Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 07:23 PM GMT

PDB ID	:	4RQE
Title	:	human Seryl-tRNA synthetase dimer complexed with two molecules of tRNAsec
Authors	:	Xie, W.; Wang, C.; Guo, Y.; Tian, Q.; Jia, Q.
Deposited on	:	2014-11-03
Resolution	:	4.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

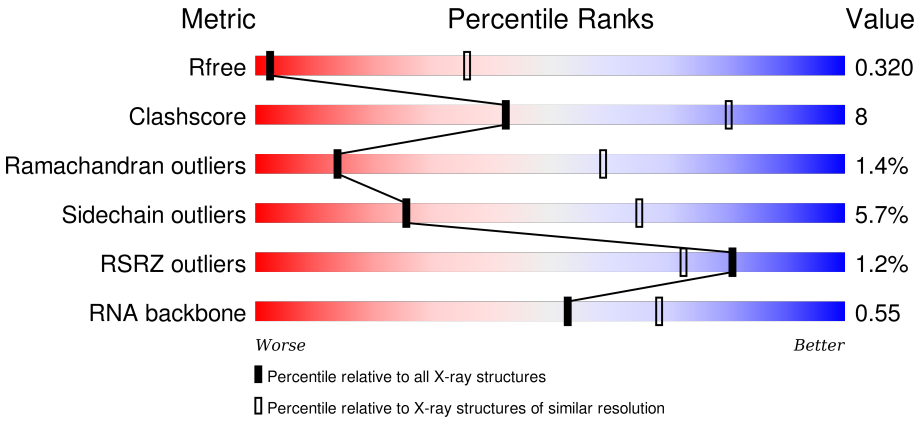
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026982
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20026982

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 4.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1010 (4.42-3.56)
Clashscore	102246	1052 (4.40-3.60)
Ramachandran outliers	100387	1005 (4.40-3.60)
Sidechain outliers	100360	1013 (4.42-3.58)
RSRZ outliers	91569	1013 (4.42-3.56)
RNA backbone	2183	1079 (5.04-2.80)

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 <=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	522	% 72% 13% • 12%
1	C	522	% 69% 15% • 13%
2	B	90	% 43% 40% 9% • 7%
2	D	90	43% 41% 8% 8%

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	SER	A	601	-	-	-	X
3	SER	C	601	-	-	-	X
4	ANP	A	602	-	-	-	X

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 10599 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 Serine–tRNA ligase, cytoplasmic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	460	Total	C	N	O	S	0	0	0
			3513	2220	607	670	16			
1	C	452	Total	C	N	O	S	0	0	0
			3448	2177	596	659	16			

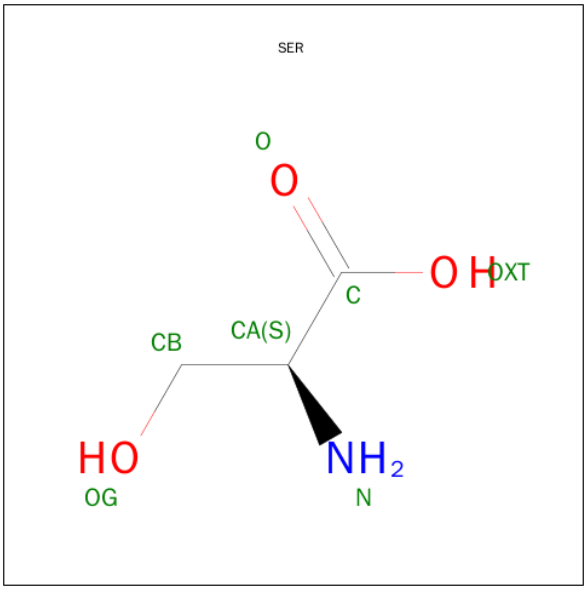
There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	156	THR	GLU	ENGINEERED MUTATION	UNP P49591
A	157	SER	ARG	ENGINEERED MUTATION	UNP P49591
A	515	LEU	-	EXPRESSION TAG	UNP P49591
A	516	GLU	-	EXPRESSION TAG	UNP P49591
A	517	HIS	-	EXPRESSION TAG	UNP P49591
A	518	HIS	-	EXPRESSION TAG	UNP P49591
A	519	HIS	-	EXPRESSION TAG	UNP P49591
A	520	HIS	-	EXPRESSION TAG	UNP P49591
A	521	HIS	-	EXPRESSION TAG	UNP P49591
A	522	HIS	-	EXPRESSION TAG	UNP P49591
C	156	THR	GLU	ENGINEERED MUTATION	UNP P49591
C	157	SER	ARG	ENGINEERED MUTATION	UNP P49591
C	515	LEU	-	EXPRESSION TAG	UNP P49591
C	516	GLU	-	EXPRESSION TAG	UNP P49591
C	517	HIS	-	EXPRESSION TAG	UNP P49591
C	518	HIS	-	EXPRESSION TAG	UNP P49591
C	519	HIS	-	EXPRESSION TAG	UNP P49591
C	520	HIS	-	EXPRESSION TAG	UNP P49591
C	521	HIS	-	EXPRESSION TAG	UNP P49591
C	522	HIS	-	EXPRESSION TAG	UNP P49591

