



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 1, 2026 – 01:38 AM UTC

PDB ID : 3FSL / pdb_00003fsl
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

<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>.

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

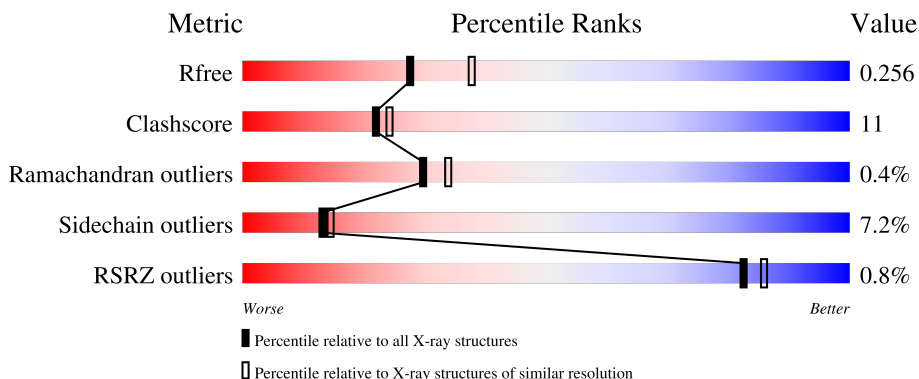
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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.



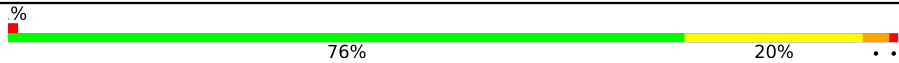
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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 ≥ 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	397	 77% 19% . .
1	B	397	 76% 20% .
1	C	397	 80% 17% .
1	D	397	 2% 75% 21% . .
1	E	397	 3% 70% 24% 5% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	397	 <p>A horizontal bar chart representing the quality of the chain. The bar is divided into segments: a small red segment at the start, followed by a large green segment labeled '76%', then a yellow segment labeled '20%', and a small red segment at the end. Above the bar is a '%' symbol, and below the bar are two dots '••'.</p>

2 Entry composition [i](#)

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
			Total	C	N	O	S			
1	A	397	3064	1949	527	572	16	0	0	0
1	B	397	3064	1949	527	572	16	0	0	0
1	C	397	3064	1949	527	572	16	0	0	0
1	D	397	3067	1951	527	572	17	0	1	0
1	E	397	3064	1949	527	572	16	0	0	0
1	F	397	3064	1949	527	572	16	0	0	0

There are 18 discrepancies between the modelled and reference sequences:

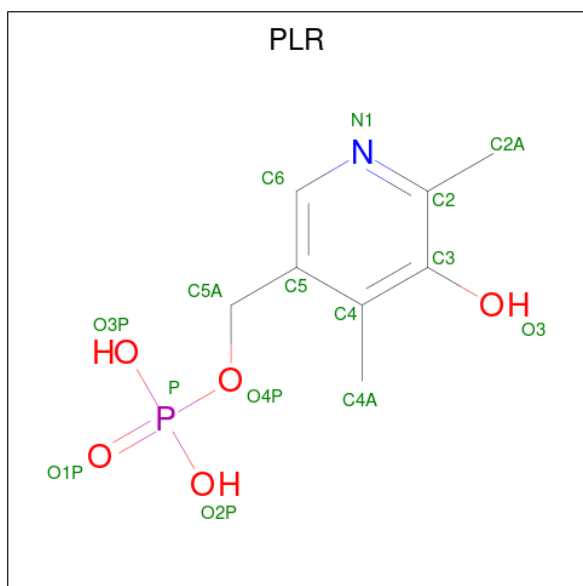
Chain	Residue	Modelled	Actual	Comment	Reference
A	181	GLN	PRO	engineered mutation	UNP P04693
A	183	GLY	ARG	engineered mutation	UNP P04693
A	321	LYS	ALA	engineered mutation	UNP P04693
B	181	GLN	PRO	engineered mutation	UNP P04693
B	183	GLY	ARG	engineered mutation	UNP P04693
B	321	LYS	ALA	engineered mutation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

Continued on next page...

Continued from previous page...

