



wwPDB X-ray Structure Validation Summary Report

Feb 1, 2016 – 10:32 AM GMT

PDB ID : 3MAU
Title : Crystal structure of StSPL in complex with phosphoethanolamine
Authors : Bourquin, F.; Grutter, M.G.; Capitani, G.
Deposited on : 2010-03-24
Resolution : 2.90 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
<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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
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) : trunk26865

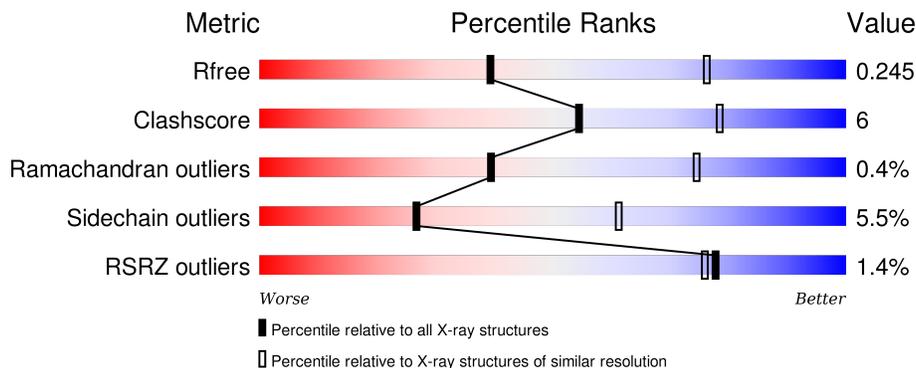
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

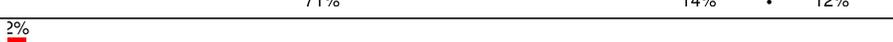
The reported resolution of this entry is 2.90 Å.

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	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (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 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	514	 72% 14% • 12%
1	B	514	 71% 14% • 12%
1	C	514	 71% 16% • 12%
1	D	514	 72% 14% • 12%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 13842 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 sphingosine-1-phosphate lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	452	3429	2195	600	621	13	0	1	0
1	B	451	3429	2195	602	619	13	0	2	0
1	C	452	3423	2191	599	620	13	0	0	0
1	D	452	3423	2191	599	620	13	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

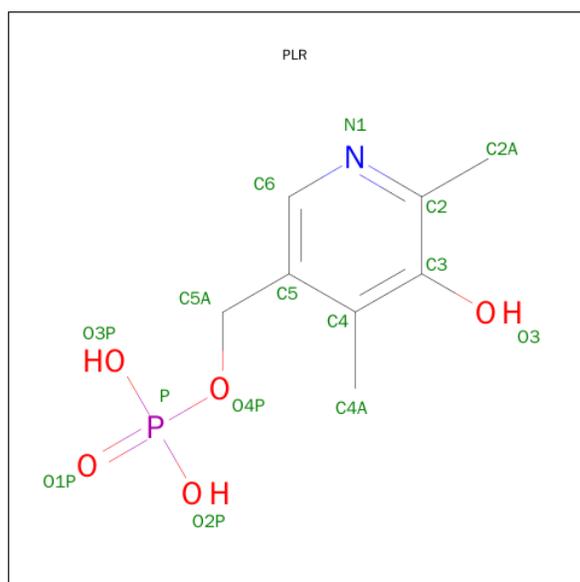
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	EXPRESSION TAG	UNP Q67PY4
A	1	PRO	-	EXPRESSION TAG	UNP Q67PY4
A	311	ALA	LYS	ENGINEERED MUTATION	UNP Q67PY4
A	508	HIS	-	EXPRESSION TAG	UNP Q67PY4
A	509	HIS	-	EXPRESSION TAG	UNP Q67PY4
A	510	HIS	-	EXPRESSION TAG	UNP Q67PY4
A	511	HIS	-	EXPRESSION TAG	UNP Q67PY4
A	512	HIS	-	EXPRESSION TAG	UNP Q67PY4
A	513	HIS	-	EXPRESSION TAG	UNP Q67PY4
B	0	MET	-	EXPRESSION TAG	UNP Q67PY4
B	1	PRO	-	EXPRESSION TAG	UNP Q67PY4
B	311	ALA	LYS	ENGINEERED MUTATION	UNP Q67PY4
B	508	HIS	-	EXPRESSION TAG	UNP Q67PY4
B	509	HIS	-	EXPRESSION TAG	UNP Q67PY4
B	510	HIS	-	EXPRESSION TAG	UNP Q67PY4
B	511	HIS	-	EXPRESSION TAG	UNP Q67PY4
B	512	HIS	-	EXPRESSION TAG	UNP Q67PY4
B	513	HIS	-	EXPRESSION TAG	UNP Q67PY4
C	0	MET	-	EXPRESSION TAG	UNP Q67PY4
C	1	PRO	-	EXPRESSION TAG	UNP Q67PY4
C	311	ALA	LYS	ENGINEERED MUTATION	UNP Q67PY4