- Molecule 2 is a RNA chain called selenocysteine tRNA.

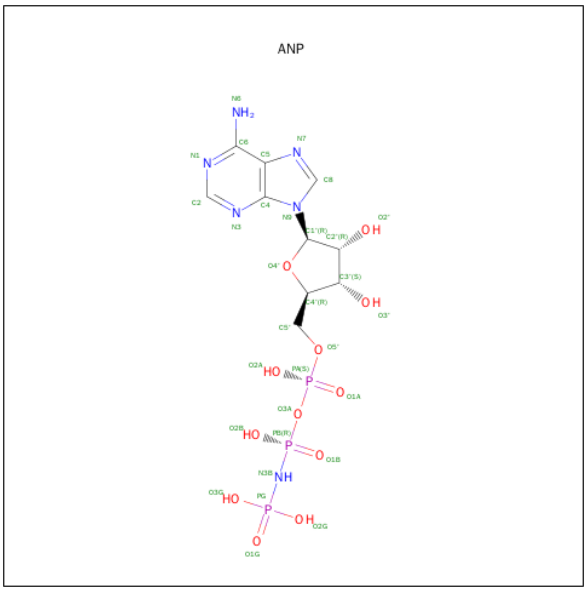
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	84	Total	C	N	O	P	0	0	0
			1791	798	315	594	84			
2	D	83	Total	C	N	O	P	0	0	0
			1771	789	312	587	83			

- Molecule 3 is SERINE (three-letter code: SER) (formula: $C_3H_7NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			7	3	1	3		
3	C	1	Total	C	N	O	0	0
			7	3	1	3		

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).



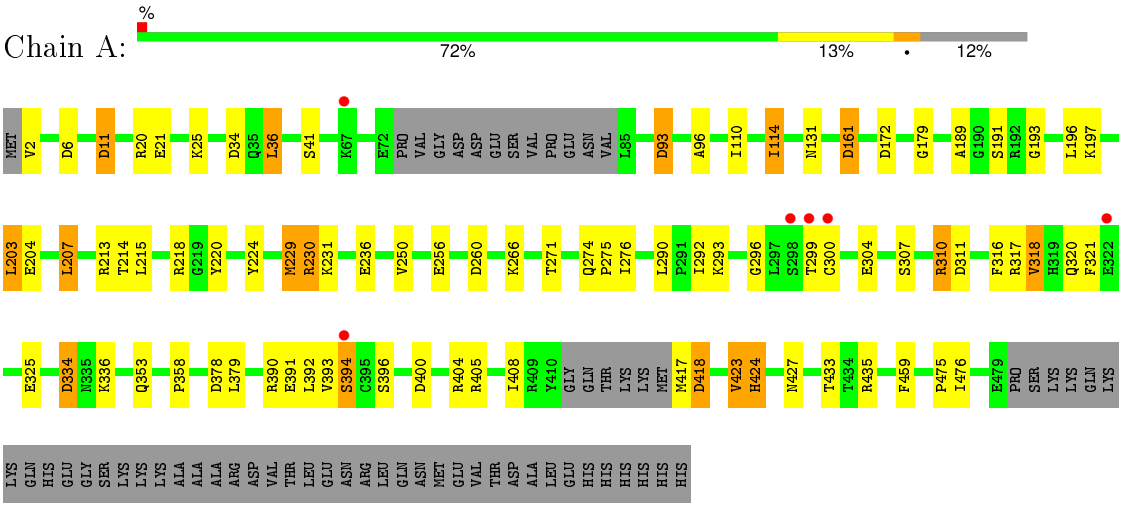
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	C	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