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

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



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
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					

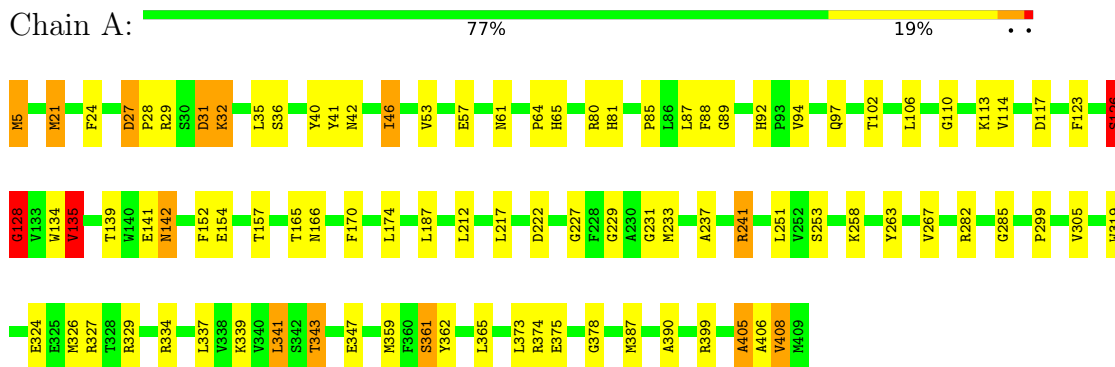
- Molecule 3 is water.

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

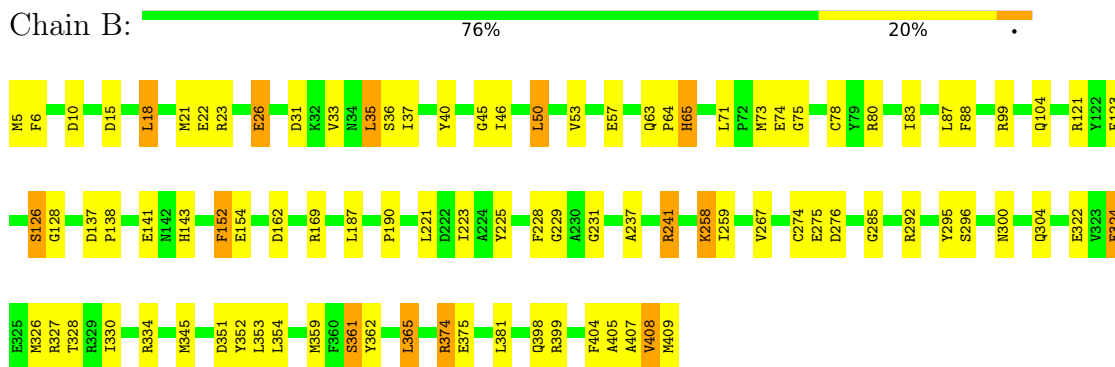
3 Residue-property plots

These plots are drawn for all protein, RNA, 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.

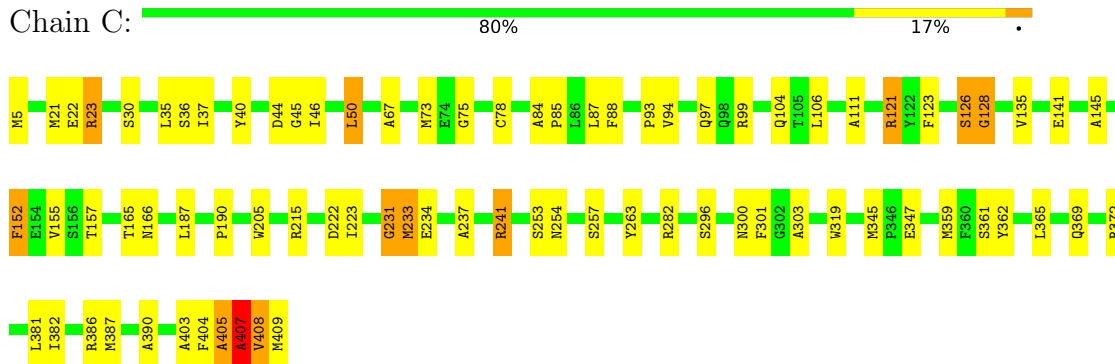
- Molecule 1: Aromatic-amino-acid aminotransferase



