



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:19 PM GMT

PDB ID : 4L9P  
Title : Crystal structure of Aspergillus fumigatus protein farnesyltransferase complexed with the FII analog, FPT-II, and the KCVVM peptide  
Authors : Mabanglo, M.F.; Hast, M.A.; Beese, L.S.  
Deposited on : 2013-06-18  
Resolution : 1.45 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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  
<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

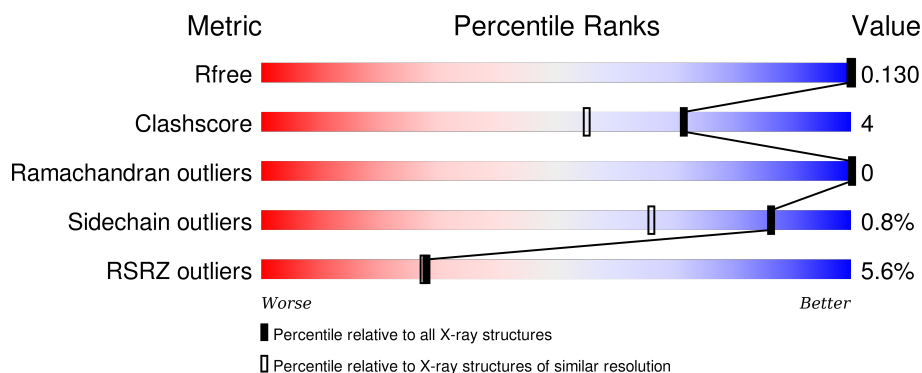
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

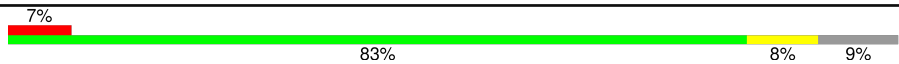
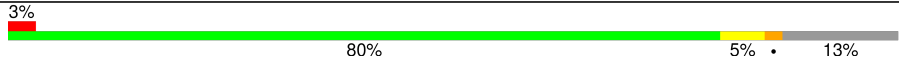

The reported resolution of this entry is 1.45 Å.

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	1278 (1.48-1.44)
Clashscore	102246	1336 (1.48-1.44)
Ramachandran outliers	100387	1320 (1.48-1.44)
Sidechain outliers	100360	1320 (1.48-1.44)
RSRZ outliers	91569	1279 (1.48-1.44)

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  $\geq 3$ , 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	367	
2	B	519	
3	C	5	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	CL	B	603	-	-	-	X
5	EDO	A	404	-	-	-	X
5	EDO	B	607	-	-	-	X

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 7369 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 CaaX farnesyltransferase alpha subunit Ram2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	335	Total	C	N	O	S	0	17	0
			2861	1821	501	529	10			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	INITIATING METHIONINE	UNP Q4WP27
A	-12	GLY	-	EXPRESSION TAG	UNP Q4WP27
A	-11	SER	-	EXPRESSION TAG	UNP Q4WP27
A	-10	SER	-	EXPRESSION TAG	UNP Q4WP27
A	-9	HIS	-	EXPRESSION TAG	UNP Q4WP27
A	-8	HIS	-	EXPRESSION TAG	UNP Q4WP27
A	-7	HIS	-	EXPRESSION TAG	UNP Q4WP27
A	-6	HIS	-	EXPRESSION TAG	UNP Q4WP27
A	-5	HIS	-	EXPRESSION TAG	UNP Q4WP27
A	-4	HIS	-	EXPRESSION TAG	UNP Q4WP27
A	-3	SER	-	EXPRESSION TAG	UNP Q4WP27
A	-2	GLN	-	EXPRESSION TAG	UNP Q4WP27
A	-1	ASP	-	EXPRESSION TAG	UNP Q4WP27
A	0	PRO	-	EXPRESSION TAG	UNP Q4WP27
A	146	SER	ASN	ENGINEERED MUTATION	UNP Q4WP27

- Molecule 2 is a protein called CaaX farnesyltransferase beta subunit Ram1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	452	Total	C	N	O	S	0	21	0
			3628	2303	613	687	25			