3 Residue-property plots (i)

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

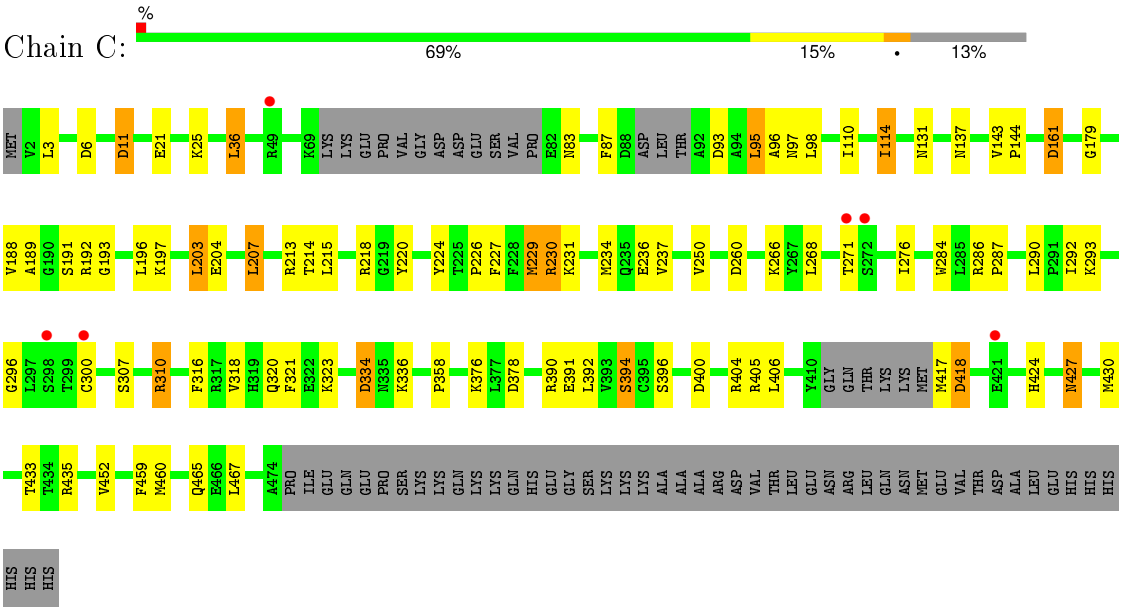
- Molecule 1: Serine–tRNA ligase, cytoplasmic

Chain A:



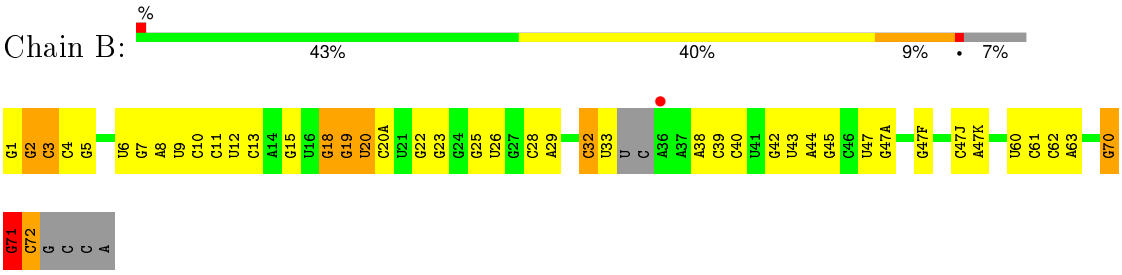
- Molecule 1: Serine–tRNA ligase, cytoplasmic

Chain C:



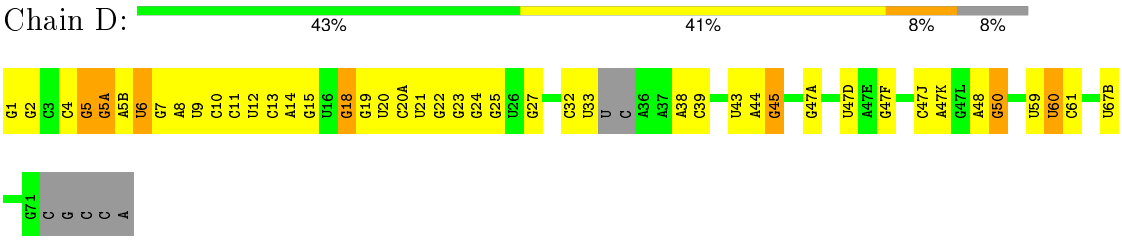
- Molecule 2: selenocysteine tRNA

Chain B:



- Molecule 2: selenocysteine tRNA

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	55.81Å 142.02Å 115.46Å 90.00° 101.95° 90.00°	Depositor
Resolution (Å)	36.39 – 4.00 36.39 – 3.95	Depositor EDS
% Data completeness (in resolution range)	97.1 (36.39-4.00) 97.2 (36.39-3.95)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.14 (at 3.99Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.274 , 0.322 0.271 , 0.320	Depositor DCC
R_{free} test set	738 reflections (4.97%)	DCC
Wilson B-factor (Å^2)	157.9	Xtriage
Anisotropy	0.526	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.23 , 93.5	EDS
Estimated twinning fraction	0.041 for h,-k,-h-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Outliers	0 of 15040 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	10599	wwPDB-VP
Average B, all atoms (Å^2)	189.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: ANP

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	0.24	0/3579	0.43	0/4844
1	C	0.22	0/3512	0.43	0/4753
2	B	0.24	0/1999	0.82	3/3112 (0.1%)
2	D	0.17	0/1977	0.75	0/3078
All	All	0.22	0/11067	0.59	3/15787 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	2	G	C5-N7-C8	-5.83	101.39	104.30
2	B	71	G	C5-C6-N1	5.56	114.28	111.50
2	B	2	G	C5-C6-O6	-5.32	125.41	128.60