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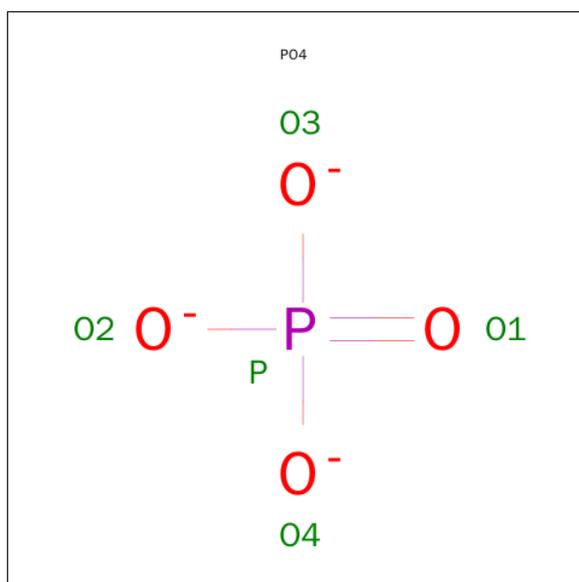
Chain	Residue	Modelled	Actual	Comment	Reference
C	508	HIS	-	EXPRESSION TAG	UNP Q67PY4
C	509	HIS	-	EXPRESSION TAG	UNP Q67PY4
C	510	HIS	-	EXPRESSION TAG	UNP Q67PY4
C	511	HIS	-	EXPRESSION TAG	UNP Q67PY4
C	512	HIS	-	EXPRESSION TAG	UNP Q67PY4
C	513	HIS	-	EXPRESSION TAG	UNP Q67PY4
D	0	MET	-	EXPRESSION TAG	UNP Q67PY4
D	1	PRO	-	EXPRESSION TAG	UNP Q67PY4
D	311	ALA	LYS	ENGINEERED MUTATION	UNP Q67PY4
D	508	HIS	-	EXPRESSION TAG	UNP Q67PY4
D	509	HIS	-	EXPRESSION TAG	UNP Q67PY4
D	510	HIS	-	EXPRESSION TAG	UNP Q67PY4
D	511	HIS	-	EXPRESSION TAG	UNP Q67PY4
D	512	HIS	-	EXPRESSION TAG	UNP Q67PY4
D	513	HIS	-	EXPRESSION TAG	UNP Q67PY4

- Molecule 2 is (5-HYDROXY-4,6-DIMETHYLPYRIDIN-3-YL)METHYL DIHYDROGEN PHOSPHATE (three-letter code: PLR) (formula: C₈H₁₂NO₅P).



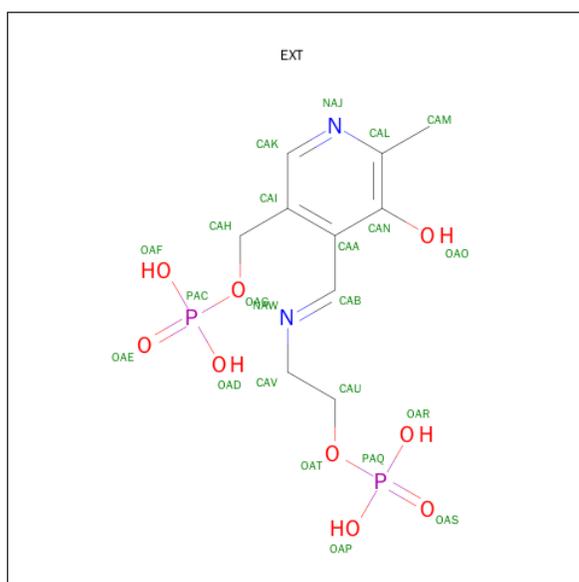
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	15	8	1	5	1	0	0

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



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

- Molecule 4 is {5-HYDROXY-6-METHYL-4-[(E)-{[2-(PHOSPHONOOXY)ETHYL]IMINO O}METHYL]PYRIDIN-3-YL}METHYL DIHYDROGEN PHOSPHATE (three-letter code: EXT) (formula: C₁₀H₁₆N₂O₉P₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C N O P	0	0
			23 10 2 9 2		
4	C	1	Total C N O P	0	0
			23 10 2 9 2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
4	D	1	23	10	2	9	2	0	0