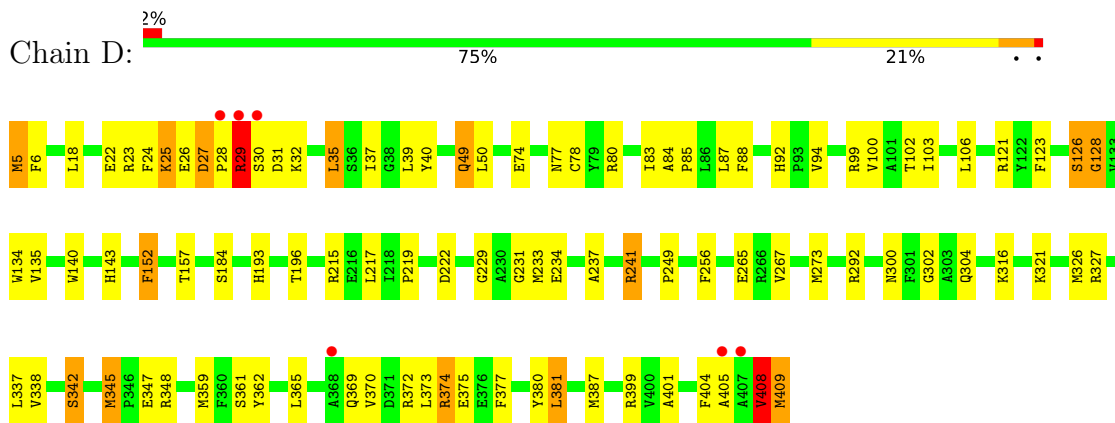
- Molecule 1: Aromatic-amino-acid aminotransferase



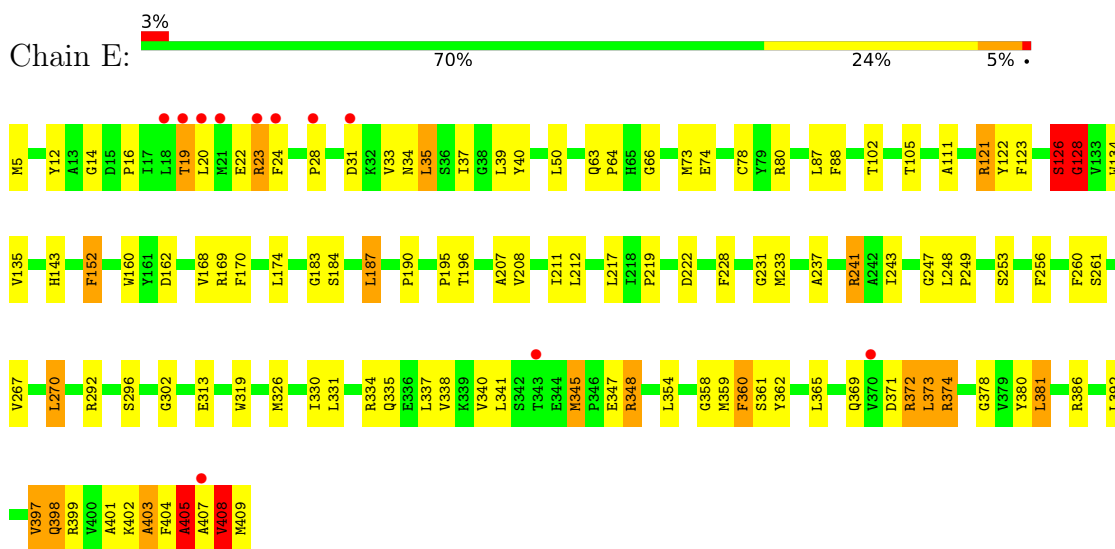
- Molecule 1: Aromatic-amino-acid aminotransferase