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	3513	0	3309	56	0
1	C	3448	0	3233	54	1
2	B	1791	0	905	27	1
2	D	1771	0	894	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	7	0	4	3	0
3	C	7	0	4	2	0
4	A	31	0	12	8	0
4	C	31	0	13	4	0
All	All	10599	0	8374	151	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (151) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:394:SER:HB2	4:A:602:ANP:H5'1	1.53	0.89
1:C:229:MET:SD	1:C:229:MET:N	2.46	0.88
2:B:1:G:H2'	2:B:2:G:C8	2.09	0.87
1:A:435:ARG:NH2	4:A:602:ANP:O1G	2.14	0.80
2:B:1:G:H2'	2:B:2:G:H8	1.48	0.79
1:A:21:GLU:HG2	1:A:25:LYS:HD2	1.72	0.71
4:A:602:ANP:O3G	4:A:602:ANP:O1B	2.08	0.70
1:A:196:LEU:HB3	1:C:224:TYR:HB3	1.72	0.70
2:B:1:G:O6	2:B:72:C:N4	2.24	0.70
1:C:21:GLU:HG2	1:C:25:LYS:HD2	1.75	0.68
1:A:418:ASP:OD1	1:A:418:ASP:N	2.26	0.68
1:A:224:TYR:HB3	1:C:196:LEU:HB3	1.78	0.65
1:A:172:ASP:HA	1:A:475:PRO:HG3	1.78	0.65
1:A:320:GLN:HE22	1:C:226:PRO:HA	1.60	0.65
1:C:418:ASP:N	1:C:418:ASP:OD1	2.30	0.63
1:A:250:VAL:HG22	1:C:250:VAL:HG22	1.80	0.62
2:B:28:C:H42	2:B:42:G:H1	1.47	0.62
1:C:400:ASP:OD1	1:C:404:ARG:NH2	2.32	0.62
2:B:2:G:H1	2:B:71:G:H1	1.48	0.61
2:D:22:G:H2'	2:D:23:G:H8	1.65	0.60
2:B:28:C:H2'	2:B:29:A:C8	2.37	0.60
1:C:276:ILE:HD11	1:C:296:GLY:HA3	1.84	0.59
1:C:394:SER:HB2	4:C:602:ANP:H4'	1.85	0.59
1:A:271:THR:HG21	3:A:601:SER:N	2.17	0.59
1:A:400:ASP:OD1	1:A:404:ARG:NH2	2.37	0.58
1:A:276:ILE:HD11	1:A:296:GLY:HA3	1.86	0.56
1:A:318:VAL:H	4:A:602:ANP:HN62	1.54	0.55
2:D:22:G:H2'	2:D:23:G:C8	2.42	0.55
1:C:11:ASP:N	1:C:11:ASP:OD1	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:21:U:H2'	2:D:22:G:C8	2.43	0.54
1:C:392:LEU:HD22	1:C:435:ARG:HB3	1.90	0.54
1:A:459:PHE:O	1:C:213:ARG:NH2	2.40	0.54
1:C:321:PHE:HE1	1:C:323:LYS:HD3	1.73	0.53
1:A:379:LEU:HB3	1:A:393:VAL:HB	1.91	0.53
1:C:230:ARG:O	1:C:266:LYS:HA	2.10	0.52
1:A:394:SER:HB2	4:A:602:ANP:C5'	2.35	0.51
1:A:230:ARG:O	1:A:266:LYS:HA	2.09	0.51
2:D:12:U:H2'	2:D:13:C:C6	2.46	0.51
1:A:423:VAL:HG23	1:A:424:HIS:N	2.24	0.50
2:B:18:G:H4'	2:B:60:U:N3	2.26	0.50
2:B:62:C:H2'	2:B:63:A:H8	1.74	0.50
2:D:5(A):G:H2'	2:D:5(B):A:C8	2.46	0.50
2:D:5(A):G:H1	2:D:67(B):U:H3	1.59	0.49
1:A:11:ASP:OD1	1:A:11:ASP:N	2.42	0.49
2:B:22:G:H2'	2:B:23:G:H8	1.76	0.49
1:C:161:ASP:H	1:C:358:PRO:HB3	1.76	0.49
1:A:334:ASP:HB2	1:A:336:LYS:HG3	1.94	0.49
1:A:353:GLN:OE1	1:A:353:GLN:HA	2.12	0.49
2:D:48:A:H4'	2:D:50:G:H5"	1.95	0.49
1:C:300:CYS:SG	1:C:323:LYS:HE3	2.53	0.49
1:C:307:SER:HB2	1:C:310:ARG:HG3	1.93	0.49
1:A:161:ASP:H	1:A:358:PRO:HB3	1.78	0.48
2:B:39:C:H2'	2:B:40:C:H6	1.78	0.48
1:C:394:SER:HB3	3:C:601:SER:OXT	2.14	0.47
2:B:13:C:H42	2:B:22:G:H1	1.62	0.47
2:D:47(J):C:H2'	2:D:47(K):A:H8	1.79	0.47
1:A:179:GLY:HA2	1:A:197:LYS:HG3	1.96	0.47
1:C:417:MET:HA	1:C:418:ASP:HA	1.57	0.47
1:C:189:ALA:HB3	1:C:193:GLY:HA3	1.96	0.47
1:C:95:LEU:HB2	1:C:96:ALA:H	1.54	0.47
1:C:376:LYS:HG2	1:C:378:ASP:OD1	2.15	0.46
1:A:394:SER:CB	4:A:602:ANP:H5'1	2.36	0.46
1:C:316:PHE:CZ	1:C:390:ARG:HB3	2.51	0.46
2:B:12:U:H2'	2:B:13:C:C6	2.50	0.46
2:B:2:G:O6	2:B:71:G:O6	2.34	0.46
1:C:236:GLU:HA	1:C:405:ARG:CZ	2.46	0.46
1:A:316:PHE:CZ	1:A:390:ARG:HB3	2.50	0.46
1:C:215:LEU:HB3	1:C:220:TYR:HB2	1.98	0.46
1:A:256:GLU:OE1	1:C:192:ARG:NH1	2.49	0.46
1:A:213:ARG:NH2	1:C:459:PHE:O	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:196:LEU:O	1:C:224:TYR:N	2.43	0.45
