



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2018 – 12:49 pm GMT

PDB ID : 3HL2
Title : The crystal structure of the human SepSecS-tRNA^{Sec} complex
Authors : Palioura, S.; Steitz, T.A.; Soll, D.; Simonovic, M.
Deposited on : 2009-05-26
Resolution : 2.81 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/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 : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk30967
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30967

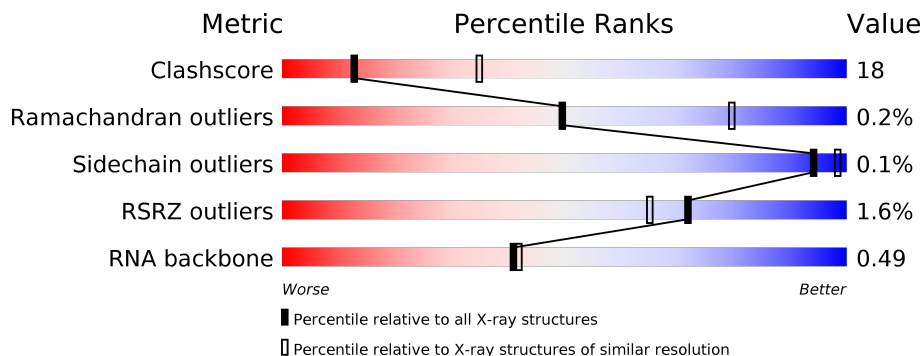
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.81 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	122126	3606 (2.84-2.80)
Ramachandran outliers	120053	3547 (2.84-2.80)
Sidechain outliers	120020	3549 (2.84-2.80)
RSRZ outliers	108989	3108 (2.84-2.80)
RNA backbone	2636	1089 (3.14-2.50)

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	501	<div> <div>66%</div> <div>21%</div> <div>12%</div> </div>
1	B	501	<div> <div>65%</div> <div>24%</div> <div>12%</div> </div>
1	C	501	<div> <div>68%</div> <div>21%</div> <div>11%</div> </div>
1	D	501	<div> <div>%</div> <div>69%</div> <div>19%</div> <div>12%</div> </div>
2	E	90	<div> <div>24%</div> <div>19%</div> <div>67%</div> <div>6%</div> <div>9%</div> </div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 17628 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.

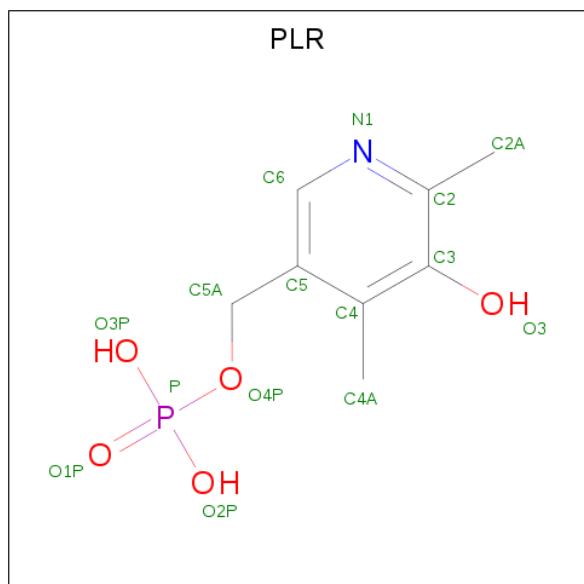
- Molecule 1 is a protein called O-phosphoseryl-tRNA(Sec) selenium transferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	441	Total	C	N	O	S	0	6	0
			3426	2170	602	628	26			
1	B	443	Total	C	N	O	S	0	5	0
			3432	2179	605	621	27			
1	C	445	Total	C	N	O	S	0	3	0
			3438	2175	606	630	27			
1	D	441	Total	C	N	O	S	0	6	0
			3411	2166	602	617	26			

- Molecule 2 is a RNA chain called tRNA_{Sec}.

