Full wwPDB X-ray Structure Validation Report (i)

Nov 5, 2023 – 10:32 pm GMT

PDB ID	:	6HQF
Title	:	Structure of Phenylalanine ammonia-lyase from Petroselinum crispum in complex with (R)-APEP
Authors	:	Bata, Z.; Molnar, B.; Leveles, I.; Poppe, L.; Vertessy, G.B.
Deposited on	:	2018-09-24
Resolution	:	1.76 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

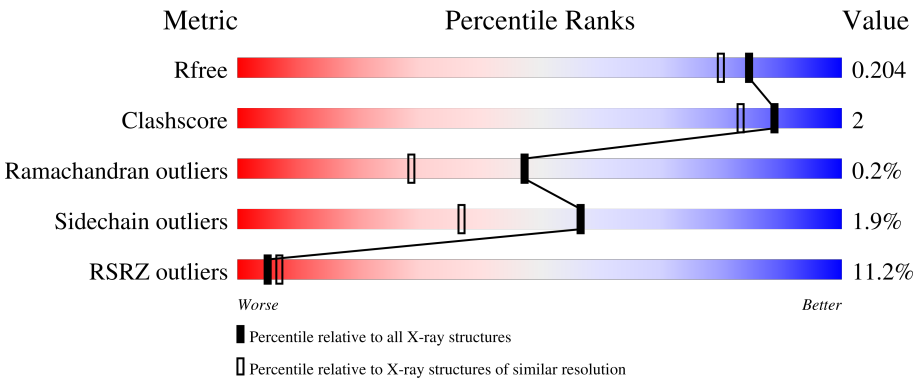
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.76 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}	130704	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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 <=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	714	9% 88% 6% 6%
1	B	714	12% 89% 5% 6%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 10955 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.

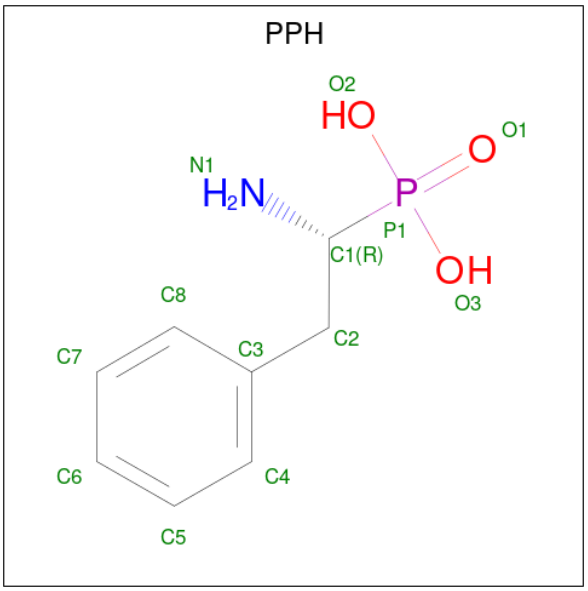
- Molecule 1 is a protein called Phenylalanine ammonia-lyase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	673	5142	3246	884	989	23	0	4	0
1	B	673	5135	3243	880	988	24	0	2	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	MDO	ALA	chromophore	UNP P24481
A	?	MDO	SER	chromophore	UNP P24481
A	203	MDO	GLY	chromophore	UNP P24481
A	704	SER	CYS	engineered mutation	UNP P24481
A	716	SER	CYS	engineered mutation	UNP P24481
B	?	MDO	ALA	chromophore	UNP P24481
B	?	MDO	SER	chromophore	UNP P24481
B	203	MDO	GLY	chromophore	UNP P24481
B	704	SER	CYS	engineered mutation	UNP P24481
B	716	SER	CYS	engineered mutation	UNP P24481

- Molecule 2 is [(1R)-1-amino-2-phenylethyl]phosphonic acid (three-letter code: PPH) (formula: $C_8H_{12}NO_3P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	13	8	1	3	1	0	0
			Total	C	N	O	P		
2	B	1	13	8	1	3	1	0	0

- Molecule 3 is water.