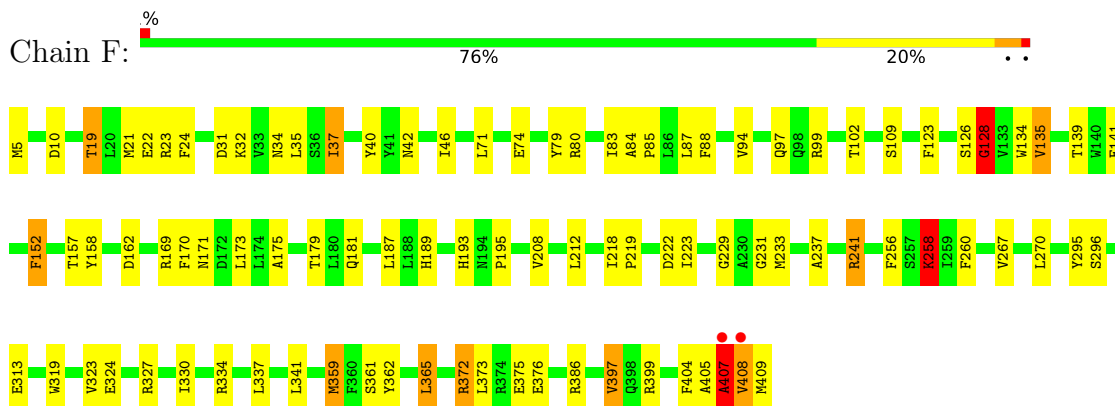
- Molecule 1: Aromatic-amino-acid aminotransferase



- 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 19.96 – 2.35	Depositor EDS
% Data completeness (in resolution range)	91.0 (19.96-2.35) 90.8 (19.96-2.35)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 2.35Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.213 , 0.260 0.192 , 0.256	Depositor DCC
R_{free} test set	5379 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	36.7	Xtrriage
Anisotropy	0.067	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 47.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	19356	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtrriage'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, 0.333 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: 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	1.01	2/3128 (0.1%)	1.33	18/4243 (0.4%)
1	B	0.96	4/3128 (0.1%)	1.33	12/4243 (0.3%)
1	C	0.99	4/3128 (0.1%)	1.33	12/4243 (0.3%)
1	D	0.95	4/3134 (0.1%)	1.27	14/4251 (0.3%)
1	E	0.88	2/3128 (0.1%)	1.40	19/4243 (0.4%)
1	F	0.90	2/3128 (0.1%)	1.42	19/4243 (0.4%)
All	All	0.95	18/18774 (0.1%)	1.35	94/25466 (0.4%)

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 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	231	GLY	CA-C	11.81	1.63	1.51
1	B	231	GLY	CA-C	11.61	1.62	1.51
1	F	231	GLY	CA-C	8.97	1.63	1.51
1	C	231	GLY	N-CA	8.61	1.57	1.45
1	E	408	VAL	CA-CB	-8.54	1.44	1.54

The worst 5 of 94 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	126	SER	CA-C-N	29.82	150.46	122.73
1	E	126	SER	C-N-CA	29.82	150.46	122.73
1	F	126	SER	CA-C-N	29.29	147.92	120.10
1	F	126	SER	C-N-CA	29.29	147.92	120.10
1	B	128	GLY	O-C-N	-27.58	88.98	122.91

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 [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	3064	0	3031	61	0
1	B	3064	0	3032	72	0
1	C	3064	0	3032	59	0
1	D	3067	0	3037	63	0
1	E	3064	0	3032	99	0
1	F	3064	0	3033	62	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	0	0
2	F	15	0	8	1	0
3	A	879	0	0	23	0
All	All	19356	0	18244	393	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 11.

The worst 5 of 393 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:A:123:PHE:CE2	1:B:5:MET:HE2	1.79	1.16
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	1.12

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%)	16	17
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%)	24	27
1	E	395/397 (100%)	365 (92%)	26 (7%)	4 (1%)	12	12
1	F	395/397 (100%)	373 (94%)	21 (5%)	1 (0%)	36	43
All	All	2371/2382 (100%)	2253 (95%)	108 (5%)	10 (0%)	30	34