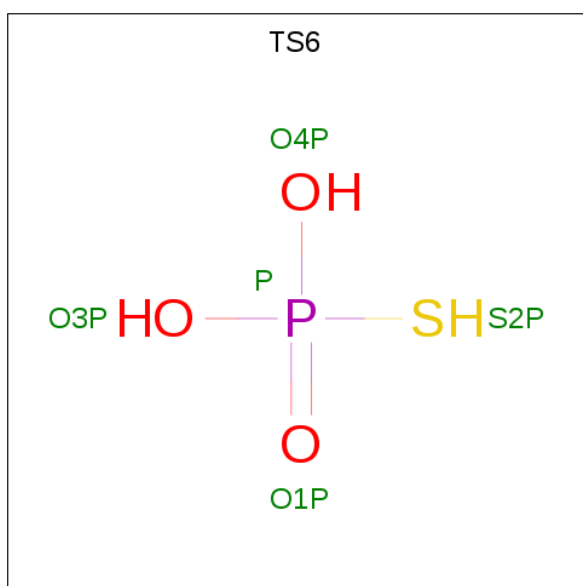
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	82	Total	C	N	O	P	0	82	0
			3492	1554	608	1166	164			

- Molecule 3 is (5-HYDROXY-4,6-DIMETHYLPYRIDIN-3-YL)METHYL DIHYDROGEN PHOSPHATE (three-letter code: PLR) (formula: C₈H₁₂NO₅P).



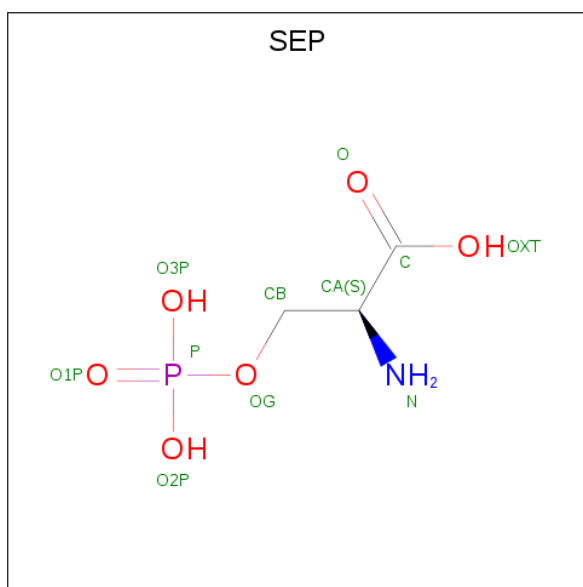
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
3	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
3	C	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
3	D	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 4 is Monothiophosphate (three-letter code: TS6) (formula: $\text{H}_3\text{O}_3\text{PS}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	O	P	S	0	0
			5	3	1	1		
4	A	1	Total	O	P	S	0	0
			5	3	1	1		
4	C	1	Total	O	P	S	0	0
			5	3	1	1		

- Molecule 5 is PHOSPHOSERINE (three-letter code: SEP) (formula: $\text{C}_3\text{H}_8\text{NO}_6\text{P}$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	P	0	1
			22	6	2	12	2		
5	B	1	Total	C	N	O	P	0	0
			11	3	1	6	1		
5	D	1	Total	C	N	O	P	0	1
			22	6	2	12	2		
5	D	1	Total	C	N	O	P	0	0
			11	3	1	6	1		