2:B:11:C:C2	2:B:25:G:C2	3.04	0.45
1:C:36:LEU:HD23	1:C:131:ASN:HB2	1.97	0.45
1:A:317:ARG:NH1	4:A:602:ANP:O1G	2.50	0.45
1:A:427:ASN:HD22	3:A:601:SER:N	2.13	0.45
2:B:19:G:H4'	2:B:20:U:O5'	2.15	0.45
1:A:417:MET:HA	1:A:418:ASP:HA	1.55	0.45
2:D:14:A:H2'	2:D:15:G:C8	2.52	0.45
1:A:93:ASP:N	1:A:93:ASP:OD2	2.50	0.45
1:C:215:LEU:HD11	1:C:430:MET:HG2	1.99	0.45
1:C:271:THR:HG21	3:C:601:SER:N	2.31	0.45
1:A:236:GLU:HA	1:A:405:ARG:CZ	2.47	0.45
1:A:307:SER:HB2	1:A:310:ARG:HG3	1.99	0.45
2:D:38:A:H2'	2:D:39:C:O4'	2.17	0.44
1:A:214:THR:O	1:A:218:ARG:HG2	2.18	0.44
1:C:110:ILE:O	1:C:114:ILE:HG23	2.16	0.44
1:C:204:GLU:HG3	1:C:433:THR:HB	2.00	0.44
1:C:334:ASP:HB2	1:C:336:LYS:HG3	1.99	0.44
1:C:179:GLY:HA2	1:C:197:LYS:HG3	1.98	0.44
2:D:1:G:H2'	2:D:2:G:C8	2.53	0.44
1:C:427:ASN:HD22	1:C:427:ASN:N	2.14	0.44
1:A:304:GLU:OE2	4:A:602:ANP:O3G	2.36	0.44
2:D:47(A):G:H1	2:D:47(J):C:H42	1.65	0.44
2:D:32:C:H2'	2:D:33:U:O4'	2.17	0.44
2:B:47(J):C:H2'	2:B:47(K):A:H8	1.83	0.44
1:C:286:ARG:HA	1:C:287:PRO:HD3	1.82	0.44
2:B:3:C:C4	2:B:4:C:C4	3.06	0.44
2:D:18:G:H4'	2:D:60:U:N3	2.32	0.43
1:C:3:LEU:HD21	1:C:137:ASN:HA	1.99	0.43
1:A:110:ILE:O	1:A:114:ILE:HG23	2.18	0.43
2:B:22:G:H2'	2:B:23:G:C8	2.53	0.43
2:D:47(J):C:H2'	2:D:47(K):A:C8	2.53	0.43
2:B:32:C:H2'	2:B:33:U:C6	2.53	0.43
2:B:25:G:C2	2:B:26:U:C4	3.07	0.43
1:A:189:ALA:HB3	1:A:193:GLY:HA3	2.00	0.43
1:A:299:THR:HG21	1:C:227:PHE:HE2	1.84	0.43
1:C:214:THR:O	1:C:218:ARG:HG2	2.19	0.43
1:C:143:VAL:HA	1:C:144:PRO:HD3	1.90	0.43
2:B:4:C:O2	2:B:70:G:N2	2.52	0.43
1:A:215:LEU:HB3	1:A:220:TYR:HB2	2.01	0.43
1:A:274:GLN:HB2	1:A:275:PRO:HD3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:5(B):A:C6	2:D:6:U:C4	3.07	0.43
2:B:32:C:H2'	2:B:33:U:H6	1.84	0.43
2:D:9:U:H4'	2:D:45:G:C4	2.54	0.42
4:C:602:ANP:O2G	4:C:602:ANP:O2B	2.37	0.42
1:A:325:GLU:OE1	3:A:601:SER:N	2.52	0.42
1:A:20:ARG:NH2	1:A:34:ASP:OD1	2.52	0.42
2:D:5:G:H2'	2:D:5(A):G:H5'	2.01	0.42
1:C:229:MET:HE3	1:C:268:LEU:C	2.40	0.42
2:B:28:C:H2'	2:B:29:A:H8	1.79	0.42
1:A:290:LEU:O	1:A:292:ILE:N	2.53	0.42
2:B:47:U:H2'	2:B:47(A):G:C8	2.54	0.42
1:A:2:VAL:HG21	1:A:405:ARG:HD3	2.01	0.42
1:A:300:CYS:HB2	1:A:321:PHE:CZ	2.55	0.42
1:A:229:MET:HB3	1:C:188:VAL:HG13	2.01	0.42
2:B:71:G:OP1	2:B:71:G:H4'	2.19	0.42
1:C:394:SER:HB2	4:C:602:ANP:C4'	2.47	0.42
1:A:220:TYR:CD1	1:A:293:LYS:HB3	2.54	0.42
2:D:1:G:C6	2:D:2:G:C6	3.08	0.42
1:C:220:TYR:CD1	1:C:293:LYS:HB3	2.55	0.41
1:A:290:LEU:O	1:A:292:ILE:HG13	2.20	0.41
1:A:204:GLU:HG3	1:A:433:THR:HB	2.01	0.41
1:C:391:GLU:O	1:C:435:ARG:NH1	2.53	0.41
2:D:43:U:H2'	2:D:44:A:C8	2.55	0.41
1:C:435:ARG:NH1	4:C:602:ANP:H2'	2.35	0.41
1:C:460:MET:O	1:C:465:GLN:NE2	2.53	0.41
1:C:237:VAL:HG13	1:C:406:LEU:HD21	2.02	0.41
1:C:290:LEU:O	1:C:292:ILE:N	2.53	0.41
1:A:203:LEU:O	1:A:207:LEU:HD12	2.20	0.41
1:A:378:ASP:HB2	1:A:393:VAL:O	2.21	0.41
1:C:452:VAL:HG23	1:C:467:LEU:HA	2.02	0.41
2:D:14:A:H2'	2:D:15:G:H8	1.85	0.41
1:C:203:LEU:O	1:C:207:LEU:HD12	2.20	0.41
2:D:24:G:H2'	2:D:25:G:H8	1.85	0.41
1:A:236:GLU:HG2	1:A:405:ARG:HE	1.86	0.41
1:A:311:ASP:OD1	1:A:317:ARG:NH2	2.54	0.41
2:B:43:U:O4	2:B:44:A:N6	2.54	0.41
2:B:43:U:H2'	2:B:44:A:C8	2.56	0.41
1:A:36:LEU:HD23	1:A:131:ASN:HB2	2.03	0.40
1:C:396:SER:HB2	1:C:427:ASN:HD21	1.87	0.40
1:A:396:SER:HB2	1:A:427:ASN:OD1	2.22	0.40