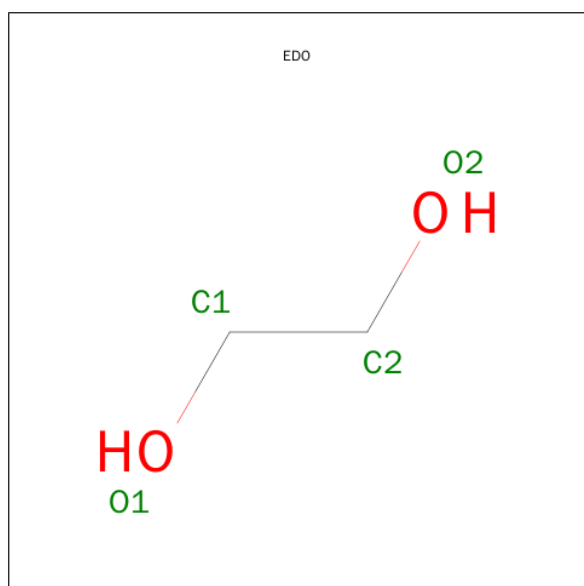
- Molecule 3 is a protein called LYS-CYS-VAL-VAL-MET (CAAX peptide).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	5	Total	C	N	O	S	0	5	0
			38	24	6	6	2			

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

*Continued on next page...*

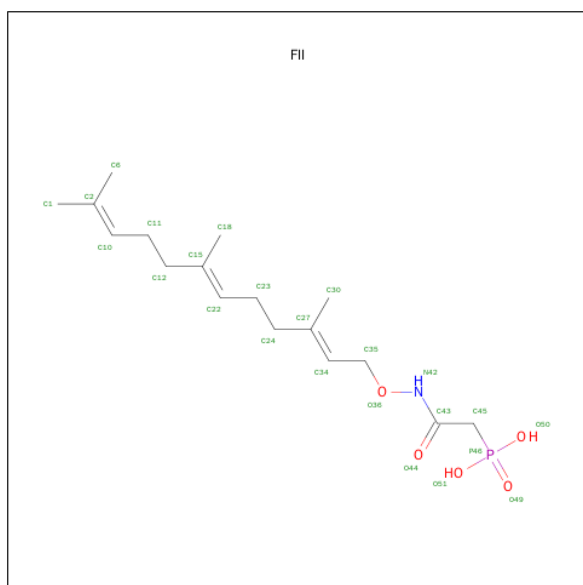
*Continued from previous page...*

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Zn	0	0
			1	1		

- Molecule 7 is [(3,7,11-TRIMETHYL-DODECA-2,6,10-TRIENYLOXYCARBAMOYL)-METHYL]-PHOSPHONIC ACID (three-letter code: FII) (formula: C<sub>17</sub>H<sub>30</sub>NO<sub>5</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	B	1	Total	C	N	O	P	0	0
			24	17	1	5	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	349	Total	O	0	0
			349	349		
8	B	420	Total	O	0	0
			420	420		

*Continued on next page...*

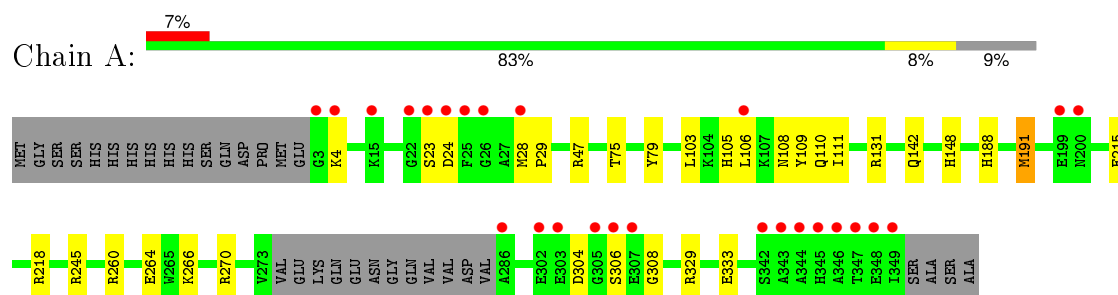
*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	C	9	Total	O	0	0
			9	9		

