



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 08:45 AM GMT

PDB ID : 3FSL
Title : Crystal structure of tyrosine aminotransferase tripple mutant (P181Q,R183G,A321K) from Escherichia coli at 2.35 Å resolution
Authors : Malashkevich, V.N.; Ng, B.; Kirsch, J.F.
Deposited on : 2009-01-09
Resolution : 2.35 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

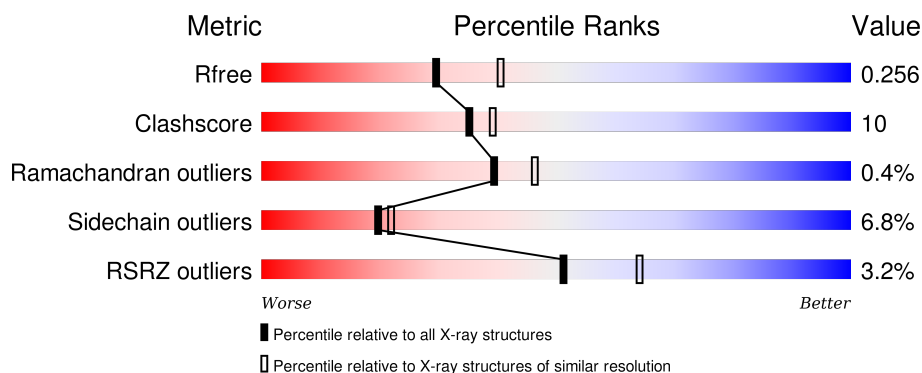
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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}	91344	1352 (2.38-2.34)
Clashscore	102246	1456 (2.38-2.34)
Ramachandran outliers	100387	1435 (2.38-2.34)
Sidechain outliers	100360	1436 (2.38-2.34)
RSRZ outliers	91569	1358 (2.38-2.34)

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	397	<div> <div></div> <div>78%19%..</div> </div>
1	B	397	<div> <div>2%</div> <div>77%21%..</div> </div>
1	C	397	<div> <div>%</div> <div>82%15%..</div> </div>
1	D	397	<div> <div>6%</div> <div>78%18%..</div> </div>
1	E	397	<div> <div>9%</div> <div>70%26%..</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	397	<div><div></div><div>2%</div><div>78%</div><div>19%</div><div>••</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 19356 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 Aromatic-amino-acid aminotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	397	Total	C	N	O	S	0	0	0
			3064	1949	527	572	16			
1	B	397	Total	C	N	O	S	0	0	0
			3064	1949	527	572	16			
1	C	397	Total	C	N	O	S	0	0	0
			3064	1949	527	572	16			
1	D	397	Total	C	N	O	S	0	1	0
			3067	1951	527	572	17			
1	E	397	Total	C	N	O	S	0	0	0
			3064	1949	527	572	16			
1	F	397	Total	C	N	O	S	0	0	0
			3064	1949	527	572	16			

There are 18 discrepancies between the modelled and reference sequences:

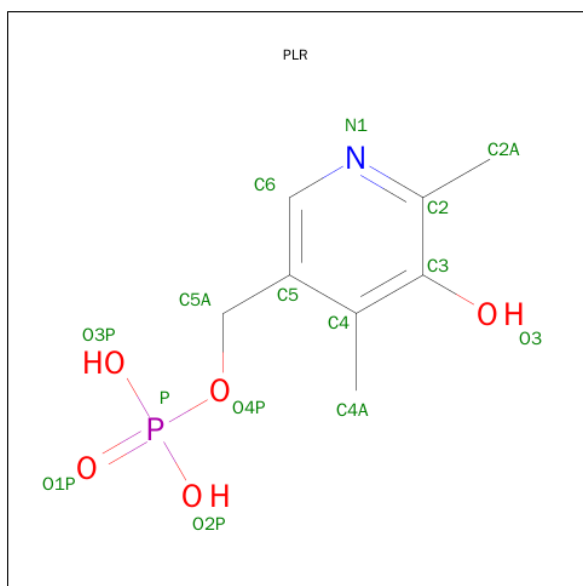
Chain	Residue	Modelled	Actual	Comment	Reference
A	181	GLN	PRO	engineered	UNP P04693
A	183	GLY	ARG	engineered	UNP P04693
A	321	LYS	ALA	engineered	UNP P04693
B	181	GLN	PRO	engineered	UNP P04693
B	183	GLY	ARG	engineered	UNP P04693
B	321	LYS	ALA	engineered	UNP P04693
C	181	GLN	PRO	engineered	UNP P04693
C	183	GLY	ARG	engineered	UNP P04693
C	321	LYS	ALA	engineered	UNP P04693
D	181	GLN	PRO	engineered	UNP P04693
D	183	GLY	ARG	engineered	UNP P04693
D	321	LYS	ALA	engineered	UNP P04693
E	181	GLN	PRO	engineered	UNP P04693
E	183	GLY	ARG	engineered	UNP P04693
E	321	LYS	ALA	engineered	UNP P04693
F	181	GLN	PRO	engineered	UNP P04693
F	183	GLY	ARG	engineered	UNP P04693

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Chain	Residue	Modelled	Actual	Comment	Reference
F	321	LYS	ALA	engineered	UNP P04693

- 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
2	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	C	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	D	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	E	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	F	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

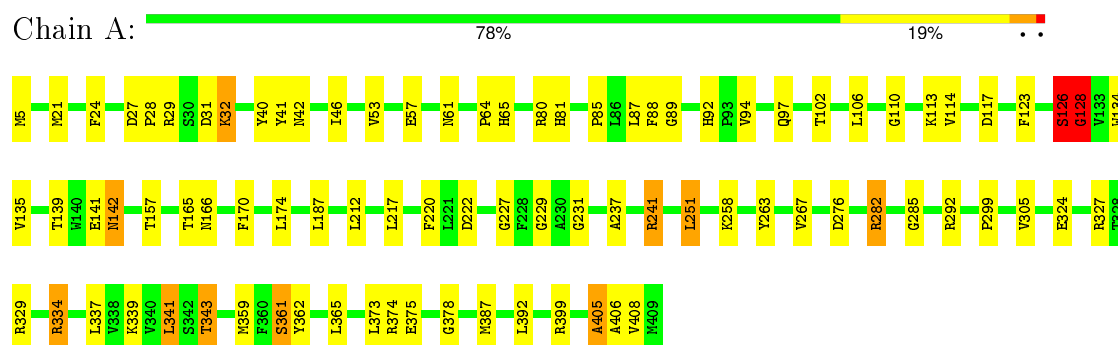
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	879	Total	O	0	0
			879	879		

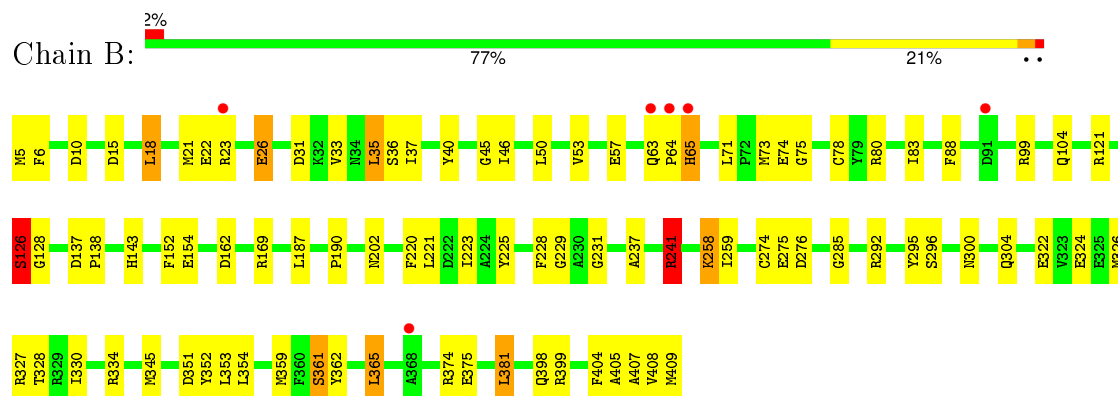
3 Residue-property plots

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.