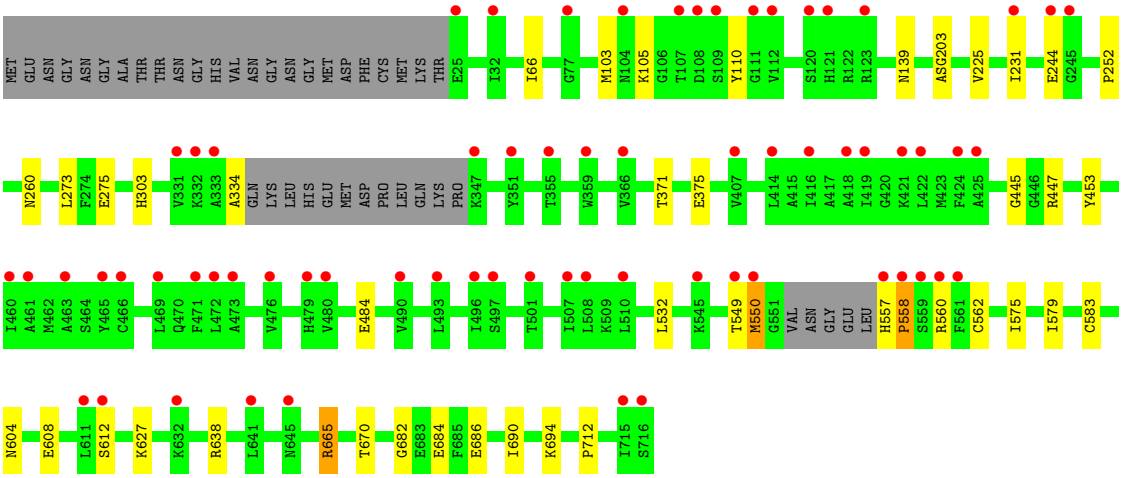
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	327	334	334	0	7
			Total	O		
3	B	310	318	318	0	8

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.

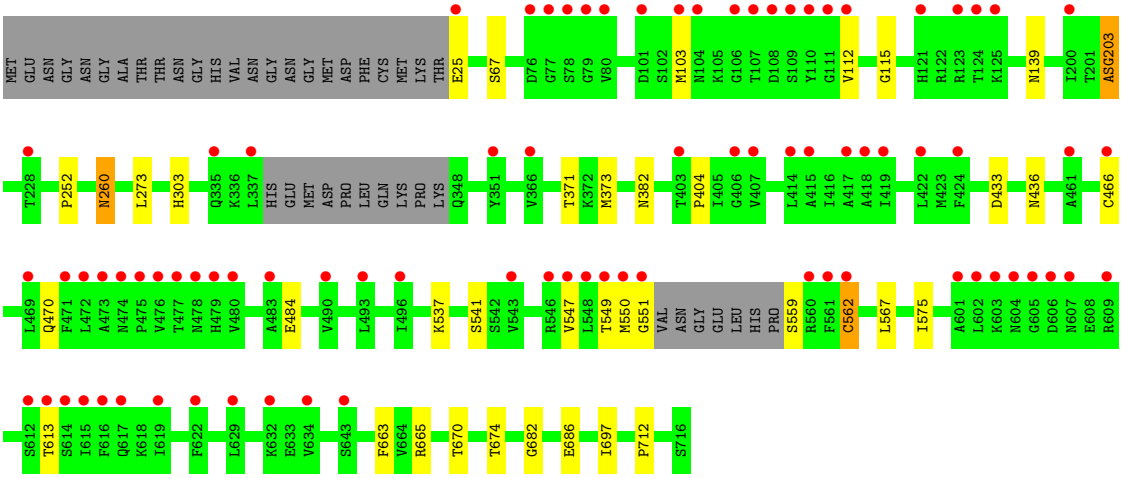
• Molecule 1: Phenylalanine ammonia-lyase 1

