



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 08:28 PM UTC

PDB ID : 3VBB / pdb\_00003vbb  
Title : Crystal Structure of Seryl-tRNA Synthetase from Human at 2.9 angstroms  
Authors : Xu, X.L.; Yang, X.-L.  
Deposited on : 2012-01-02  
Resolution : 2.89 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](mailto: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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

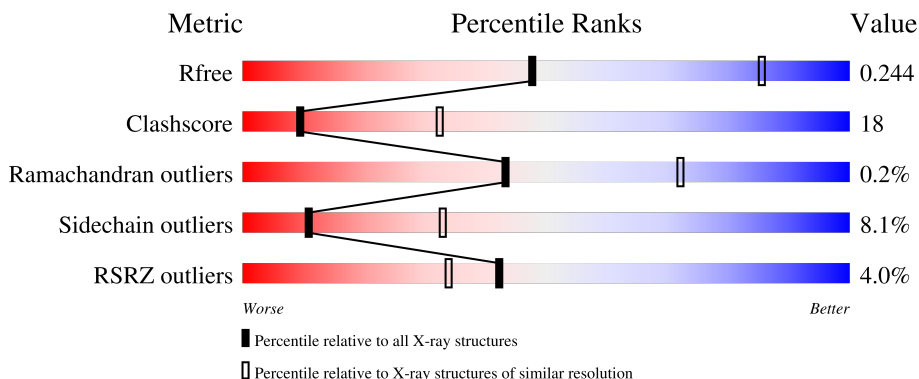
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.89 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.



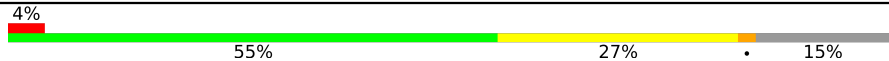
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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	522	 2% 54% 30% 14%
1	B	522	 2% 56% 27% 13%
1	C	522	 4% 53% 30% 13%
1	D	522	 4% 51% 30% 5% 14%
1	E	522	 4% 57% 24% 16%

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Mol	Chain	Length	Quality of chain
1	F	522	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into four segments: a small red segment (4%), a large green segment (55%), a yellow segment (27%), and a small grey segment (15%).</p>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 21387 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 Seryl-tRNA synthetase, cytoplasmic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	451	Total 3606	C 2301	N 619	O 668	S 18	5	1	0
1	B	454	Total 3625	C 2311	N 623	O 671	S 20	0	1	0
1	C	456	Total 3588	C 2291	N 609	O 669	S 19	3	1	0
1	D	450	Total 3533	C 2264	N 602	O 649	S 18	7	1	0
1	E	440	Total 3469	C 2216	N 596	O 638	S 19	1	1	0
1	F	443	Total 3519	C 2247	N 604	O 650	S 18	11	1	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
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
B	515	LEU	-	expression tag	UNP P49591
B	516	GLU	-	expression tag	UNP P49591
B	517	HIS	-	expression tag	UNP P49591
B	518	HIS	-	expression tag	UNP P49591
B	519	HIS	-	expression tag	UNP P49591
B	520	HIS	-	expression tag	UNP P49591
B	521	HIS	-	expression tag	UNP P49591
B	522	HIS	-	expression tag	UNP P49591
C	515	LEU	-	expression tag	UNP P49591