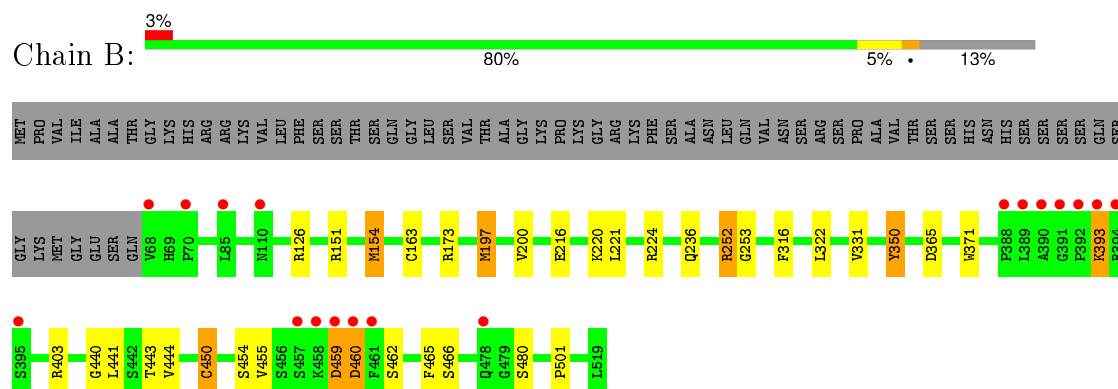
### 3 Residue-property plots [i](#)

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.

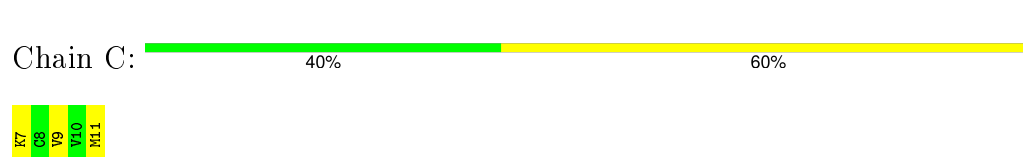
- Molecule 1: CaaX farnesyltransferase alpha subunit Ram2



- Molecule 2: CaaX farnesyltransferase beta subunit Ram1



- Molecule 3: LYS-CYS-VAL-VAL-MET (CAAX peptide)



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	63.24Å 90.33Å 83.01Å 90.00° 111.01° 90.00°	Depositor
Resolution (Å)	22.42 – 1.45 22.42 – 1.45	Depositor EDS
% Data completeness (in resolution range)	98.9 (22.42-1.45) 93.7 (22.42-1.45)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.19 (at 1.44Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, $R_{free}$	0.125 , 0.152 0.128 , 0.130	Depositor DCC
$R_{free}$ test set	7550 reflections (5.49%)	DCC
Wilson B-factor (Å <sup>2</sup> )	12.8	Xtriage
Anisotropy	0.374	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 53.0	EDS
Estimated twinning fraction	0.016 for h,-k,-h-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 153559 reflections	Xtriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	7369	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.04% 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, 0.375 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: ZN, FII, EDO, CL

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	0.86	1/2972 (0.0%)	0.90	5/4028 (0.1%)
2	B	0.94	2/3752 (0.1%)	0.99	14/5103 (0.3%)
3	C	0.86	0/37	1.21	0/46
All	All	0.91	3/6761 (0.0%)	0.95	19/9177 (0.2%)

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	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	450[A]	CYS	CB-SG	-8.48	1.67	1.82
2	B	450[B]	CYS	CB-SG	-8.48	1.67	1.82
1	A	79	TYR	CD1-CE1	5.08	1.47	1.39

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	224	ARG	NE-CZ-NH2	-13.58	113.51	120.30
2	B	460	ASP	CB-CG-OD1	-9.58	109.68	118.30
2	B	224	ARG	NE-CZ-NH1	8.62	124.61	120.30
2	B	126	ARG	NE-CZ-NH2	-8.17	116.21	120.30
1	A	47	ARG	NE-CZ-NH2	-7.41	116.59	120.30
2	B	350	TYR	CB-CG-CD2	-7.22	116.67	121.00
2	B	403	ARG	NE-CZ-NH2	-6.13	117.24	120.30