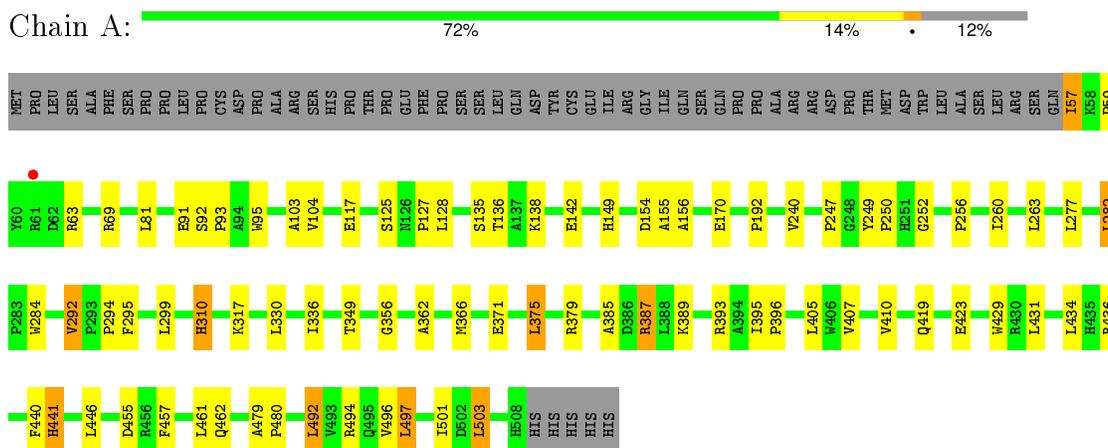
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	12	Total 12	O 12	0	0
5	B	17	Total 17	O 17	0	0
5	C	10	Total 10	O 10	0	0
5	D	10	Total 10	O 10	0	0

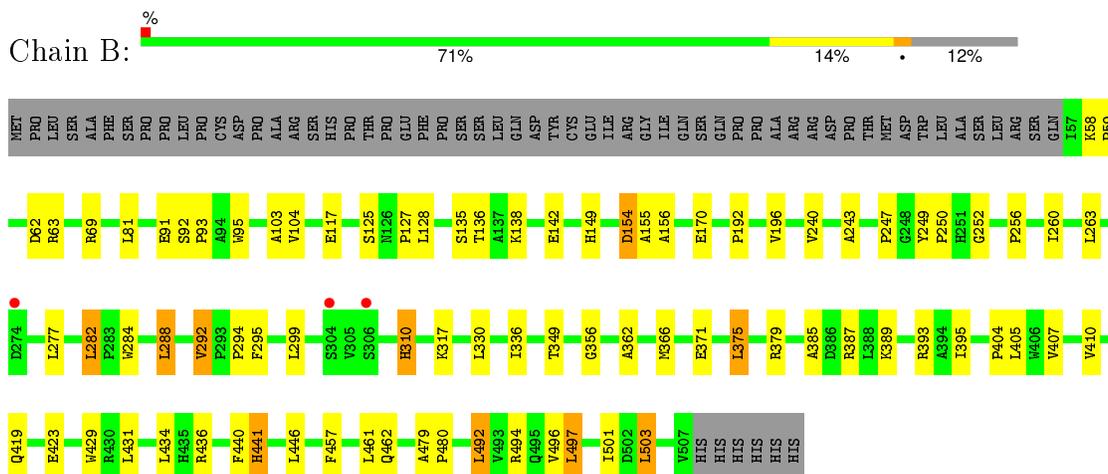
3 Residue-property plots [i](#)

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.

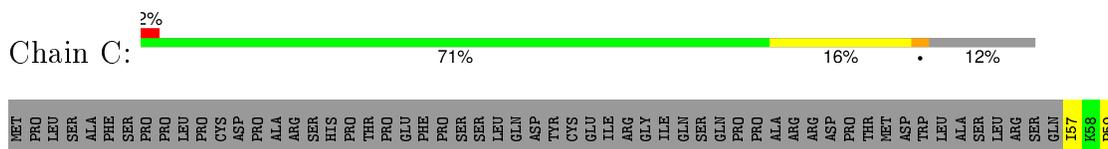
- Molecule 1: sphingosine-1-phosphate lyase