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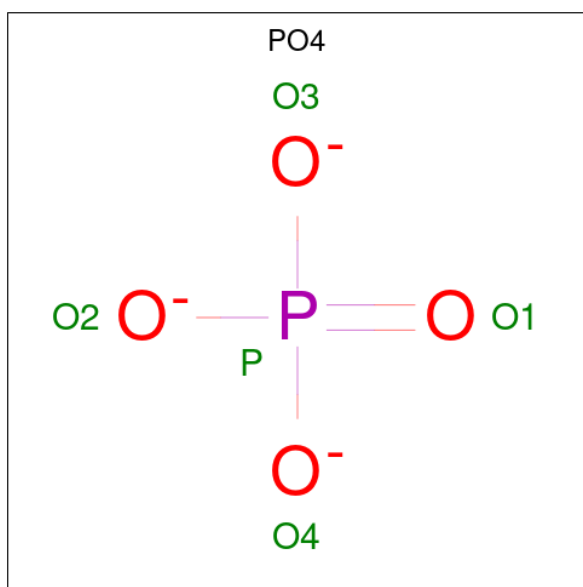
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Chain	Residue	Modelled	Actual	Comment	Reference
C	516	GLU	-	expression tag	UNP P49591
C	517	HIS	-	expression tag	UNP P49591
C	518	HIS	-	expression tag	UNP P49591
C	519	HIS	-	expression tag	UNP P49591
C	520	HIS	-	expression tag	UNP P49591
C	521	HIS	-	expression tag	UNP P49591
C	522	HIS	-	expression tag	UNP P49591
D	515	LEU	-	expression tag	UNP P49591
D	516	GLU	-	expression tag	UNP P49591
D	517	HIS	-	expression tag	UNP P49591
D	518	HIS	-	expression tag	UNP P49591
D	519	HIS	-	expression tag	UNP P49591
D	520	HIS	-	expression tag	UNP P49591
D	521	HIS	-	expression tag	UNP P49591
D	522	HIS	-	expression tag	UNP P49591
E	515	LEU	-	expression tag	UNP P49591
E	516	GLU	-	expression tag	UNP P49591
E	517	HIS	-	expression tag	UNP P49591
E	518	HIS	-	expression tag	UNP P49591
E	519	HIS	-	expression tag	UNP P49591
E	520	HIS	-	expression tag	UNP P49591
E	521	HIS	-	expression tag	UNP P49591
E	522	HIS	-	expression tag	UNP P49591
F	515	LEU	-	expression tag	UNP P49591
F	516	GLU	-	expression tag	UNP P49591
F	517	HIS	-	expression tag	UNP P49591
F	518	HIS	-	expression tag	UNP P49591
F	519	HIS	-	expression tag	UNP P49591
F	520	HIS	-	expression tag	UNP P49591
F	521	HIS	-	expression tag	UNP P49591
F	522	HIS	-	expression tag	UNP P49591

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mg 1 1	0	0
2	B	1	Total Mg 1 1	0	0

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	C	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		
3	E	1	Total	O	P	0	0
			5	4	1		
3	F	1	Total	O	P	0	0
			5	4	1		

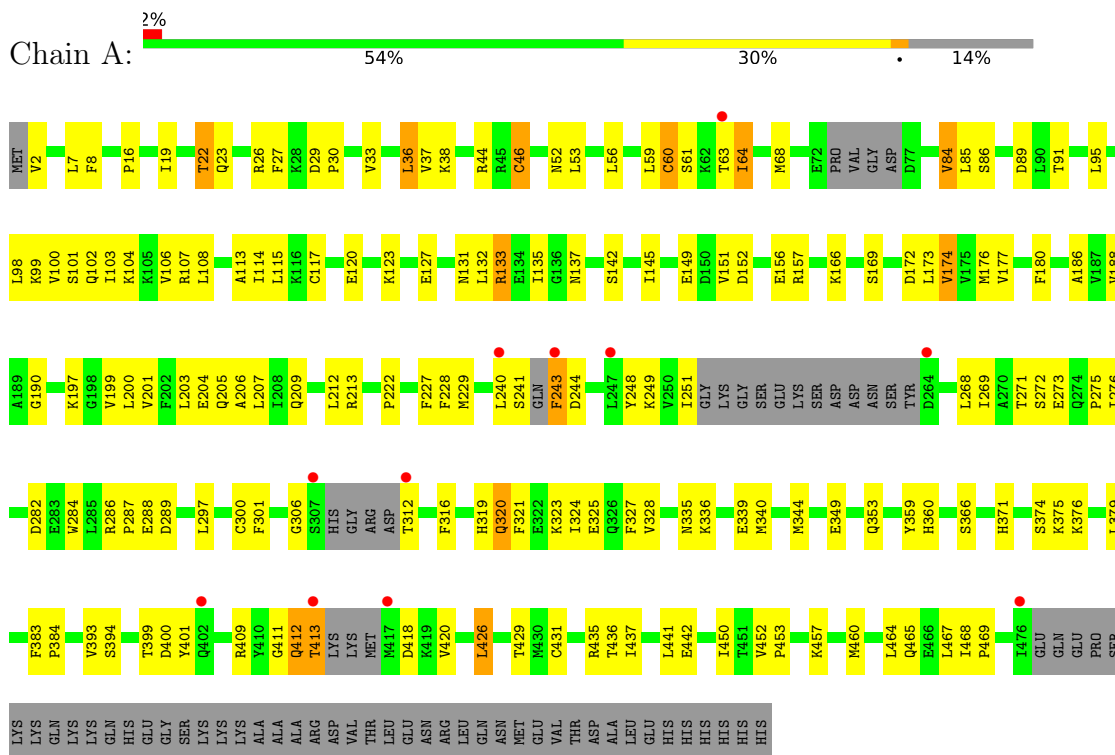
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	5	Total	O	0	0
			5	5		
4	B	3	Total	O	0	0
			3	3		
4	C	1	Total	O	0	0
			1	1		
4	D	2	Total	O	0	0
			2	2		
4	E	2	Total	O	0	0
			2	2		
4	F	2	Total	O	0	0
			2	2		