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	154[A]	MET	CG-SD-CE	-6.04	90.53	100.20
2	B	154[B]	MET	CG-SD-CE	-6.04	90.53	100.20
1	A	245[A]	ARG	NE-CZ-NH2	-5.97	117.32	120.30
1	A	245[B]	ARG	NE-CZ-NH2	-5.97	117.32	120.30
2	B	459	ASP	CB-CG-OD2	-5.85	113.04	118.30
1	A	131	ARG	NE-CZ-NH2	-5.82	117.39	120.30
2	B	365	ASP	CB-CG-OD1	5.75	123.48	118.30
1	A	47	ARG	NE-CZ-NH1	5.73	123.17	120.30
2	B	252	ARG	NE-CZ-NH2	-5.46	117.57	120.30
2	B	173	ARG	NE-CZ-NH2	-5.23	117.68	120.30
2	B	403	ARG	NE-CZ-NH1	5.17	122.88	120.30
2	B	460	ASP	OD1-CG-OD2	5.10	132.99	123.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	105	HIS	Mainchain
1	A	306	SER	Peptide

## 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	2861	0	2781	33	0
2	B	3628	0	3485	22	0
3	C	38	0	43	3	0
4	A	1	0	0	0	0
4	B	2	0	0	0	0
5	A	20	0	30	0	0
5	B	16	0	24	4	0
6	B	1	0	0	0	0
7	B	24	0	28	0	0
8	A	349	0	0	16	0
8	B	420	0	0	3	0
8	C	9	0	0	4	0
All	All	7369	0	6391	56	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 4.

All (56) 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:C:11[C]:MET:HB3	8:C:109:HOH:O	1.49	1.12
1:A:191:MET:SD	8:A:749:HOH:O	2.40	0.79
1:A:4:LYS:NZ	8:A:789:HOH:O	2.15	0.79
1:A:108[A]:ASN:HB3	1:A:111:ILE:HD12	1.67	0.76
1:A:215[B]:GLU:OE1	8:A:609:HOH:O	2.08	0.72
3:C:9[C]:VAL:HB	8:C:108:HOH:O	1.89	0.71
1:A:28[B]:MET:HE3	1:A:29:PRO:HD2	1.71	0.70
3:C:7[C]:LYS:N	8:C:107:HOH:O	2.23	0.70
2:B:450[B]:CYS:SG	8:B:991:HOH:O	2.47	0.70
1:A:110[A]:GLN:OE1	8:A:799:HOH:O	2.11	0.68
1:A:109[A]:TYR:HB3	1:A:148:HIS:CE1	2.30	0.67
1:A:142:GLN:NE2	8:A:822:HOH:O	2.30	0.65
8:A:750:HOH:O	2:B:252:ARG:NE	2.31	0.63
2:B:236:GLN:HB3	5:B:606:EDO:H12	1.80	0.62
1:A:218:ARG:NH2	8:A:657:HOH:O	2.33	0.62
1:A:333[A]:GLU:OE1	8:A:632:HOH:O	2.16	0.61
1:A:106[B]:LEU:O	8:A:771:HOH:O	2.16	0.61
1:A:304:ASP:OD1	8:A:824:HOH:O	2.17	0.60
2:B:440:GLY:O	2:B:443[A]:THR:HG22	2.03	0.58
1:A:329[A]:ARG:CZ	2:B:480:SER:HB3	2.36	0.55
1:A:106[A]:LEU:CD2	1:A:106[A]:LEU:N	2.71	0.54
1:A:108[A]:ASN:ND2	1:A:110[A]:GLN:OE1	2.41	0.54
2:B:154[B]:MET:HE1	5:B:604:EDO:H11	1.91	0.52
1:A:103:LEU:O	1:A:106[A]:LEU:HD21	2.10	0.52
1:A:260:ARG:HD3	1:A:264:GLU:OE2	2.09	0.52
1:A:106[A]:LEU:HD23	8:A:717:HOH:O	2.10	0.52
1:A:308:GLY:HA2	8:A:769:HOH:O	2.11	0.49
2:B:216:GLU:HG2	2:B:220:LYS:HD3	1.94	0.49
1:A:109[B]:TYR:CE2	8:A:750:HOH:O	2.64	0.49
2:B:200:VAL:HG21	2:B:253:GLY:HA2	1.96	0.47
1:A:188:HIS:CE1	1:A:191:MET:HE1	2.49	0.46
2:B:393:LYS:HD3	2:B:393:LYS:HA	1.48	0.46
1:A:106[B]:LEU:HD12	8:A:780:HOH:O	2.14	0.46
1:A:148:HIS:HE1	8:C:108:HOH:O	1.99	0.46
1:A:108[A]:ASN:CB	1:A:111:ILE:HD12	2.42	0.45
2:B:350:TYR:CG	5:B:605:EDO:H12	2.51	0.45
1:A:106[B]:LEU:HD22	8:A:717:HOH:O	2.16	0.45

