	401	FPS	C6-C7	-3.90	1.39	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	401	FPS	C2-C3	3.86	1.40	1.32
2	A	402	FPS	C11-C12	-3.84	1.39	1.50
2	B	402	FPS	C6-C7	-3.83	1.39	1.50
2	B	402	FPS	C11-C12	-3.83	1.39	1.50
2	D	401	FPS	C6-C7	-3.82	1.39	1.50
2	E	401	FPS	C11-C12	-3.80	1.39	1.50
2	D	401	FPS	C11-C12	-3.79	1.39	1.50
2	E	401	FPS	C6-C7	-3.77	1.39	1.50
2	A	401	FPS	C11-C12	-3.75	1.39	1.50
2	E	402	FPS	C6-C7	-3.76	1.39	1.50
2	B	401	FPS	C6-C7	-3.72	1.39	1.50
2	B	401	FPS	C11-C12	-3.64	1.40	1.50
2	C	401	FPS	C11-C12	-3.59	1.40	1.50
2	A	402	FPS	C2-C3	3.59	1.40	1.32
2	D	401	FPS	C2-C3	3.52	1.40	1.32
2	D	401	FPS	C7-C8	3.46	1.39	1.32
2	B	401	FPS	C7-C8	3.46	1.39	1.32
2	E	402	FPS	C7-C8	3.46	1.39	1.32
2	B	401	FPS	C2-C3	3.45	1.39	1.32
2	A	402	FPS	PB-O2B	3.37	1.62	1.51
2	C	401	FPS	C7-C8	3.36	1.39	1.32
2	B	401	FPS	PB-O2B	3.35	1.62	1.51
2	E	401	FPS	C2-C3	3.34	1.39	1.32
2	E	401	FPS	C7-C8	3.34	1.39	1.32
2	B	402	FPS	C7-C8	3.34	1.39	1.32
2	E	402	FPS	PB-O2B	3.31	1.62	1.51
2	A	401	FPS	C7-C8	3.29	1.39	1.32
2	B	402	FPS	C2-C3	3.28	1.39	1.32
2	A	402	FPS	C7-C8	3.28	1.39	1.32
2	C	401	FPS	PB-O2B	3.28	1.62	1.51
2	D	401	FPS	PB-O2B	3.26	1.62	1.51
2	D	401	FPS	PA-O2A	-3.24	1.48	1.55
2	B	402	FPS	PA-O2A	-3.24	1.48	1.55
2	A	401	FPS	C2-C3	3.22	1.39	1.32
2	A	401	FPS	PB-O2B	3.21	1.62	1.51
2	B	402	FPS	PB-O2B	3.20	1.61	1.51
2	E	402	FPS	C2-C3	3.10	1.39	1.32
2	E	401	FPS	PB-O2B	3.09	1.61	1.51
2	B	401	FPS	PA-O2A	-3.09	1.48	1.55
2	A	402	FPS	PA-O2A	-3.07	1.48	1.55
2	E	401	FPS	PA-O2A	-3.06	1.48	1.55
2	C	401	FPS	PA-O2A	-2.92	1.49	1.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	402	FPS	PA-O2A	-2.90	1.49	1.55
2	A	401	FPS	PA-O2A	-2.88	1.49	1.55
2	C	401	FPS	C12-C13	2.63	1.40	1.32
2	B	401	FPS	C12-C13	2.47	1.40	1.32
2	A	401	FPS	C12-C13	2.38	1.40	1.32
2	E	401	FPS	C12-C13	2.38	1.40	1.32
2	D	401	FPS	C12-C13	2.31	1.39	1.32
2	A	402	FPS	PB-O3A	2.27	1.64	1.60
2	A	402	FPS	C12-C13	2.23	1.39	1.32
2	B	402	FPS	C12-C13	2.20	1.39	1.32
2	E	401	FPS	PB-O3B	2.15	1.62	1.54
2	B	402	FPS	PB-O3B	2.15	1.62	1.54
2	A	402	FPS	PB-O3B	2.14	1.62	1.54
2	A	401	FPS	PB-O3B	2.11	1.62	1.54
2	B	401	FPS	PB-O3B	2.09	1.62	1.54
2	E	402	FPS	C12-C13	2.07	1.39	1.32
2	D	401	FPS	PB-O3B	2.04	1.62	1.54
2	E	402	FPS	PB-O3B	2.02	1.62	1.54