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

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:83:ASN:OD1	2:B:47(F):G:O2'[1_554]	2.16	0.04

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	454/522 (87%)	415 (91%)	33 (7%)	6 (1%)	15	60
1	C	444/522 (85%)	410 (92%)	27 (6%)	7 (2%)	12	57
All	All	898/1044 (86%)	825 (92%)	60 (7%)	13 (1%)	14	59

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	230	ARG
1	C	98	LEU
1	C	230	ARG
1	C	93	ASP
1	C	97	ASN
1	A	96	ALA
1	A	191	SER
1	A	231	LYS
1	C	191	SER
1	C	231	LYS
1	A	161	ASP
1	A	391	GLU
1	C	161	ASP

5.3.2 Protein sidechains (i)

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	354/461 (77%)	334 (94%)	20 (6%)	26 65
1	C	347/461 (75%)	327 (94%)	20 (6%)	25 64
All	All	701/922 (76%)	661 (94%)	40 (6%)	25 65

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ASP
1	A	11	ASP
1	A	36	LEU
1	A	41	SER
1	A	93	ASP
1	A	114	ILE
1	A	203	LEU
1	A	207	LEU
1	A	229	MET
1	A	260	ASP
1	A	310	ARG
1	A	318	VAL
1	A	334	ASP
1	A	392	LEU
1	A	394	SER
1	A	408	ILE
1	A	418	ASP
1	A	423	VAL
1	A	424	HIS
1	A	476	ILE
1	C	6	ASP
1	C	11	ASP
1	C	36	LEU
1	C	87	PHE
1	C	95	LEU
1	C	114	ILE
1	C	203	LEU
1	C	207	LEU
1	C	229	MET
1	C	234	MET
1	C	260	ASP

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Mol	Chain	Res	Type
1	C	284	TRP
1	C	310	ARG
1	C	318	VAL
1	C	320	GLN
1	C	334	ASP
1	C	394	SER
1	C	418	ASP
1	C	424	HIS
1	C	427	ASN

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

Mol	Chain	Res	Type
1	A	335	ASN
1	C	427	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	82/90 (91%)	18 (21%)	2 (2%)
2	D	81/90 (90%)	19 (23%)	3 (3%)
All	All	163/180 (90%)	37 (22%)	5 (3%)

All (37) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	3	C
2	B	5	G
2	B	7	G
2	B	8	A
2	B	9	U
2	B	10	C
2	B	15	G
2	B	18	G
2	B	19	G
2	B	20	U
2	B	20(A)	C
2	B	32	C
2	B	38	A
2	B	45	G

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Mol	Chain	Res	Type
2	B	61	C
2	B	70	G
2	B	71	G
2	B	72	C
2	D	4	C
2	D	5(A)	G
2	D	6	U
2	D	7	G
2	D	8	A
2	D	10	C
2	D	11	C
2	D	18	G
2	D	19	G
2	D	20	U
2	D	20(A)	C
2	D	27	G
2	D	45	G
2	D	47(D)	U
2	D	47(F)	G
2	D	50	G
2	D	59	U
2	D	60	U
2	D	61	C

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	6	U
2	B	19	G
2	D	5	G
2	D	6	U
2	D	19	G

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)

4 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	SER	A	601	-	3,6,6	0.36	0	2,7,7	0.32	0
4	ANP	A	602	-	29,33,33	2.79	10 (34%)	26,52,52	3.38	10 (38%)
3	SER	C	601	-	3,6,6	0.38	0	2,7,7	0.51	0
4	ANP	C	602	-	29,33,33	2.77	7 (24%)	26,52,52	2.80	8 (30%)