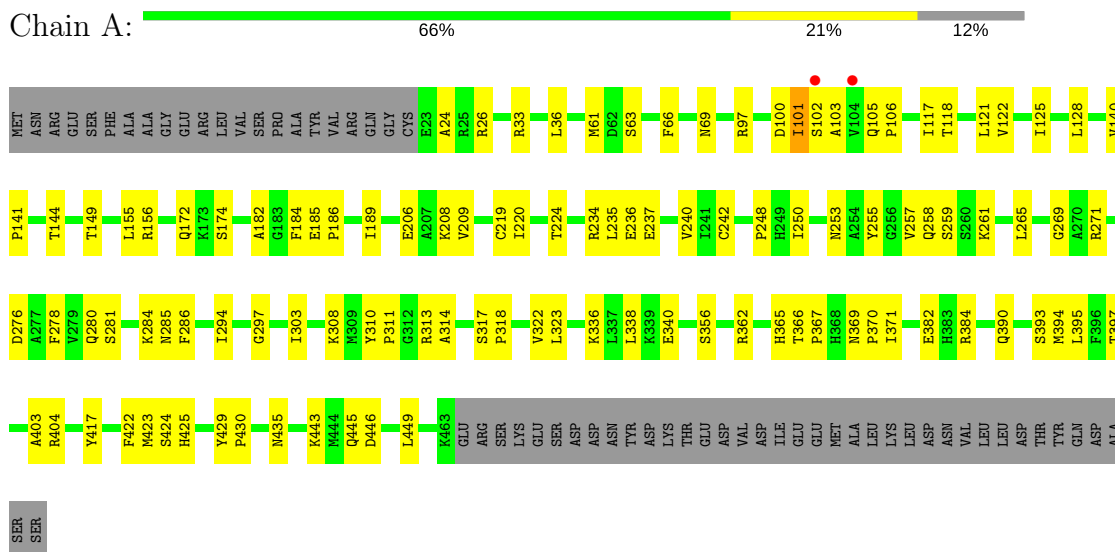
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	71	Total	O	0	0
			71	71		
6	B	87	Total	O	0	0
			87	87		
6	C	67	Total	O	0	0
			67	67		
6	D	58	Total	O	0	0
			58	58		
6	E	5	Total	O	0	0
			5	5		

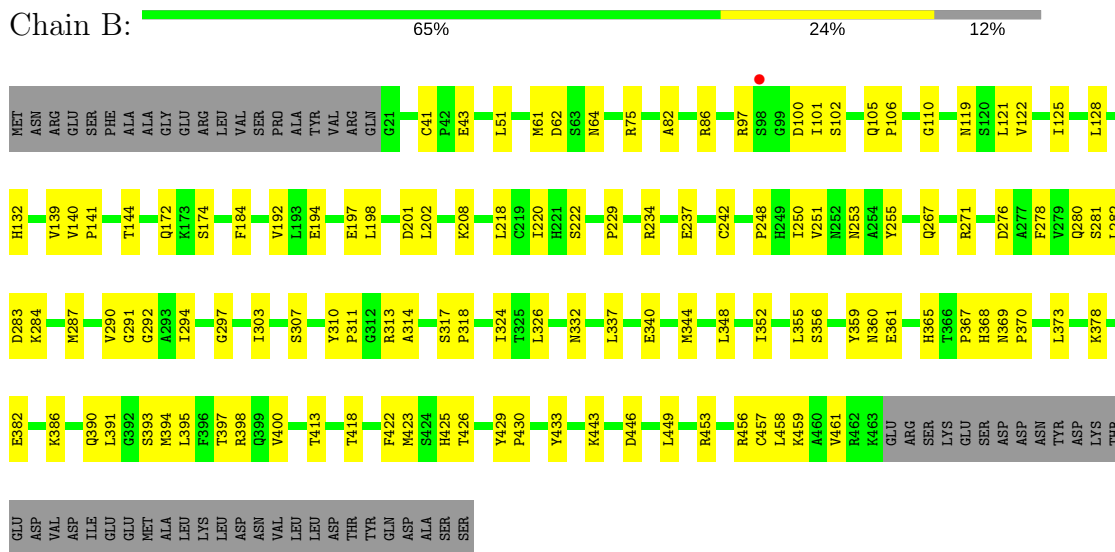
3 Residue-property plots

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: O-phosphoseryl-tRNA(Sec) selenium transferase