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109[A]:TYR:HB3	1:A:148:HIS:ND1	2.31	0.44
1:A:106[A]:LEU:N	1:A:106[A]:LEU:HD22	2.30	0.44
2:B:154[B]:MET:CE	5:B:604:EDO:H11	2.47	0.44
2:B:151:ARG:HB3	8:B:1088:HOH:O	2.18	0.44
1:A:266:LYS:O	1:A:270:ARG:HG3	2.18	0.44
1:A:23:SER:OG	1:A:23:SER:O	2.34	0.43
2:B:454:SER:HB2	2:B:466[B]:SER:OG	2.17	0.43
2:B:163[B]:CYS:SG	2:B:501:PRO:HG2	2.59	0.43
1:A:110[A]:GLN:CD	8:A:799:HOH:O	2.55	0.43
2:B:163[B]:CYS:SG	2:B:501:PRO:CG	3.07	0.42
1:A:23:SER:O	1:A:24:ASP:HB2	2.19	0.42
2:B:322:LEU:O	2:B:331[B]:VAL:HG21	2.20	0.42
1:A:75:THR:HG23	2:B:197:MET:HE3	2.02	0.41
2:B:154[B]:MET:HE3	8:B:734:HOH:O	2.19	0.41
2:B:455:VAL:HG22	2:B:465:PHE:HB3	2.01	0.41
1:A:106[A]:LEU:H	1:A:106[A]:LEU:HD23	1.84	0.41
2:B:441:LEU:O	2:B:444:VAL:HG22	2.21	0.41
2:B:459:ASP:HA	2:B:462[B]:SER:OG	2.21	0.40
2:B:316:PHE:HB2	2:B:371:TRP:O	2.22	0.40

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	348/367 (95%)	339 (97%)	9 (3%)	0	100	100
2	B	471/519 (91%)	465 (99%)	6 (1%)	0	100	100
3	C	3/5 (60%)	3 (100%)	0	0	100	100
All	All	822/891 (92%)	807 (98%)	15 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	304/315 (96%)	303 (100%)	1 (0%)	94	84
2	B	393/428 (92%)	389 (99%)	4 (1%)	82	56
3	C	5/5 (100%)	5 (100%)	0	100	100
All	All	702/748 (94%)	697 (99%)	5 (1%)	86	69

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	191	MET
2	B	197	MET
2	B	221	LEU
2	B	393	LYS
2	B	460	ASP

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

Mol	Chain	Res	Type
1	A	148	HIS
2	B	236	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 carbohydrates in this entry.

## 5.6 Ligand geometry

Of 14 ligands modelled in this entry, 4 are monoatomic - leaving 10 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$
5	EDO	A	402	-	3,3,3	0.57	0	2,2,2	0.50	0
5	EDO	A	403	-	3,3,3	0.65	0	2,2,2	0.58	0
5	EDO	A	404	-	3,3,3	0.37	0	2,2,2	0.19	0
5	EDO	A	405	-	3,3,3	0.59	0	2,2,2	0.59	0
5	EDO	A	406	-	3,3,3	0.37	0	2,2,2	0.57	0
5	EDO	B	604	-	3,3,3	0.18	0	2,2,2	0.70	0
5	EDO	B	605	-	3,3,3	0.40	0	2,2,2	0.80	0
5	EDO	B	606	-	3,3,3	0.48	0	2,2,2	0.96	0
5	EDO	B	607	-	3,3,3	0.54	0	2,2,2	0.17	0
7	FII	B	608	-	23,23,23	3.19	5 (21%)	27,29,29	2.02	7 (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
5	EDO	A	402	-	-	0/1/1/1	0/0/0/0
5	EDO	A	403	-	-	0/1/1/1	0/0/0/0
5	EDO	A	404	-	-	0/1/1/1	0/0/0/0
5	EDO	A	405	-	-	0/1/1/1	0/0/0/0
5	EDO	A	406	-	-	0/1/1/1	0/0/0/0
5	EDO	B	604	-	-	0/1/1/1	0/0/0/0
5	EDO	B	605	-	-	0/1/1/1	0/0/0/0
5	EDO	B	606	-	-	0/1/1/1	0/0/0/0
5	EDO	B	607	-	-	0/1/1/1	0/0/0/0
7	FII	B	608	-	-	0/23/24/24	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	608	FII	C10-C2	5.06	1.47	1.32
7	B	608	FII	P46-C45	5.20	1.87	1.79
7	B	608	FII	C43-N42	5.24	1.40	1.33
7	B	608	FII	C34-C27	7.97	1.48	1.33
7	B	608	FII	C22-C15	8.69	1.50	1.33