All (75) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	FPS	PB-O3A-PA	-5.87	114.46	131.68
2	C	401	FPS	PA-S1-C1	5.83	109.21	102.27
2	B	401	FPS	PA-S1-C1	5.36	108.64	102.27
2	C	401	FPS	C9-C8-C7	-5.30	113.02	123.52
2	C	401	FPS	C6-C7-C8	5.21	139.04	127.80
2	E	402	FPS	C4-C3-C5	5.20	123.30	115.39
2	B	401	FPS	O2A-PA-S1	4.79	116.41	104.29
2	C	401	FPS	O2A-PA-S1	4.77	116.36	104.29
2	E	402	FPS	PB-O3A-PA	-4.48	118.54	131.68
2	E	401	FPS	PB-O3A-PA	-4.38	118.83	131.68
2	C	401	FPS	PB-O3A-PA	-4.21	119.35	131.68
2	D	401	FPS	C4-C3-C5	4.16	121.72	115.39
2	A	401	FPS	PB-O3A-PA	-4.00	119.96	131.68
2	A	401	FPS	C4-C3-C5	3.96	121.42	115.39
2	C	401	FPS	C2-C1-S1	3.90	117.98	111.69
2	C	401	FPS	C1-C2-C3	3.80	133.69	127.43
2	B	402	FPS	C4-C3-C2	-3.80	116.00	123.52
2	A	401	FPS	C9-C8-C7	-3.59	116.41	123.52
2	E	401	FPS	C4-C3-C5	3.54	120.78	115.39
2	E	401	FPS	O2A-PA-S1	3.53	113.22	104.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	402	FPS	O2A-PA-S1	3.52	113.19	104.29
2	E	401	FPS	C9-C8-C7	-3.46	116.66	123.52
2	D	401	FPS	C9-C8-C7	-3.44	116.70	123.52
2	D	401	FPS	O2A-PA-S1	3.43	112.97	104.29
2	D	401	FPS	PB-O3A-PA	-3.43	121.63	131.68
2	E	402	FPS	C4-C3-C2	-3.38	116.83	123.52
2	C	401	FPS	C10-C8-C7	3.36	127.55	121.08
2	E	402	FPS	O2A-PA-O3A	3.36	115.79	104.51
2	B	401	FPS	C4-C3-C5	3.31	120.42	115.39
2	C	401	FPS	O1A-PA-S1	-3.30	101.43	112.36
2	E	402	FPS	PA-S1-C1	-3.27	98.38	102.27
2	A	402	FPS	O2A-PA-S1	3.25	112.51	104.29
2	B	401	FPS	C9-C8-C7	-3.20	117.18	123.52
2	B	402	FPS	O2A-PA-S1	3.16	112.28	104.29
2	A	402	FPS	PB-O3A-PA	-3.12	122.53	131.68
2	B	402	FPS	C4-C3-C5	3.09	120.09	115.39
2	E	401	FPS	C9-C8-C10	3.08	120.07	115.39
2	A	401	FPS	O2A-PA-S1	3.05	112.02	104.29
2	D	401	FPS	O2A-PA-O3A	3.03	114.67	104.51
2	C	401	FPS	O2A-PA-O3A	3.02	114.65	104.51
2	B	401	FPS	C2-C1-S1	-2.96	106.93	111.69
2	B	402	FPS	O2A-PA-O3A	2.93	114.34	104.51
2	E	402	FPS	O1A-PA-S1	-2.91	102.73	112.36
2	A	402	FPS	C1-C2-C3	2.88	132.17	127.43
2	B	401	FPS	C9-C8-C10	2.86	119.74	115.39
2	B	402	FPS	PB-O3A-PA	-2.84	123.36	131.68
2	D	401	FPS	PA-S1-C1	2.81	105.62	102.27
2	D	401	FPS	C9-C8-C10	2.80	119.64	115.39
2	E	402	FPS	C1-C2-C3	-2.77	122.85	127.43
2	A	401	FPS	C9-C8-C10	2.76	119.59	115.39
2	D	401	FPS	C1-C2-C3	2.75	131.96	127.43
2	E	401	FPS	O2A-PA-O3A	2.74	113.70	104.51
2	A	401	FPS	O1A-PA-S1	-2.68	103.51	112.36
2	C	401	FPS	C9-C8-C10	2.65	119.42	115.39
2	A	402	FPS	C9-C8-C10	2.45	119.12	115.39
2	B	402	FPS	C14-C13-C12	-2.36	114.92	122.62
2	B	401	FPS	C14-C13-C12	-2.35	114.93	122.62
2	B	402	FPS	C2-C1-S1	-2.33	107.93	111.69
2	E	402	FPS	C15-C13-C14	2.30	120.49	114.62
2	C	401	FPS	O1B-PB-O3A	2.23	115.74	105.14
2	C	401	FPS	C10-C11-C12	2.22	117.97	111.62
2	B	401	FPS	O1A-PA-S1	-2.21	105.04	112.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	FPS	O2A-PA-O3A	2.20	111.91	104.51
2	B	402	FPS	C10-C11-C12	-2.20	105.33	111.62
2	B	402	FPS	C15-C13-C14	2.20	120.22	114.62
2	B	401	FPS	C6-C7-C8	2.14	132.41	127.80
2	B	401	FPS	O2A-PA-O3A	2.12	111.64	104.51
2	E	402	FPS	C10-C8-C7	-2.11	117.02	121.08
2	A	401	FPS	C6-C7-C8	2.11	132.35	127.80
2	A	401	FPS	C4-C3-C2	-2.11	119.35	123.52
2	A	402	FPS	O1A-PA-S1	-2.08	105.47	112.36
2	B	401	FPS	C1-C2-C3	2.04	130.78	127.43
2	D	401	FPS	C2-C1-S1	-2.03	108.42	111.69
2	E	401	FPS	C6-C7-C8	2.01	132.13	127.80
2	B	402	FPS	O1B-PB-O3A	2.00	114.63	105.14