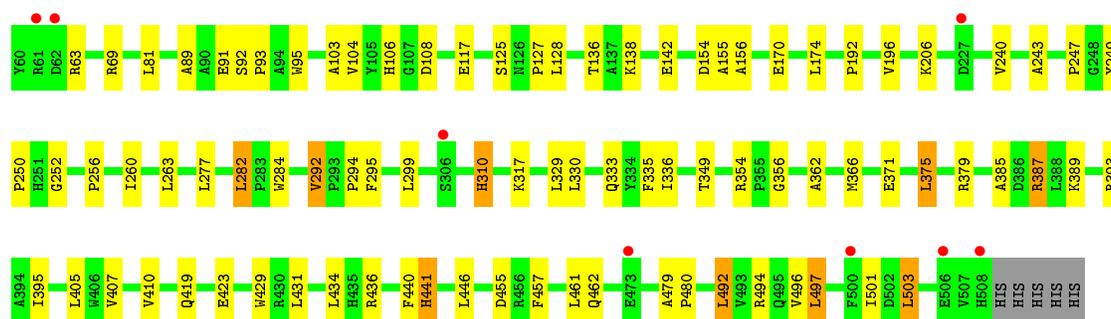


- Molecule 1: sphingosine-1-phosphate lyase

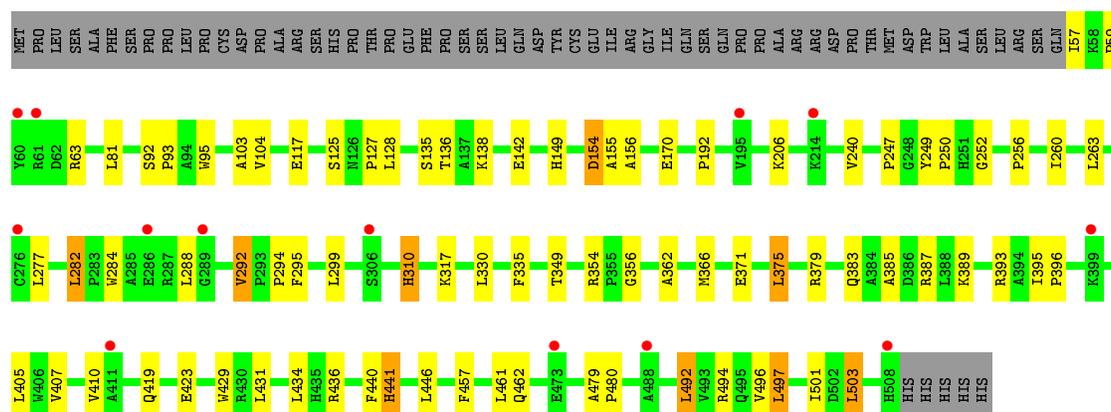


- Molecule 1: sphingosine-1-phosphate lyase





- Molecule 1: sphingosine-1-phosphate lyase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	64.36Å 243.45Å 280.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.89 – 2.90 29.89 – 2.90	Depositor EDS
% Data completeness (in resolution range)	97.7 (29.89-2.90) 97.8 (29.89-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.48 (at 2.90Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.4_29)	Depositor
R, R_{free}	0.229 , 0.252 0.225 , 0.245	Depositor DCC
R_{free} test set	2421 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	67.5	Xtriage
Anisotropy	0.477	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 12.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Outliers	0 of 48404 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13842	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: PO4, EXT, PLR

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	0.30	0/3530	0.62	8/4824 (0.2%)
1	B	0.30	0/3532	0.71	9/4825 (0.2%)
1	C	0.29	0/3521	0.62	8/4812 (0.2%)
1	D	0.30	0/3521	0.61	8/4812 (0.2%)
All	All	0.30	0/14104	0.64	33/19273 (0.2%)

There are no bond length outliers.

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	393	ARG	NE-CZ-NH1	-18.07	111.26	120.30
1	B	393	ARG	NE-CZ-NH2	17.57	129.08	120.30
1	D	387	ARG	NE-CZ-NH1	-13.26	113.67	120.30
1	C	387	ARG	NE-CZ-NH2	-13.10	113.75	120.30
1	A	387	ARG	NE-CZ-NH2	-12.82	113.89	120.30

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	3429	0	3370	44	0
1	B	3429	0	3381	49	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3423	0	3362	51	0
1	D	3423	0	3362	44	0
2	A	15	0	10	2	0
3	A	5	0	0	0	0
4	B	23	0	11	1	0
4	C	23	0	12	0	0
4	D	23	0	11	0	0
5	A	12	0	0	0	0
5	B	17	0	0	3	0
5	C	10	0	0	0	0
5	D	10	0	0	0	0
All	All	13842	0	13519	175	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 6.