Chain A: 9% 88% 6% 6%



• Molecule 1: Phenylalanine ammonia-lyase 1

Chain B: 12% 89% 5% 6%



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	118.88Å 160.95Å 141.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.70 – 1.76 46.22 – 1.72	Depositor EDS
% Data completeness (in resolution range)	99.7 (38.70-1.76) 98.6 (46.22-1.72)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.95 (at 1.72Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.168 , 0.205 0.168 , 0.204	Depositor DCC
R_{free} test set	2098 reflections (1.49%)	wwPDB-VP
Wilson B-factor (Å^2)	30.8	Xtriage
Anisotropy	0.078	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 41.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	10955	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.64% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: MDO, PPH

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	0.36	0/5230	0.52	0/7078
1	B	0.35	0/5215	0.51	0/7052
All	All	0.35	0/10445	0.52	0/14130

There are no bond length outliers.

There are no bond angle outliers.

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	5142	0	5136	21	0
1	B	5135	0	5136	16	0
2	A	13	0	10	2	0
2	B	13	0	9	1	0
3	A	334	0	0	3	0
3	B	318	0	0	0	0
All	All	10955	0	10291	38	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 2.

All (38) 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:583:CYS:HB3	1:A:627:LYS:HG2	1.83	0.60
1:B:682:GLY:O	1:B:686:GLU:HG2	2.02	0.59
1:B:112:VAL:HG13	1:B:252:PRO:HB3	1.87	0.56
1:A:447:ARG:CZ	1:A:638[B]:ARG:HD2	2.39	0.53
1:B:559:SER:HB3	1:B:562:CYS:HB2	1.94	0.49
1:A:549:THR:HG23	1:A:549:THR:O	2.13	0.49
1:B:665:ARG:HD3	1:B:670:THR:O	2.13	0.48
1:A:445:GLY:O	1:A:638[A]:ARG:NH2	2.45	0.48
1:B:663:PHE:CE2	1:B:697:ILE:HD13	2.49	0.48
1:A:334:ALA:HA	3:A:912:HOH:O	2.15	0.47
1:A:66:ILE:HG23	1:A:375:GLU:HG2	1.96	0.47
1:A:682:GLY:O	1:A:686:GLU:HG2	2.14	0.46
1:B:273:LEU:HD13	1:B:371:THR:HA	1.97	0.46
1:B:103:MET:HG3	1:B:252:PRO:HG2	1.98	0.46
1:A:558:PRO:HD2	3:A:1205:HOH:O	2.16	0.45
1:A:103:MET:HG3	1:A:252:PRO:HG2	1.97	0.45
1:B:373:MET:HG2	1:B:404:PRO:HB3	1.99	0.45
1:B:466:CYS:O	1:B:470:GLN:HG2	2.17	0.45
1:A:604:ASN:HB3	1:A:608:GLU:HB2	1.99	0.44
1:A:690:ILE:HG22	1:A:694:LYS:HE2	1.98	0.44
2:A:801:PPH:H7	2:A:801:PPH:H2	1.65	0.44
1:A:453:TYR:OH	1:B:115:GLY:HA2	2.18	0.44
1:B:537:LYS:HG3	1:B:567:LEU:HD22	1.99	0.43
1:A:670:THR:HG23	1:A:684:GLU:HB3	2.00	0.43
1:A:225:VAL:HG22	1:A:231:ILE:HD13	2.01	0.43
1:A:303:HIS:CE1	1:A:712:PRO:HG3	2.54	0.43
1:B:551:GLY:HA3	1:B:613:THR:HA	2.01	0.43
1:A:110:TYR:OH	2:A:801:PPH:O2	2.31	0.42
1:A:273:LEU:HD13	1:A:371:THR:HA	2.02	0.42
1:B:203:MDO:O2	1:B:260:ASN:ND2	2.52	0.42
2:B:801:PPH:H2	2:B:801:PPH:H11	1.64	0.41
1:A:275:GLU:OE2	3:A:901:HOH:O	2.22	0.41
1:B:433:ASP:HA	1:B:436:ASN:OD1	2.21	0.41
1:A:550:MET:O	1:A:557:HIS:HA	2.21	0.40
1:B:303:HIS:CE1	1:B:712:PRO:HG3	2.57	0.40
1:A:532:LEU:HD13	1:A:579:ILE:HG12	2.04	0.40
1:A:665:ARG:HA	1:A:665:ARG:HD3	1.95	0.40
1:B:541:SER:HB2	1:B:567:LEU:HD21	2.03	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	668/714 (94%)	658 (98%)	8 (1%)	2 (0%)	41	22
1	B	666/714 (93%)	654 (98%)	11 (2%)	1 (0%)	47	29
All	All	1334/1428 (93%)	1312 (98%)	19 (1%)	3 (0%)	47	29