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	402	FPS	O1A-PA-S1-C1
2	B	402	FPS	C2-C1-S1-PA
2	E	401	FPS	O1A-PA-S1-C1
2	B	401	FPS	O1A-PA-S1-C1
2	D	401	FPS	O1A-PA-S1-C1
2	C	401	FPS	O1A-PA-S1-C1

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	327/343 (95%)	-0.17	9 (2%) 50 54	19, 34, 60, 99	0
1	B	333/343 (97%)	-0.14	12 (3%) 41 44	22, 37, 65, 97	0
1	C	333/343 (97%)	0.26	18 (5%) 25 28	23, 48, 102, 120	0
1	D	329/343 (95%)	0.23	20 (6%) 21 23	29, 56, 102, 126	0
1	E	329/343 (95%)	0.33	26 (7%) 13 15	24, 51, 103, 125	0
1	F	322/343 (93%)	0.57	39 (12%) 5 6	35, 77, 131, 151	0
All	All	1973/2058 (95%)	0.18	124 (6%) 19 22	19, 48, 109, 151	0

All (124) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	316	ILE	10.7
1	C	321	ALA	8.3
1	F	312	GLY	7.4
1	E	159	ASP	6.9
1	F	313	ALA	6.6
1	C	318	LYS	6.4
1	E	315	LYS	6.3
1	B	319	GLY	6.1
1	E	312	GLY	5.9
1	C	316	ILE	5.9
1	F	241	LYS	5.8
1	F	247	ALA	5.1
1	C	319	GLY	5.1
1	D	322	VAL	5.1
1	C	312	GLY	5.0
1	F	314	VAL	4.9
1	E	313	ALA	4.9
1	E	368	THR	4.9
1	A	317	ARG	4.9