The worst 5 of 175 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:503:LEU:O	1:A:503:LEU:HD22	1.98	0.64
1:B:138:LYS:HE2	1:B:142:GLU:OE2	1.98	0.63
1:C:503:LEU:O	1:C:503:LEU:HD22	1.98	0.63
1:A:138:LYS:HE2	1:A:142:GLU:OE2	2.00	0.61
1:B:404:PRO:HG3	5:B:528:HOH:O	2.01	0.61

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	451/514 (88%)	430 (95%)	19 (4%)	2 (0%)	39 74

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	451/514 (88%)	430 (95%)	19 (4%)	2 (0%)	39	74
1	C	450/514 (88%)	428 (95%)	20 (4%)	2 (0%)	39	74
1	D	450/514 (88%)	430 (96%)	18 (4%)	2 (0%)	39	74
All	All	1802/2056 (88%)	1718 (95%)	76 (4%)	8 (0%)	39	74

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	155	ALA
1	C	155	ALA
1	B	155	ALA
1	D	103	ALA
1	A	103	ALA

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	339/395 (86%)	321 (95%)	18 (5%)	28	63
1	B	339/395 (86%)	320 (94%)	19 (6%)	26	60
1	C	338/395 (86%)	321 (95%)	17 (5%)	30	65
1	D	338/395 (86%)	318 (94%)	20 (6%)	24	58
All	All	1354/1580 (86%)	1280 (94%)	74 (6%)	27	61

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	492	LEU
1	C	310	HIS
1	D	446	LEU
1	B	494	ARG
1	C	128	LEU

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

Mol	Chain	Res	Type
1	C	435	HIS
1	D	435	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

5 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	PLR	A	514	-	15,15,15	0.95	1 (6%)	21,22,22	1.12	2 (9%)
3	PO4	A	515	-	4,4,4	0.39	0	6,6,6	0.26	0
4	EXT	B	514	-	23,23,23	1.71	5 (21%)	30,33,33	1.37	4 (13%)
4	EXT	C	514	-	23,23,23	1.77	5 (21%)	30,33,33	1.47	7 (23%)
4	EXT	D	514	-	23,23,23	1.75	5 (21%)	30,33,33	1.19	2 (6%)

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	PLR	A	514	-	-	0/6/6/6	0/1/1/1
3	PO4	A	515	-	-	0/0/0/0	0/0/0/0
4	EXT	B	514	-	-	0/15/15/15	0/1/1/1
4	EXT	C	514	-	-	1/15/15/15	0/1/1/1
4	EXT	D	514	-	-	1/15/15/15	0/1/1/1

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	514	EXT	CAA-CAB	-4.16	1.39	1.46
4	C	514	EXT	CAA-CAB	-4.12	1.39	1.46
4	B	514	EXT	CAA-CAB	-3.82	1.40	1.46
4	D	514	EXT	CAN-CAL	-2.21	1.39	1.40
4	B	514	EXT	PAC-OAF	2.01	1.61	1.54

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	514	EXT	CAU-CAV-NAW	-2.98	105.18	111.02
4	C	514	EXT	CAN-CAA-CAI	2.01	119.61	118.11
4	C	514	EXT	OAO-CAN-CAL	2.04	121.21	117.66
4	C	514	EXT	OAG-PAC-OAE	2.10	112.50	107.14
2	A	514	PLR	O3-C3-C2	2.17	121.44	117.66

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	514	EXT	CAU-CAV-NAW-CAB
4	D	514	EXT	CAU-CAV-NAW-CAB

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	514	PLR	2	0
4	B	514	EXT	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	452/514 (87%)	-0.06	1 (0%) 95 95	54, 70, 86, 104	0
1	B	451/514 (87%)	-0.11	3 (0%) 89 88	54, 70, 86, 101	0
1	C	452/514 (87%)	-0.09	8 (1%) 71 68	55, 70, 86, 111	0
1	D	452/514 (87%)	0.02	13 (2%) 55 49	54, 70, 86, 101	0
All	All	1807/2056 (87%)	-0.06	25 (1%) 78 76	54, 70, 86, 111	0

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	306	SER	3.8
1	D	289	GLY	3.7
1	C	508	HIS	3.5
1	C	506	GLU	2.9
1	D	214	LYS	2.9

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	PO4	A	515	5/5	0.94	0.17	0.13	70,73,80,81	0
4	EXT	C	514	23/23	0.95	0.16	-0.32	60,64,78,87	0
4	EXT	D	514	23/23	0.95	0.16	-0.54	53,63,72,82	0
4	EXT	B	514	23/23	0.95	0.18	-0.69	54,60,76,82	0
2	PLR	A	514	15/15	0.97	0.15	-1.00	56,58,61,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.