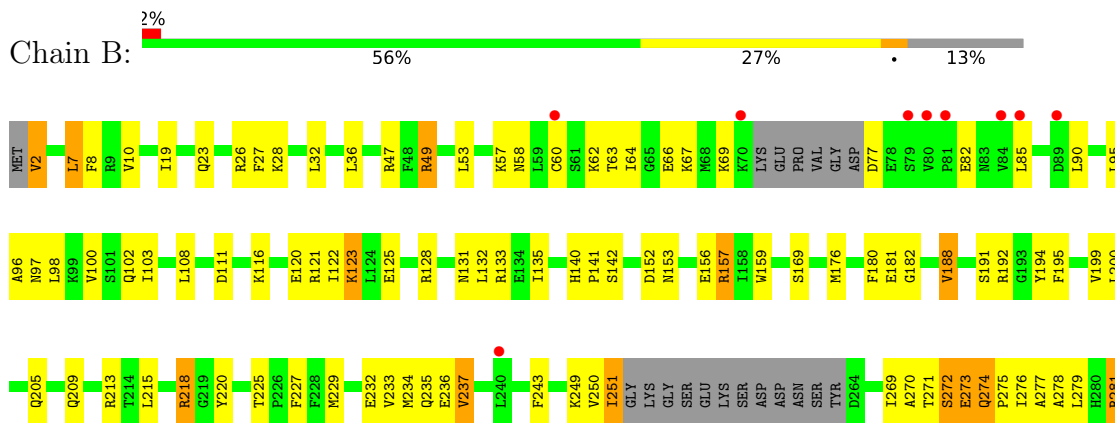
### 3 Residue-property plots i

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

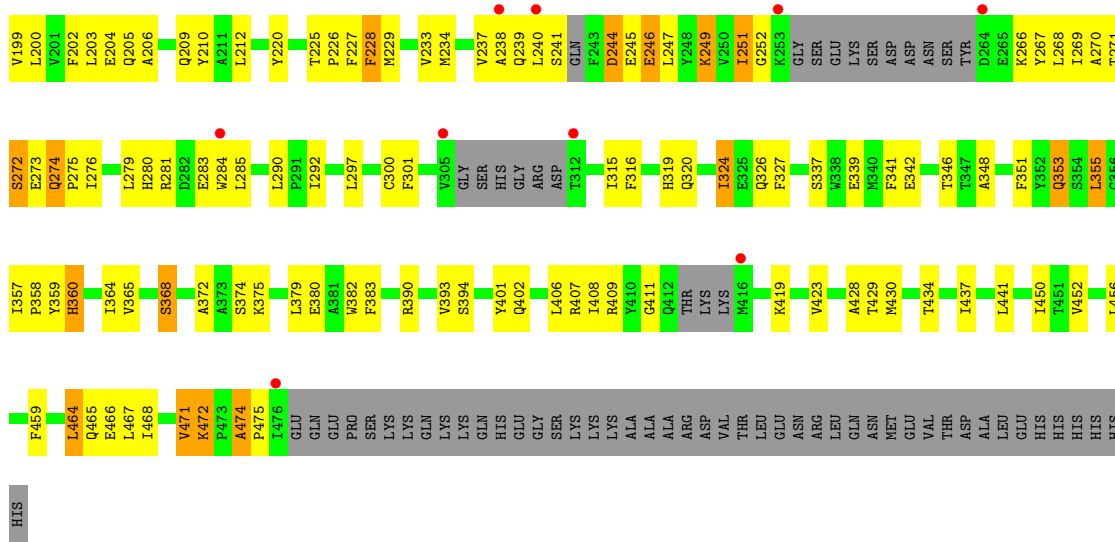