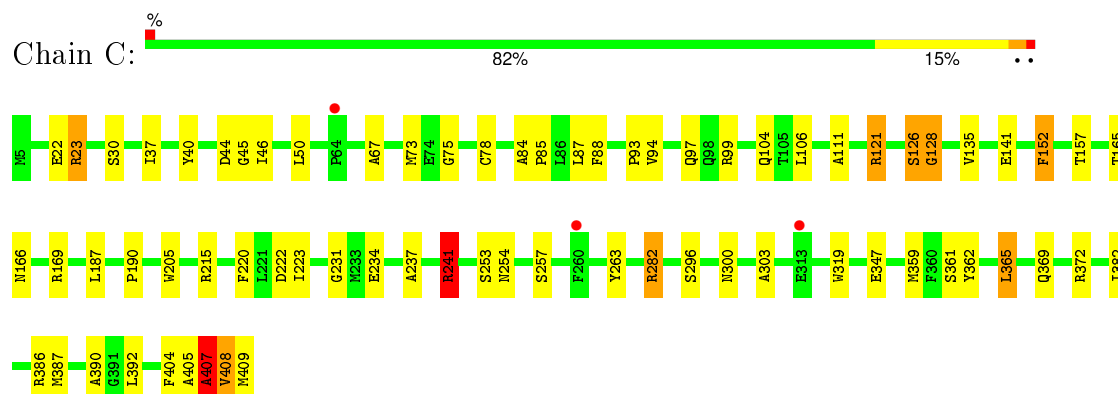
• Molecule 1: Aromatic-amino-acid aminotransferase



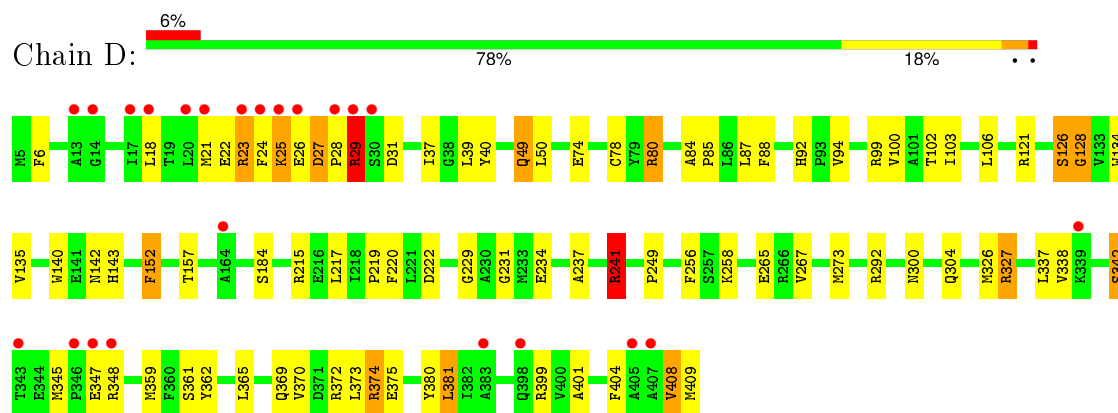
• Molecule 1: Aromatic-amino-acid aminotransferase