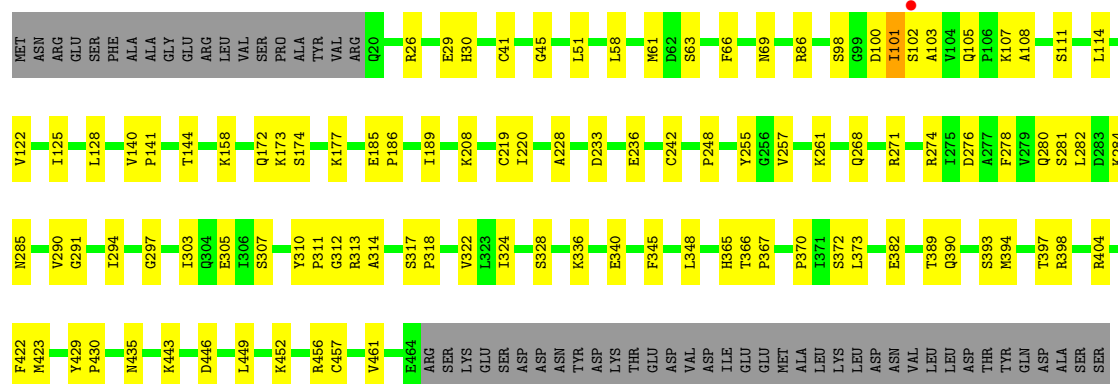


- Molecule 1: O-phosphoseryl-tRNA(Sec) selenium transferase



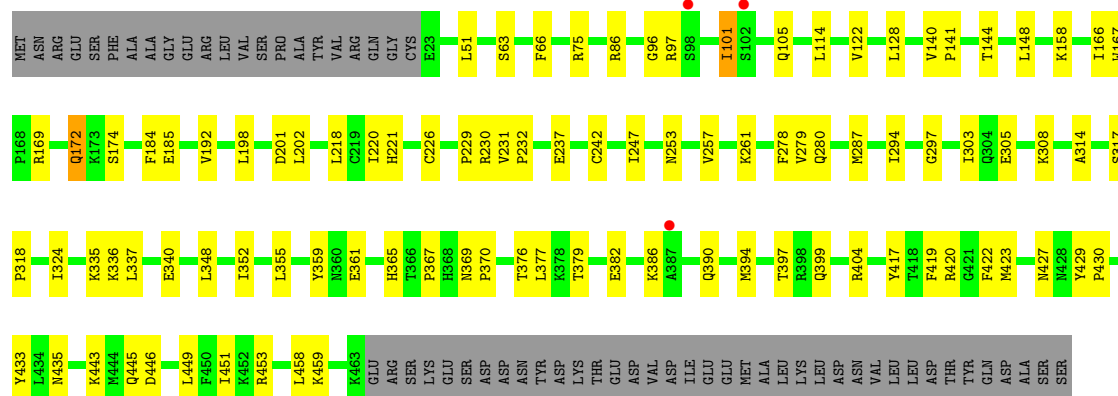
- Molecule 1: O-phosphoseryl-tRNA(Sec) selenium transferase

Chain C: 



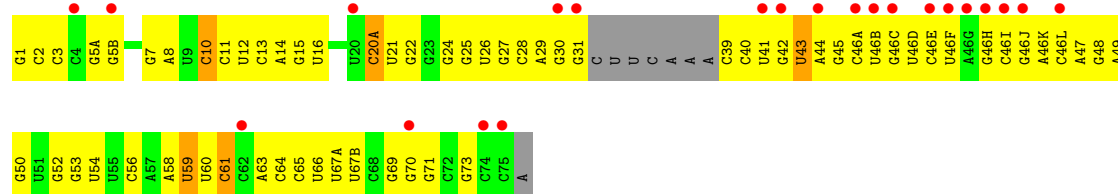
• Molecule 1: O-phosphoseryl-tRNA(Sec) selenium transferase

Chain D: 



• Molecule 2: tRNA^{Sec}

Chain E: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 1 2	Depositor
Cell constants a, b, c, α , β , γ	166.82Å 166.82Å 236.32Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	37.95 – 2.81 39.55 – 2.81	Depositor EDS
% Data completeness (in resolution range)	97.1 (37.95-2.81) 97.1 (39.55-2.81)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.17	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 2.81Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.203 , 0.238 0.194 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	65.4	Xtriage
Anisotropy	0.234	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 35.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.458 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	17628	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.54% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TS6, PLR, SEP

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	0.29	0/3507	0.48	0/4740
1	B	0.30	0/3509	0.46	0/4741
1	C	0.29	0/3510	0.47	0/4745
1	D	0.29	0/3493	0.46	0/4723
2	E	0.42	2/3894 (0.1%)	1.03	26/6058 (0.4%)
All	All	0.32	2/17913 (0.0%)	0.65	26/25007 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	43[A]	U	N3-C4	-5.00	1.33	1.38
2	E	43[B]	U	N3-C4	-5.00	1.33	1.38