#### • Molecule 1: Seryl-tRNA synthetase, cytoplasmic



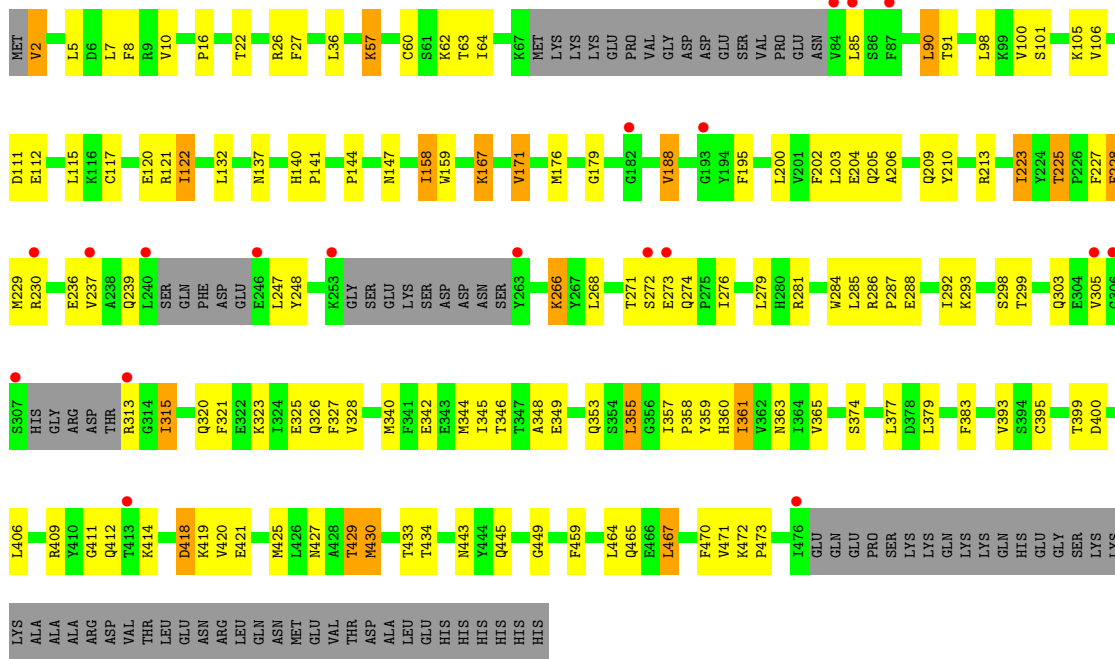
#### • Molecule 1: Seryl-tRNA synthetase, cytoplasmic