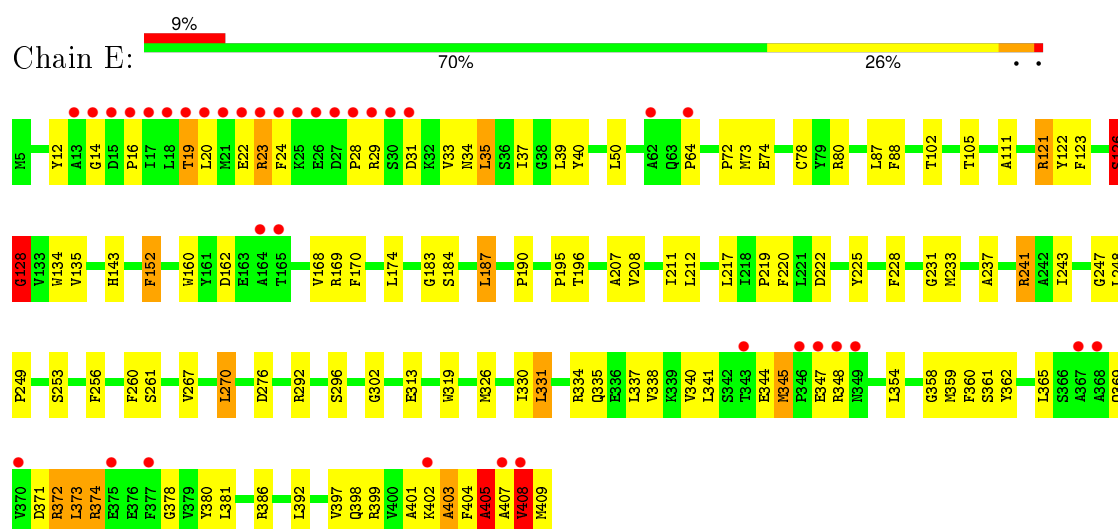
• Molecule 1: Aromatic-amino-acid aminotransferase



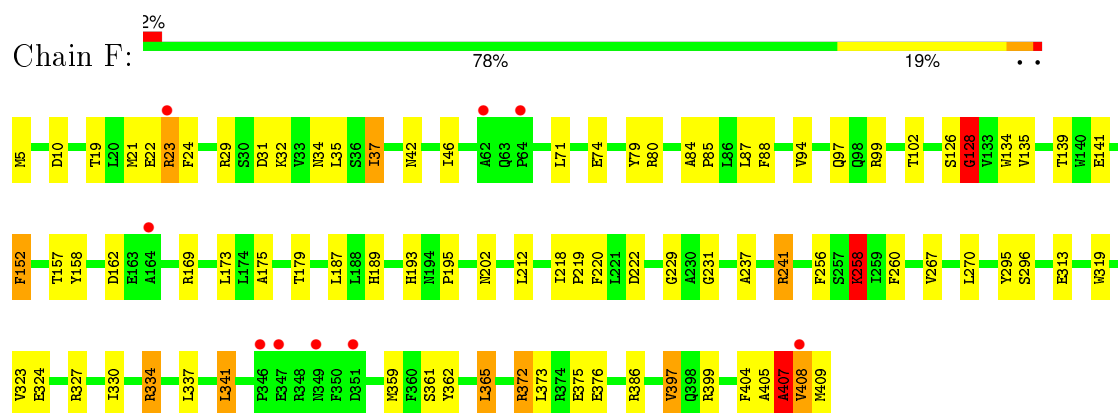
• Molecule 1: Aromatic-amino-acid aminotransferase