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	558	PRO
1	A	550	MET
1	B	550	MET

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	552/591 (93%)	542 (98%)	10 (2%)	59	40
1	B	550/591 (93%)	539 (98%)	11 (2%)	55	34
All	All	1102/1182 (93%)	1081 (98%)	21 (2%)	57	37

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	105	LYS
1	A	139	ASN
1	A	244	GLU

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Mol	Chain	Res	Type
1	A	260	ASN
1	A	484	GLU
1	A	560	ARG
1	A	562	CYS
1	A	575	ILE
1	A	612	SER
1	A	665	ARG
1	B	25	GLU
1	B	67	SER
1	B	139	ASN
1	B	260	ASN
1	B	382	ASN
1	B	484	GLU
1	B	547	VAL
1	B	549	THR
1	B	562	CYS
1	B	575	ILE
1	B	674	THR

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

Mol	Chain	Res	Type
1	A	260	ASN
1	B	260	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)

2 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	MDO	B	203	1,2	12,13,14	1.88	5 (41%)	15,18,20	3.87	10 (66%)
1	MDO	A	203	1,2	12,13,14	2.03	4 (33%)	15,18,20	3.48	9 (60%)

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
1	MDO	B	203	1,2	-	1/4/23/24	0/1/1/1
1	MDO	A	203	1,2	-	1/4/23/24	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	203	MDO	CA3-N3	-3.91	1.39	1.47
1	A	203	MDO	CA2-C2	3.42	1.50	1.43
1	B	203	MDO	CA2-C2	2.97	1.49	1.43
1	B	203	MDO	CA2-N2	-2.95	1.33	1.39
1	B	203	MDO	O2-C2	-2.86	1.17	1.23
1	A	203	MDO	O2-C2	-2.85	1.17	1.23
1	B	203	MDO	CA3-N3	-2.59	1.42	1.47
1	A	203	MDO	CB-CA1	-2.28	1.44	1.52
1	B	203	MDO	C2-N3	-2.15	1.34	1.39

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	203	MDO	CA3-N3-C1	8.32	137.15	127.16
1	A	203	MDO	CA3-N3-C1	7.43	136.09	127.16
1	B	203	MDO	CA2-C2-N3	6.46	106.43	103.37
1	A	203	MDO	O2-C2-CA2	-5.85	127.67	130.96
1	B	203	MDO	O2-C2-CA2	-5.75	127.73	130.96
1	A	203	MDO	C2-CA2-N2	-4.83	105.55	108.93
1	A	203	MDO	CA2-C2-N3	4.59	105.54	103.37
1	B	203	MDO	O3-C3-CA3	-3.88	114.69	126.39
1	B	203	MDO	C2-N3-C1	-3.57	106.16	107.97
1	B	203	MDO	C2-CA2-N2	-3.49	106.49	108.93
1	A	203	MDO	CA3-N3-C2	-3.42	115.94	123.80
1	B	203	MDO	CA3-N3-C2	-3.31	116.21	123.80
1	A	203	MDO	O3-C3-CA3	-3.28	116.49	126.39
1	A	203	MDO	N3-C1-N2	3.21	113.68	111.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	203	MDO	CA1-C1-N2	-3.20	119.95	124.05
1	B	203	MDO	CA2-N2-C1	2.56	107.71	105.40
1	A	203	MDO	CA1-C1-N2	-2.49	120.86	124.05
1	B	203	MDO	N3-C1-N2	2.38	113.11	111.45
1	A	203	MDO	CA2-N2-C1	2.26	107.44	105.40