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	43[A]	U	N3-C4-C5	11.95	121.77	114.60
2	E	43[B]	U	N3-C4-C5	11.95	121.77	114.60
2	E	43[A]	U	C2-N3-C4	-10.91	120.45	127.00
2	E	43[B]	U	C2-N3-C4	-10.91	120.45	127.00
2	E	59[A]	U	N1-C1'-C2'	-10.59	100.23	114.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	3426	0	3465	84	0
1	B	3432	0	3468	100	0
1	C	3438	0	3455	85	0
1	D	3411	0	3447	77	0
2	E	3492	0	1728	250	0
3	A	15	0	8	2	0
3	B	15	0	8	1	0
3	C	15	0	8	4	0
3	D	15	0	8	1	0
4	A	10	0	2	0	0
4	C	5	0	1	0	0
5	B	33	0	15	5	0
5	D	33	0	15	5	0
6	A	71	0	0	2	0
6	B	87	0	0	3	0
6	C	67	0	0	4	0
6	D	58	0	0	0	0
6	E	5	0	0	0	0
All	All	17628	0	15628	584	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 18.

The worst 5 of 584 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:128:LEU:HD11	1:D:335:LYS:CE	1.74	1.17
2:E:46(C)[A]:G:O2'	2:E:46(D)[A]:U:H5'	1.45	1.15
2:E:49[B]:A:H4'	2:E:50[B]:G:H5'	1.16	1.13
2:E:46(C)[B]:G:O2'	2:E:46(D)[B]:U:H5'	1.45	1.13
2:E:46(C)[B]:G:C2'	2:E:46(D)[B]:U:H5'	1.80	1.11

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	445/501 (89%)	422 (95%)	21 (5%)	2 (0%)	36	68
1	B	446/501 (89%)	420 (94%)	26 (6%)	0	100	100
1	C	446/501 (89%)	420 (94%)	25 (6%)	1 (0%)	49	79
1	D	445/501 (89%)	424 (95%)	20 (4%)	1 (0%)	49	79
All	All	1782/2004 (89%)	1686 (95%)	92 (5%)	4 (0%)	49	79

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	384	ARG
1	D	101	ILE
1	A	101	ILE
1	C	101	ILE

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	375/430 (87%)	375 (100%)	0	100	100
1	B	371/430 (86%)	371 (100%)	0	100	100
1	C	372/430 (86%)	372 (100%)	0	100	100
1	D	369/430 (86%)	368 (100%)	1 (0%)	93	98
All	All	1487/1720 (86%)	1486 (100%)	1 (0%)	94	98

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	172	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	267	GLN
1	C	105	GLN
1	D	267	GLN
1	B	332	ASN
1	B	350	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	E	0/90	-	-

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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](#)

13 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	PLR	A	1001	1	15,15,15	0.96	1 (6%)	20,22,22	1.03	1 (5%)
4	TS6	A	3001	-	2,4,4	1.98	0	3,6,6	1.37	0
4	TS6	A	3002	-	2,4,4	1.96	1 (50%)	3,6,6	1.21	0
3	PLR	B	1001	1	15,15,15	1.00	1 (6%)	20,22,22	1.41	3 (15%)
5	SEP	B	2001[A]	-	6,10,10	1.68	1 (16%)	8,14,14	1.78	2 (25%)
5	SEP	B	2001[B]	-	6,10,10	1.66	1 (16%)	8,14,14	1.71	2 (25%)
5	SEP	B	2002	-	6,10,10	1.72	1 (16%)	8,14,14	1.90	2 (25%)
3	PLR	C	1001	1	15,15,15	0.93	0	20,22,22	1.10	2 (10%)
4	TS6	C	3001	-	2,4,4	1.99	1 (50%)	3,6,6	1.32	0
3	PLR	D	1001	1	15,15,15	1.06	2 (13%)	20,22,22	1.06	1 (5%)
5	SEP	D	2001[A]	-	6,10,10	1.72	1 (16%)	8,14,14	2.16	2 (25%)
5	SEP	D	2001[B]	-	6,10,10	1.67	1 (16%)	8,14,14	1.75	2 (25%)
5	SEP	D	2002	-	6,10,10	1.71	1 (16%)	8,14,14	1.70	2 (25%)