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%)	293 (93%)	23 (7%)	13	14
1	B	316/316 (100%)	293 (93%)	23 (7%)	13	14
1	C	316/316 (100%)	301 (95%)	15 (5%)	23	30
1	D	317/316 (100%)	292 (92%)	25 (8%)	11	12
1	E	316/316 (100%)	289 (92%)	27 (8%)	10	11
1	F	316/316 (100%)	292 (92%)	24 (8%)	12	13
All	All	1897/1896 (100%)	1760 (93%)	137 (7%)	13	14

5 of 137 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	35	LEU
1	F	135	VAL
1	F	362	TYR
1	C	37	ILE
1	C	23	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	97	GLN
1	F	202	ASN
1	C	335	GLN
1	C	202	ASN
1	F	300	ASN

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](#)

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	E	500	1	15,15,15	1.13	1 (6%)	21,22,22	2.41	5 (23%)
2	PLR	C	500	1	15,15,15	1.79	2 (13%)	21,22,22	2.59	9 (42%)
2	PLR	F	500	1	15,15,15	0.96	0	21,22,22	1.88	5 (23%)
2	PLR	A	500	1	15,15,15	1.48	2 (13%)	21,22,22	1.82	5 (23%)
2	PLR	B	500	1	15,15,15	1.19	2 (13%)	21,22,22	1.97	5 (23%)
2	PLR	D	500	1	15,15,15	1.21	1 (6%)	21,22,22	2.68	10 (47%)

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	E	500	1	-	3/6/6/6	0/1/1/1
2	PLR	C	500	1	-	2/6/6/6	0/1/1/1
2	PLR	F	500	1	-	2/6/6/6	0/1/1/1
2	PLR	A	500	1	-	1/6/6/6	0/1/1/1
2	PLR	B	500	1	-	2/6/6/6	0/1/1/1
2	PLR	D	500	1	-	2/6/6/6	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	500	PLR	C4A-C4	-5.82	1.40	1.51
2	A	500	PLR	C4A-C4	-3.80	1.44	1.51
2	A	500	PLR	C2-N1	2.50	1.38	1.33
2	B	500	PLR	C2-N1	2.47	1.38	1.33
2	D	500	PLR	C2-N1	2.27	1.37	1.33

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	500	PLR	O4P-C5A-C5	6.60	121.73	109.36
2	B	500	PLR	O4P-C5A-C5	6.23	121.04	109.36
2	E	500	PLR	O4P-C5A-C5	6.01	120.62	109.36
2	C	500	PLR	O2P-P-O4P	5.89	122.02	106.67
2	C	500	PLR	O4P-C5A-C5	5.29	119.27	109.36

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	500	PLR	C5A-O4P-P-O3P
2	B	500	PLR	C4-C5-C5A-O4P
2	B	500	PLR	C6-C5-C5A-O4P
2	C	500	PLR	C4-C5-C5A-O4P
2	C	500	PLR	C6-C5-C5A-O4P

There are no ring outliers.

4 monomers are involved in 4 short contacts:

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

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

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	397/397 (100%)	-0.56	0 100 100	16, 26, 49, 75	0
1	B	397/397 (100%)	-0.44	0 100 100	15, 26, 51, 74	0
1	C	397/397 (100%)	-0.53	0 100 100	15, 26, 48, 72	0
1	D	397/397 (100%)	-0.01	6 (1%) 72 77	16, 28, 62, 82	1 (0%)
1	E	397/397 (100%)	0.03	11 (2%) 55 61	16, 31, 62, 83	0
1	F	397/397 (100%)	-0.34	2 (0%) 87 90	19, 32, 53, 73	0
All	All	2382/2382 (100%)	-0.31	19 (0%) 82 86	15, 28, 54, 83	1 (0%)

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	370	VAL	3.6
1	D	28	PRO	3.5
1	D	405	ALA	3.3
1	D	30	SER	3.0
1	E	407	ALA	2.8

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, 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
2	PLR	E	500	15/15	0.96	0.08	21,28,33,33	0
2	PLR	F	500	15/15	0.97	0.07	21,33,37,41	0
2	PLR	D	500	15/15	0.98	0.05	19,26,30,33	0
2	PLR	A	500	15/15	0.98	0.05	19,24,27,28	0
2	PLR	B	500	15/15	0.98	0.05	12,20,27,30	0
2	PLR	C	500	15/15	0.99	0.05	18,23,29,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.