• Molecule 1: Aromatic-amino-acid aminotransferase



• Molecule 1: Aromatic-amino-acid aminotransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	98.88Å 119.16Å 242.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.96 – 2.35 19.95 – 2.35	Depositor EDS
% Data completeness (in resolution range)	91.0 (19.96-2.35) 91.0 (19.95-2.35)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 2.35Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.213 , 0.260 0.192 , 0.256	Depositor DCC
R_{free} test set	5379 reflections (5.22%)	DCC
Wilson B-factor (Å ²)	36.7	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 46.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 108456 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	19356	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.14% 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: 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	0.81	1/3128 (0.0%)	1.02	15/4243 (0.4%)
1	B	0.77	2/3128 (0.1%)	0.96	8/4243 (0.2%)
1	C	0.79	1/3128 (0.0%)	0.92	12/4243 (0.3%)
1	D	0.76	2/3134 (0.1%)	0.92	13/4251 (0.3%)
1	E	0.71	1/3128 (0.0%)	0.91	10/4243 (0.2%)
1	F	0.74	1/3128 (0.0%)	0.94	15/4243 (0.4%)
All	All	0.77	8/18774 (0.0%)	0.94	73/25466 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	4
1	C	0	4
1	D	0	2
1	E	0	4
1	F	0	3
All	All	0	19

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	231	GLY	N-CA	7.87	1.57	1.46
1	D	231	GLY	CA-C	7.39	1.63	1.51
1	F	231	GLY	CA-C	7.07	1.63	1.51
1	B	231	GLY	CA-C	6.96	1.62	1.51
1	B	231	GLY	C-O	6.41	1.33	1.23

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	128	GLY	O-C-N	-21.07	88.98	122.70
1	A	126	SER	C-N-CA	20.36	165.06	122.30
1	D	126	SER	C-N-CA	18.97	162.13	122.30
1	B	128	GLY	CA-C-N	14.85	149.87	117.20
1	F	128	GLY	O-C-N	-14.20	99.98	122.70

There are no chirality outliers.

5 of 19 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	126	SER	Peptide
1	A	64	PRO	Peptide
1	B	126	SER	Mainchain
1	B	152	PHE	Peptide
1	B	407	ALA	Mainchain

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	3064	0	3031	56	0
1	B	3064	0	3030	71	0
1	C	3064	0	3031	45	0
1	D	3067	0	3037	55	0
1	E	3064	0	3031	97	0
1	F	3064	0	3031	59	0
2	A	15	0	8	1	0
2	B	15	0	8	0	0
2	C	15	0	8	1	0
2	D	15	0	8	1	0
2	E	15	0	7	1	0
2	F	15	0	8	1	0
3	A	879	0	0	21	0
All	All	19356	0	18238	361	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 10.

The worst 5 of 361 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)
3:A:908:HOH:O	1:B:78:CYS:HB3	1.30	1.31
1:E:404:PHE:O	1:E:409:MET:HB2	1.39	1.21
1:D:404:PHE:O	1:D:409:MET:HG3	1.42	1.15
1:E:405:ALA:O	1:E:407:ALA:C	1.88	1.08
1:E:404:PHE:O	1:E:409:MET:CB	2.12	0.98

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	395/397 (100%)	379 (96%)	13 (3%)	3 (1%)	24	26
1	B	395/397 (100%)	383 (97%)	12 (3%)	0	100	100
1	C	395/397 (100%)	382 (97%)	13 (3%)	0	100	100
1	D	396/397 (100%)	371 (94%)	23 (6%)	2 (0%)	34	39
1	E	395/397 (100%)	365 (92%)	26 (7%)	4 (1%)	19	20
1	F	395/397 (100%)	373 (94%)	21 (5%)	1 (0%)	46	55
All	All	2371/2382 (100%)	2253 (95%)	108 (5%)	10 (0%)	39	46

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	32	LYS
1	A	128	GLY
1	F	407	ALA
1	A	263	TYR
1	D	29	ARG

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	316/316 (100%)	297 (94%)	19 (6%)	24	28
1	B	316/316 (100%)	295 (93%)	21 (7%)	21	23
1	C	316/316 (100%)	302 (96%)	14 (4%)	35	44
1	D	317/316 (100%)	294 (93%)	23 (7%)	17	19
1	E	316/316 (100%)	287 (91%)	29 (9%)	11	11
1	F	316/316 (100%)	293 (93%)	23 (7%)	17	19
All	All	1897/1896 (100%)	1768 (93%)	129 (7%)	20	22