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	PLR	A	1001	1	-	0/6/6/6	0/1/1/1
4	TS6	A	3001	-	-	0/0/0/0	0/0/0/0
4	TS6	A	3002	-	-	0/0/0/0	0/0/0/0
3	PLR	B	1001	1	-	0/6/6/6	0/1/1/1
5	SEP	B	2001[A]	-	-	0/6/10/10	0/0/0/0
5	SEP	B	2001[B]	-	-	0/6/10/10	0/0/0/0
5	SEP	B	2002	-	-	0/6/10/10	0/0/0/0
3	PLR	C	1001	1	-	0/6/6/6	0/1/1/1
4	TS6	C	3001	-	-	0/0/0/0	0/0/0/0
3	PLR	D	1001	1	-	0/6/6/6	0/1/1/1
5	SEP	D	2001[A]	-	-	0/6/10/10	0/0/0/0
5	SEP	D	2001[B]	-	-	0/6/10/10	0/0/0/0
5	SEP	D	2002	-	-	0/6/10/10	0/0/0/0

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1001	PLR	C3-C2	-2.26	1.39	1.40
4	C	3001	TS6	P-O4P	-2.03	1.51	1.56
4	A	3002	TS6	P-O4P	-2.01	1.51	1.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1001	PLR	C2-N1	2.02	1.38	1.33
3	B	1001	PLR	C2-N1	2.13	1.38	1.33

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	2001[B]	SEP	P-OG-CB	-3.21	109.45	118.30
5	D	2001[A]	SEP	P-OG-CB	-3.08	109.81	118.30
5	B	2001[B]	SEP	P-OG-CB	-3.05	109.89	118.30
5	D	2002	SEP	P-OG-CB	-2.76	110.69	118.30
5	B	2001[A]	SEP	P-OG-CB	-2.70	110.87	118.30

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1001	PLR	2	0
3	B	1001	PLR	1	0
5	B	2001[A]	SEP	2	0
5	B	2001[B]	SEP	2	0
5	B	2002	SEP	1	0
3	C	1001	PLR	4	0
3	D	1001	PLR	1	0
5	D	2001[A]	SEP	2	0
5	D	2001[B]	SEP	3	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	441/501 (88%)	-0.48	2 (0%) 90 88	36, 52, 86, 117	0
1	B	443/501 (88%)	-0.45	1 (0%) 94 94	36, 54, 87, 136	0
1	C	445/501 (88%)	-0.47	1 (0%) 94 94	37, 52, 88, 113	0
1	D	441/501 (88%)	-0.45	3 (0%) 87 84	37, 54, 87, 141	0
2	E	82/90 (91%)	1.60	22 (26%) 0 0	66, 95, 104, 112	0
All	All	1852/2094 (88%)	-0.37	29 (1%) 72 65	36, 54, 96, 141	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	46(A)[A]	C	7.7
2	E	75[A]	C	5.4
2	E	46(C)[A]	G	4.7
2	E	74[A]	C	4.7
2	E	46(L)[A]	C	4.1

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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	B-factors(Å ²)	Q<0.9
5	SEP	B	2001[B]	11/11	0.82	0.33	65,68,78,78	11
5	SEP	B	2001[A]	11/11	0.82	0.33	65,75,83,88	11
5	SEP	D	2001[B]	11/11	0.85	0.30	63,67,77,78	11
5	SEP	D	2001[A]	11/11	0.85	0.30	71,79,86,95	11
4	TS6	C	3001	5/5	0.89	0.21	65,71,79,84	5
5	SEP	D	2002	11/11	0.90	0.14	63,72,85,85	11
4	TS6	A	3001	5/5	0.91	0.18	61,66,83,86	5
5	SEP	B	2002	11/11	0.92	0.13	66,75,86,90	11
4	TS6	A	3002	5/5	0.93	0.16	57,65,74,80	5
3	PLR	D	1001	15/15	0.98	0.18	46,52,57,61	0
3	PLR	A	1001	15/15	0.98	0.16	44,49,55,59	0
3	PLR	C	1001	15/15	0.98	0.15	45,53,60,61	0
3	PLR	B	1001	15/15	0.98	0.17	46,52,57,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.