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	SER	A	601	-	-	0/2/6/6	0/0/0/0
4	ANP	A	602	-	-	0/13/38/38	0/3/3/3
3	SER	C	601	-	-	0/2/6/6	0/0/0/0
4	ANP	C	602	-	-	0/13/38/38	0/3/3/3

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	602	ANP	O3'-C3'	-2.92	1.36	1.43
4	A	602	ANP	C2'-C3'	-2.71	1.46	1.53
4	A	602	ANP	C3'-C4'	-2.55	1.46	1.53
4	C	602	ANP	C3'-C4'	-2.46	1.46	1.53
4	A	602	ANP	O4'-C4'	-2.42	1.39	1.45
4	C	602	ANP	O3'-C3'	-2.05	1.38	1.43
4	A	602	ANP	O2'-C2'	-2.03	1.38	1.43
4	C	602	ANP	C6-N6	2.25	1.43	1.34
4	C	602	ANP	PB-N3B	2.32	1.69	1.63
4	A	602	ANP	C6-N6	2.35	1.43	1.34
4	A	602	ANP	C8-N7	2.67	1.39	1.34
4	A	602	ANP	PB-N3B	2.95	1.71	1.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	602	ANP	C8-N7	3.08	1.40	1.34
4	A	602	ANP	PG-O1G	3.99	1.50	1.46
4	C	602	ANP	PG-O1G	4.48	1.50	1.46
4	A	602	ANP	PB-O1B	11.62	1.58	1.46
4	C	602	ANP	PB-O1B	12.19	1.59	1.46

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	602	ANP	N3-C2-N1	-12.18	119.30	128.87
4	C	602	ANP	N3-C2-N1	-11.09	120.16	128.87
4	A	602	ANP	C4'-O4'-C1'	-5.64	103.66	109.64
4	A	602	ANP	C1'-N9-C4	-5.63	120.52	126.81
4	A	602	ANP	PA-O3A-PB	-3.63	119.54	132.71
4	A	602	ANP	C5'-C4'-C3'	-3.26	102.59	115.20
4	C	602	ANP	PA-O3A-PB	-3.03	121.72	132.71
4	C	602	ANP	C4'-O4'-C1'	-2.83	106.65	109.64
4	C	602	ANP	C1'-N9-C4	-2.63	123.87	126.81
4	A	602	ANP	O3A-PB-N3B	-2.56	99.00	106.07
4	C	602	ANP	O3A-PB-N3B	-2.30	99.72	106.07
4	A	602	ANP	O5'-PA-O1A	2.00	117.41	109.21
4	C	602	ANP	C2-N1-C6	2.20	122.70	118.77
4	C	602	ANP	O4'-C4'-C3'	2.31	109.85	105.16
4	A	602	ANP	O2'-C2'-C1'	2.43	119.22	111.61
4	A	602	ANP	C2-N1-C6	2.99	124.11	118.77
4	A	602	ANP	O2B-PB-O1B	4.51	118.91	110.02
4	C	602	ANP	O2B-PB-O1B	4.90	119.67	110.02

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	601	SER	3	0
4	A	602	ANP	8	0
3	C	601	SER	2	0
4	C	602	ANP	4	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, 95^{th} 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	460/522 (88%)	-0.30	6 (1%) 79 70	119, 175, 214, 246	0
1	C	452/522 (86%)	-0.32	6 (1%) 79 70	112, 174, 227, 258	0
2	B	84/90 (93%)	-0.25	1 (1%) 81 72	129, 186, 276, 307	0
2	D	83/90 (92%)	-0.05	0 100 100	166, 223, 311, 351	0
All	All	1079/1224 (88%)	-0.28	13 (1%) 81 72	112, 178, 237, 351	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	298	SER	3.7
1	A	298	SER	3.6
1	C	272	SER	2.8
1	A	322	GLU	2.8
2	B	36	A	2.7
1	C	271	THR	2.5
1	A	394	SER	2.1
1	A	67	LYS	2.1
1	C	421	GLU	2.1
1	A	299	THR	2.1
1	C	49	ARG	2.1
1	A	300	CYS	2.0
1	C	300	CYS	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, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
3	SER	A	601	7/7	0.84	0.65	1.93	141,145,149,158	0
3	SER	C	601	7/7	0.84	0.47	0.19	147,153,158,166	0
4	ANP	C	602	31/31	0.91	0.37	0.18	142,157,166,176	0
4	ANP	A	602	31/31	0.87	0.42	-0.39	130,139,146,148	0

6.5 Other polymers (i)

There are no such residues in this entry.