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	608	FII	C23-C22-C15	-6.12	114.45	127.76
7	B	608	FII	O36-N42-C43	-4.20	112.41	118.39
7	B	608	FII	C24-C27-C34	-3.34	114.72	121.05
7	B	608	FII	C12-C15-C22	-2.95	115.45	121.05
7	B	608	FII	O51-P46-C45	-2.43	101.66	107.01
7	B	608	FII	O49-P46-C45	-2.03	105.92	110.92
7	B	608	FII	C18-C15-C12	2.62	119.41	115.41

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	604	EDO	2	0
5	B	605	EDO	1	0
5	B	606	EDO	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, 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	335/367 (91%)	0.12	26 (7%) 16 16	3, 14, 37, 54	0
2	B	452/519 (87%)	-0.19	18 (3%) 42 42	3, 9, 25, 39	0
3	C	5/5 (100%)	0.92	0 100 100	10, 11, 15, 27	5 (100%)
All	All	792/891 (88%)	-0.06	44 (5%) 28 27	3, 11, 30, 54	5 (0%)

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	25	PHE	17.7
2	B	390	ALA	10.6
1	A	24	ASP	10.1
2	B	392	PRO	9.8
2	B	391	GLY	8.8
1	A	307	GLU	8.4
2	B	393	LYS	7.8
1	A	305	GLY	7.4
2	B	460	ASP	7.4
2	B	389	LEU	7.1
2	B	459	ASP	6.7
1	A	23	SER	6.3
2	B	395	SER	5.2
2	B	68	VAL	5.1
1	A	26	GLY	5.0
1	A	345	HIS	5.0
2	B	394	ARG	4.4
1	A	348	GLU	4.3
2	B	388	PRO	4.1
1	A	106[A]	LEU	4.0
1	A	200	ASN	4.0
1	A	4	LYS	3.9
1	A	346	ALA	3.9

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	22	GLY	3.8
1	A	347	THR	3.7
1	A	303	GLU	3.7
2	B	457	SER	3.5
1	A	286	ALA	3.3
1	A	306	SER	3.3
1	A	3	GLY	3.3
2	B	85	LEU	3.2
1	A	342	SER	3.0
1	A	199	GLU	2.9
2	B	70	PRO	2.8
1	A	349	ILE	2.8
2	B	478	GLN	2.8
1	A	302	GLU	2.7
2	B	458	LYS	2.7
2	B	110	ASN	2.6
2	B	461	PHE	2.5
1	A	343	ALA	2.5
1	A	15	LYS	2.4
1	A	28[A]	MET	2.3
1	A	344	ALA	2.0

## 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 ⓘ

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, 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
5	EDO	B	607	4/4	0.87	0.16	13.38	28,28,28,32	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	CL	B	603	1/1	0.87	0.09	3.26	58,58,58,58	0
5	EDO	A	404	4/4	0.96	0.11	2.34	20,22,22,22	0
5	EDO	A	405	4/4	0.95	0.08	0.93	22,22,22,23	0
5	EDO	A	403	4/4	0.97	0.07	-0.06	14,15,16,17	0
5	EDO	B	604	4/4	0.97	0.06	-0.21	14,16,17,18	0
7	FII	B	608	24/24	0.98	0.06	-0.22	4,10,14,17	0
4	CL	B	602	1/1	1.00	0.04	-1.00	19,19,19,19	0
6	ZN	B	601	1/1	1.00	0.04	-1.36	5,5,5,5	0
4	CL	A	401	1/1	0.83	0.09	-	62,62,62,62	0
5	EDO	A	402	4/4	0.93	0.15	-	12,17,20,24	0
5	EDO	B	606	4/4	0.91	0.18	-	23,25,25,26	0
5	EDO	A	406	4/4	0.94	0.08	-	36,36,36,37	0
5	EDO	B	605	4/4	0.95	0.09	-	18,19,23,23	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.