5 of 129 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	29	ARG
1	D	365	LEU
1	F	313	GLU
1	D	50	LEU
1	D	220	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	49	GLN
1	D	300	ASN
1	F	34	ASN
1	C	335	GLN
1	F	97	GLN

5.3.3 RNA [i](#)

There are no RNA molecules 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 ⓘ

6 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	500	1	15,15,15	1.41	1 (6%)	21,22,22	1.94	5 (23%)
2	PLR	B	500	1	15,15,15	1.18	1 (6%)	21,22,22	2.14	5 (23%)
2	PLR	C	500	1	15,15,15	1.71	1 (6%)	21,22,22	2.72	7 (33%)
2	PLR	D	500	1	15,15,15	1.10	0	21,22,22	2.86	10 (47%)
2	PLR	E	500	1	15,15,15	1.18	1 (6%)	21,22,22	2.72	5 (23%)
2	PLR	F	500	1	15,15,15	0.88	0	21,22,22	2.03	4 (19%)

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	500	1	-	0/6/6/6	0/1/1/1
2	PLR	B	500	1	-	0/6/6/6	0/1/1/1
2	PLR	C	500	1	-	0/6/6/6	0/1/1/1
2	PLR	D	500	1	-	0/6/6/6	0/1/1/1
2	PLR	E	500	1	-	0/6/6/6	0/1/1/1
2	PLR	F	500	1	-	0/6/6/6	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	500	PLR	C4A-C4	-5.72	1.40	1.51
2	A	500	PLR	C4A-C4	-3.74	1.44	1.51
2	E	500	PLR	C3-C2	-2.99	1.38	1.40
2	B	500	PLR	C3-C2	-2.74	1.38	1.40

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	500	PLR	C5A-C5-C6	-4.42	110.93	119.28
2	E	500	PLR	C5A-C5-C6	-4.18	111.37	119.28
2	F	500	PLR	C4A-C4-C5	-4.16	116.54	120.88
2	C	500	PLR	C5A-C5-C6	-4.01	111.70	119.28
2	D	500	PLR	C4A-C4-C3	-2.87	115.16	120.36

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	PLR	1	0
2	C	500	PLR	1	0
2	D	500	PLR	1	0
2	E	500	PLR	1	0
2	F	500	PLR	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 ⓘ

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	397/397 (100%)	-0.34	0 100 100	16, 26, 49, 75	0
1	B	397/397 (100%)	-0.35	6 (1%) 76 85	15, 26, 51, 74	0
1	C	397/397 (100%)	-0.32	3 (0%) 87 93	15, 26, 48, 72	0
1	D	397/397 (100%)	-0.05	23 (5%) 26 40	16, 28, 62, 82	0
1	E	397/397 (100%)	0.18	36 (9%) 11 18	16, 31, 62, 83	0
1	F	397/397 (100%)	-0.16	9 (2%) 64 76	19, 32, 53, 73	0
All	All	2382/2382 (100%)	-0.17	77 (3%) 51 64	15, 28, 54, 83	0

The worst 5 of 77 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	30	SER	6.7
1	E	26	GLU	6.6
1	E	22	GLU	5.5
1	E	343	THR	5.2
1	D	407	ALA	5.0

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 [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(Å ²)	Q<0.9
2	PLR	F	500	15/15	0.98	0.10	0.46	21,33,37,41	0
2	PLR	E	500	15/15	0.98	0.10	-0.16	21,28,33,33	0
2	PLR	B	500	15/15	0.98	0.09	-0.57	12,20,27,30	0
2	PLR	C	500	15/15	0.99	0.09	-0.77	18,23,29,32	0
2	PLR	A	500	15/15	0.99	0.07	-1.00	19,24,27,28	0
2	PLR	D	500	15/15	0.98	0.08	-1.15	19,26,30,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.