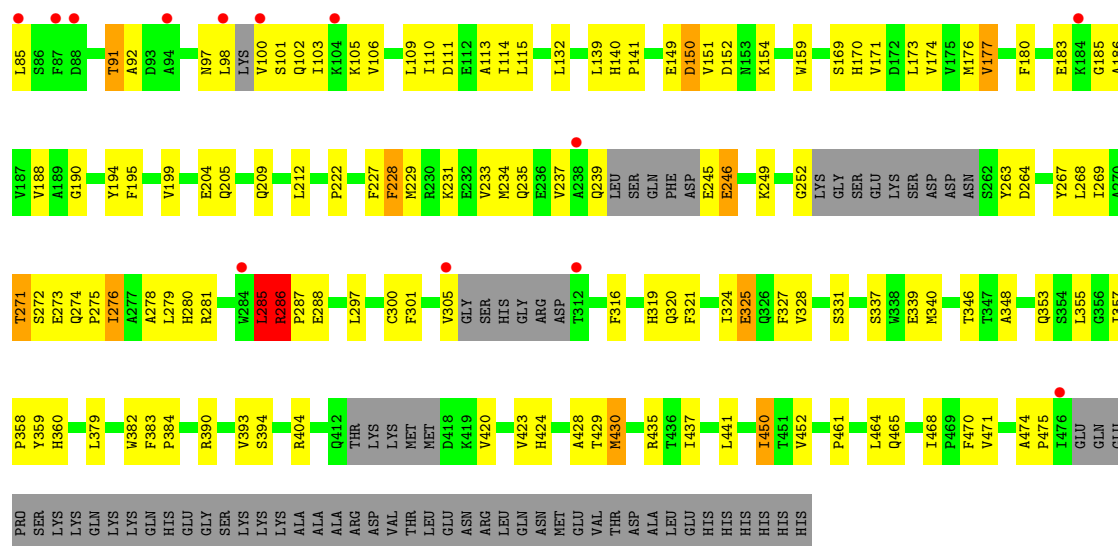


• Molecule 1: Seryl-tRNA synthetase, cytoplasmic



• Molecule 1: Seryl-tRNA synthetase, cytoplasmic





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	116.80Å 189.42Å 230.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.59 – 2.89 48.59 – 2.89	Depositor EDS
% Data completeness (in resolution range)	94.8 (48.59-2.89) 98.7 (48.59-2.89)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.12 (at 2.91Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, $R_{free}$	0.194 , 0.250 0.191 , 0.244	Depositor DCC
$R_{free}$ test set	5680 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	72.5	Xtrriage
Anisotropy	0.373	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 45.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	21387	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	80.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.34% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 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: MG, PO4

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	0.59	0/3677	0.98	10/4957 (0.2%)
1	B	0.61	0/3697	0.99	12/4982 (0.2%)
1	C	0.56	0/3661	1.01	14/4949 (0.3%)
1	D	0.60	0/3601	1.02	16/4858 (0.3%)
1	E	0.62	0/3539	0.97	7/4777 (0.1%)
1	F	0.60	0/3589	0.99	14/4841 (0.3%)
All	All	0.60	0/21764	0.99	73/29364 (0.2%)

There are no bond length outliers.

The worst 5 of 73 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	6	ASP	N-CA-C	-10.09	97.21	110.43
1	C	242	GLN	N-CA-C	-8.68	102.39	113.16
1	B	26	ARG	N-CA-C	-8.38	99.47	110.53
1	F	331	SER	CA-C-N	7.97	127.61	119.56
1	F	331	SER	C-N-CA	7.97	127.61	119.56

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	3606	0	3584	129	0
1	B	3625	0	3600	134	0
1	C	3588	0	3506	157	0
1	D	3533	0	3483	130	0
1	E	3469	0	3414	117	0
1	F	3519	0	3465	121	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
3	E	5	0	0	0	0
3	F	5	0	0	0	0
4	A	5	0	0	0	0
4	B	3	0	0	0	0
4	C	1	0	0	0	0
4	D	2	0	0	0	0
4	E	2	0	0	0	0
4	F	2	0	0	0	0
All	All	21387	0	21052	756	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 756 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:399:THR:HG22	1:E:400:ASP:H	0.97	1.08
1:B:157:ARG:HG3	1:B:157:ARG:HH11	1.20	1.05
1:B:276:ILE:HD12	1:B:327[B]:PHE:CD2	1.93	1.04
1:E:230:ARG:O	1:E:266:LYS:HA	1.58	1.03
1:A:344:MET:HE1	1:A:426:LEU:HB2	1.37	1.03

There are no symmetry-related clashes.