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	203	MDO	N3-C1-CA1-CB
1	B	203	MDO	N3-C1-CA1-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	203	MDO	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

2 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	PPH	A	801	1	13,13,13	1.18	2 (15%)	14,18,18	0.76	0
2	PPH	B	801	1	13,13,13	1.20	3 (23%)	14,18,18	0.89	0

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	PPH	A	801	1	-	4/9/10/10	0/1/1/1
2	PPH	B	801	1	-	4/9/10/10	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	PPH	P1-C1	2.51	1.86	1.84
2	B	801	PPH	P1-C1	2.39	1.86	1.84
2	B	801	PPH	P1-O2	-2.35	1.51	1.54
2	A	801	PPH	P1-O2	-2.29	1.51	1.54
2	B	801	PPH	P1-O3	-2.29	1.51	1.54

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	PPH	P1-C1-C2-C3
2	B	801	PPH	P1-C1-C2-C3
2	A	801	PPH	N1-C1-C2-C3
2	B	801	PPH	N1-C1-C2-C3
2	A	801	PPH	C1-C2-C3-C4
2	B	801	PPH	C1-C2-C3-C8
2	A	801	PPH	C1-C2-C3-C8
2	B	801	PPH	C1-C2-C3-C4

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	PPH	2	0
2	B	801	PPH	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	672/714 (94%)	0.50	67 (9%) 7 9	22, 32, 58, 102	0
1	B	672/714 (94%)	0.62	83 (12%) 4 5	22, 33, 58, 100	0
All	All	1344/1428 (94%)	0.56	150 (11%) 5 7	22, 33, 58, 102	0