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Mol	Chain	Res	Type	RSRZ
1	F	311	LYS	4.8
1	E	161	HIS	4.8
1	F	249	PRO	4.6
1	D	159	ASP	4.6
1	C	317	ARG	4.5
1	C	323	THR	4.4
1	C	315	LYS	4.3
1	E	243	LEU	4.3
1	D	315	LYS	4.3
1	D	115	LYS	4.1
1	F	87	THR	4.1
1	D	317	ARG	4.0
1	C	313	ALA	3.9
1	F	251	ASN	3.9
1	D	88	ILE	3.9
1	B	317	ARG	3.8
1	F	159	ASP	3.8
1	E	37	SER	3.8
1	E	211	LEU	3.7
1	D	37	SER	3.7
1	F	250	GLU	3.6
1	B	159	ASP	3.6
1	C	322	VAL	3.6
1	E	88	ILE	3.5
1	F	347	HIS	3.5
1	E	217	ILE	3.4
1	D	323	THR	3.4
1	B	313	ALA	3.4
1	F	310	PHE	3.3
1	E	352	SER	3.3
1	A	36	LEU	3.3
1	D	112	MET	3.3
1	F	90	VAL	3.1
1	E	242	LYS	3.0
1	E	369	GLN	3.0
1	B	316	ILE	3.0
1	D	117	LYS	2.9
1	D	313	ALA	2.9
1	D	325	MET	2.8
1	C	36	LEU	2.8
1	F	226	GLY	2.8
1	C	243	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	320	GLN	2.7
1	B	315	LYS	2.7
1	F	117	LYS	2.7
1	A	249	PRO	2.7
1	D	87	THR	2.7
1	F	230	PHE	2.7
1	F	240	VAL	2.7
1	C	324	LEU	2.6
1	F	309	VAL	2.6
1	A	159	ASP	2.6
1	A	315	LYS	2.6
1	D	41	LYS	2.6
1	D	130	LEU	2.5
1	F	91	GLU	2.5
1	F	243	LEU	2.5
1	F	224	GLN	2.5
1	F	110	ARG	2.5
1	F	358	LYS	2.4
1	D	86	MET	2.4
1	B	320	GLN	2.4
1	A	225	GLN	2.4
1	A	316	ILE	2.4
1	B	225	GLN	2.4
1	B	314	VAL	2.4
1	E	233	GLN	2.4
1	F	92	LYS	2.4
1	F	164	SER	2.4
1	F	100	PHE	2.4
1	A	247	ALA	2.4
1	F	281	ARG	2.4
1	E	325	MET	2.3
1	F	161	HIS	2.3
1	D	91	GLU	2.3
1	B	318	LYS	2.3
1	F	120	GLN	2.3
1	C	52	ARG	2.3
1	F	233	GLN	2.3
1	F	308	GLN	2.3
1	E	351	ASP	2.2
1	C	314	VAL	2.2
1	E	323	THR	2.2
1	D	225	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	248	LYS	2.2
1	E	236	TRP	2.2
1	E	117	LYS	2.2
1	F	160	LYS	2.2
1	E	52	ARG	2.1
1	C	351	ASP	2.1
1	E	314	VAL	2.1
1	F	248	LYS	2.1
1	F	220	TYR	2.1
1	B	161	HIS	2.1
1	F	88	ILE	2.1
1	E	158	LEU	2.0
1	E	160	LYS	2.0
1	E	241	LYS	2.0
1	D	281	ARG	2.0
1	F	229	GLU	2.0
1	F	201	THR	2.0
1	F	252	ILE	2.0
1	D	326	MET	2.0
1	C	211	LEU	2.0
1	B	37	SER	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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	FPS	A	402	24/24	0.32	5.26	77,106,126,126	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	FPS	D	401	24/24	0.27	3.18	72,96,118,118	0
2	FPS	E	402	24/24	0.28	2.96	56,90,119,119	0
2	FPS	B	402	24/24	0.26	2.80	44,77,98,98	0
2	FPS	C	401	24/24	0.27	2.42	44,81,105,105	0
2	FPS	A	401	24/24	0.21	2.03	48,78,107,107	0
2	FPS	B	401	24/24	0.20	1.45	33,83,107,107	0
2	FPS	E	401	24/24	0.21	0.76	52,90,109,109	0

6.5 Other polymers ⓘ

There are no such residues in this entry.