## 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	440/522 (84%)	420 (96%)	20 (4%)	0	100	100
1	B	447/522 (86%)	433 (97%)	14 (3%)	0	100	100
1	C	449/522 (86%)	421 (94%)	27 (6%)	1 (0%)	43	72
1	D	437/522 (84%)	420 (96%)	16 (4%)	1 (0%)	43	72
1	E	431/522 (83%)	422 (98%)	7 (2%)	2 (0%)	24	54
1	F	430/522 (82%)	410 (95%)	20 (5%)	0	100	100
All	All	2634/3132 (84%)	2526 (96%)	104 (4%)	4 (0%)	43	72

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	84	VAL
1	E	315	ILE
1	E	305	VAL
1	C	420	VAL

### 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	388/461 (84%)	360 (93%)	28 (7%)	13	39
1	B	388/461 (84%)	352 (91%)	36 (9%)	8	27
1	C	379/461 (82%)	355 (94%)	24 (6%)	16	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	370/461 (80%)	334 (90%)	36 (10%)	8	25
1	E	365/461 (79%)	333 (91%)	32 (9%)	9	29
1	F	373/461 (81%)	347 (93%)	26 (7%)	14	40
All	All	2263/2766 (82%)	2081 (92%)	182 (8%)	11	34

5 of 182 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	353	GLN
1	E	266	LYS
1	D	374	SER
1	E	100	VAL
1	E	421	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	445	GLN
1	F	320	GLN
1	D	326	GLN
1	F	424	HIS
1	F	102	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 for Mogul analysis.

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	PO4	D	601	-	4,4,4	0.76	0	6,6,6	0.61	0
3	PO4	A	602	-	4,4,4	0.90	0	6,6,6	0.41	0
3	PO4	B	602	-	4,4,4	0.86	0	6,6,6	0.52	0
3	PO4	E	601	-	4,4,4	0.81	0	6,6,6	0.44	0
3	PO4	F	601	-	4,4,4	0.78	0	6,6,6	0.59	0
3	PO4	C	601	-	4,4,4	0.89	0	6,6,6	0.35	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	451/522 (86%)	0.02	11 (2%) 59 50	35, 74, 146, 167	2 (0%)
1	B	454/522 (86%)	-0.10	12 (2%) 57 48	36, 70, 126, 153	1 (0%)
1	C	456/522 (87%)	0.14	21 (4%) 37 29	39, 78, 147, 165	2 (0%)
1	D	450/522 (86%)	0.18	23 (5%) 33 26	36, 72, 140, 156	4 (0%)
1	E	440/522 (84%)	0.09	19 (4%) 40 31	38, 72, 133, 149	2 (0%)
1	F	443/522 (84%)	0.10	21 (4%) 36 28	35, 71, 150, 176	4 (0%)
All	All	2694/3132 (86%)	0.07	107 (3%) 42 34	35, 73, 142, 176	15 (0%)

The worst 5 of 107 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	240	LEU	5.6
1	E	240	LEU	5.5
1	E	307	SER	5.3
1	D	305	VAL	5.1
1	D	90	LEU	4.8

### 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 oligosaccharides 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, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	PO4	D	601	5/5	0.65	0.15	117,134,150,164	0
3	PO4	E	601	5/5	0.66	0.15	125,128,143,154	0
3	PO4	B	602	5/5	0.67	0.12	134,146,154,159	0
3	PO4	C	601	5/5	0.69	0.15	126,131,151,163	0
3	PO4	F	601	5/5	0.69	0.14	121,124,146,155	0
3	PO4	A	602	5/5	0.77	0.13	115,118,145,154	0
2	MG	A	601	1/1	0.86	0.26	86,86,86,86	0
2	MG	B	601	1/1	0.91	0.19	90,90,90,90	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.