All (150) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	561	PHE	7.4
1	B	107	THR	6.9
1	A	550	MET	6.7
1	B	549	THR	6.3
1	A	558	PRO	5.3
1	B	335	GLN	5.3
1	A	331	VAL	5.3
1	B	615	ILE	5.3
1	A	245	GLY	5.0
1	B	480	VAL	4.9
1	A	549	THR	4.8
1	A	471	PHE	4.7
1	A	472	LEU	4.7
1	A	424	PHE	4.5
1	A	107	THR	4.5
1	B	550	MET	4.5
1	A	469	LEU	4.4
1	A	716	SER	4.4
1	B	414	LEU	4.4
1	A	611	LEU	4.3
1	B	493	LEU	4.2
1	A	104	ASN	4.2
1	B	609	ARG	4.2
1	A	473	ALA	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	332	LYS	4.1
1	A	466	CYS	4.0
1	A	557	HIS	4.0
1	A	561	PHE	4.0
1	B	476	VAL	4.0
1	B	108	ASP	3.9
1	A	112	VAL	3.8
1	B	622	PHE	3.7
1	B	601	ALA	3.6
1	A	715	ILE	3.6
1	B	103	MET	3.5
1	A	418	ALA	3.5
1	B	471	PHE	3.4
1	A	414	LEU	3.4
1	B	607	ASN	3.4
1	B	25	GLU	3.3
1	B	490	VAL	3.3
1	B	616	PHE	3.3
1	B	417	ALA	3.2
1	A	333	ALA	3.2
1	B	337	LEU	3.2
1	B	562	CYS	3.2
1	B	109	SER	3.2
1	B	125	LYS	3.2
1	A	645	ASN	3.2
1	B	546	ARG	3.2
1	B	104	ASN	3.1
1	B	79	GLY	3.1
1	B	77	GLY	3.1
1	B	473	ALA	3.0
1	B	619	ILE	3.0
1	A	560	ARG	3.0
1	A	416	ILE	3.0
1	B	496	ILE	3.0
1	B	613	THR	3.0
1	A	422	LEU	3.0
1	A	419	ILE	2.9
1	B	106	GLY	2.9
1	B	634	VAL	2.9
1	A	109	SER	2.9
1	A	490	VAL	2.9
1	A	507	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	612	SER	2.8
1	B	643	SER	2.8
1	B	475	PRO	2.8
1	A	476	VAL	2.8
1	A	407	VAL	2.7
1	B	560	ARG	2.7
1	B	469	LEU	2.7
1	B	543	VAL	2.7
1	A	612	SER	2.7
1	B	78	SER	2.7
1	A	108	ASP	2.7
1	B	424	PHE	2.7
1	B	422	LEU	2.6
1	B	602	LEU	2.6
1	B	112	VAL	2.6
1	B	366	VAL	2.6
1	B	466	CYS	2.6
1	A	425	ALA	2.6
1	B	121	HIS	2.6
1	A	493	LEU	2.6
1	B	472	LEU	2.6
1	B	351	TYR	2.6
1	A	347	LYS	2.6
1	B	418	ALA	2.6
1	B	629	LEU	2.5
1	B	110	TYR	2.5
1	B	477	THR	2.5
1	A	632	LYS	2.5
1	B	76	ASP	2.5
1	A	25	GLU	2.5
1	B	603	LYS	2.5
1	A	32	ILE	2.5
1	B	547	VAL	2.5
1	A	123	ARG	2.4
1	B	415	ALA	2.4
1	A	463	ALA	2.4
1	B	478	ASN	2.4
1	B	200	ILE	2.4
1	A	121	HIS	2.4
1	A	244	GLU	2.4
1	A	355	THR	2.4
1	B	80	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	508	LEU	2.3
1	B	123	ARG	2.3
1	B	479	HIS	2.3
1	A	501	THR	2.3
1	B	614	SER	2.3
1	A	120	SER	2.3
1	A	231	ILE	2.3
1	A	479	HIS	2.3
1	B	419	ILE	2.3
1	B	604	ASN	2.3
1	A	421	LYS	2.3
1	B	111	GLY	2.3
1	B	124	THR	2.3
1	B	605	GLY	2.2
1	B	407	VAL	2.2
1	A	111	GLY	2.2
1	B	406	GLY	2.2
1	B	617	GLN	2.2
1	A	77	GLY	2.2
1	B	403	THR	2.2
1	A	496	ILE	2.2
1	A	359	TRP	2.2
1	A	497	SER	2.1
1	A	510	LEU	2.1
1	A	641	LEU	2.1
1	A	351	TYR	2.1
1	A	545	LYS	2.1
1	A	366	VAL	2.1
1	A	460	ILE	2.1
1	B	606	ASP	2.1
1	B	483	ALA	2.1
1	B	474	ASN	2.1
1	A	559	SER	2.1
1	B	228	THR	2.0
1	A	480	VAL	2.0
1	B	548	LEU	2.0
1	B	632	LYS	2.0
1	B	551	GLY	2.0
1	A	461	ALA	2.0
1	B	461	ALA	2.0
1	A	465	TYR	2.0
1	B	101	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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
1	MDO	B	203	13/14	0.92	0.12	20,24,31,34	0
1	MDO	A	203	13/14	0.93	0.12	22,24,32,34	0

6.3 Carbohydrates (i)

There are no monosaccharides 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	PPH	A	801	13/13	0.96	0.08	23,28,33,35	0
2	PPH	B	801	13/13	0.97	0.09	25,30,35,36	0

6.5 Other polymers (i)

There are no such residues in this entry.