



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:46 AM GMT

PDB ID : 2SFP
Title : ALANINE RACEMASE WITH BOUND PROPIONATE INHIBITOR
Authors : Morollo, A.A.; Petsko, G.A.; Ringe, D.
Deposited on : 1999-02-16
Resolution : 1.90 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
<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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

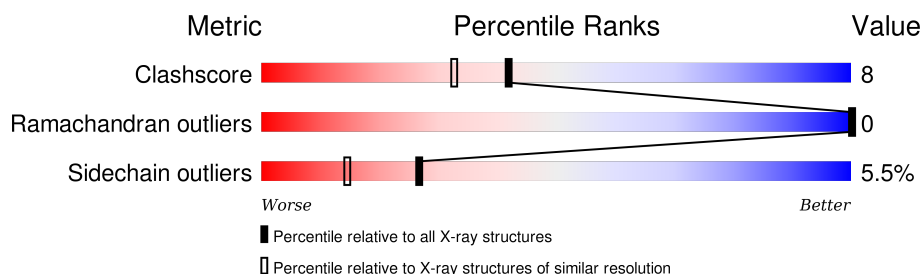
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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))
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	388	 78% 18% ..
1	B	388	 81% 15% ..

2 Entry composition [i](#)

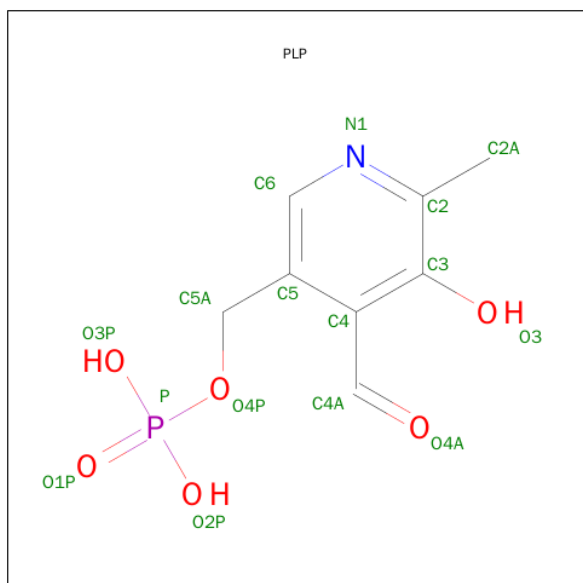
There are 4 unique types of molecules in this entry. The entry contains 6279 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PROTEIN (ALANINE RACEMASE).

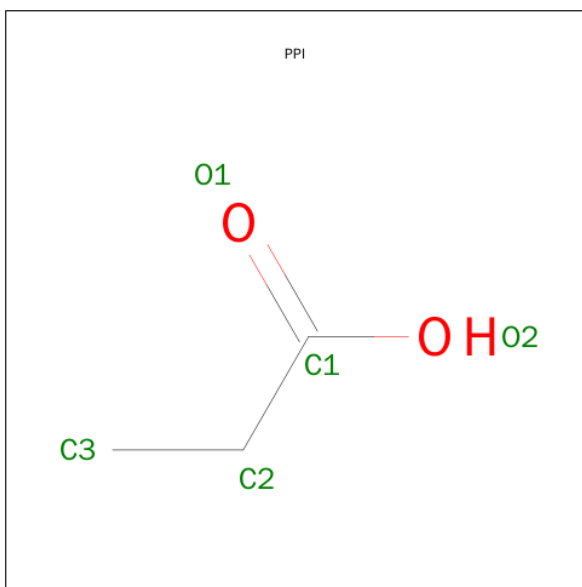
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	379	Total	C	N	O	S	0	0	0
			3016	1932	534	537	13			
1	B	379	Total	C	N	O	S	0	0	0
			3016	1932	534	537	13			

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: $C_8H_{10}NO_6P$).



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		

- Molecule 3 is PROPANOIC ACID (three-letter code: PPI) (formula: $C_3H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			5	3	2		
3	A	1	Total	C	O	0	0
			5	3	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	102	Total	O	0	0
			102	102		
4	B	105	Total	O	0	0
			105	105		

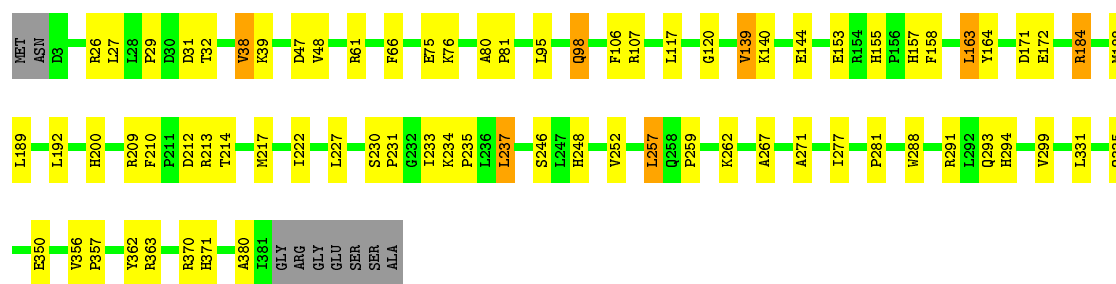
3 Residue-property plots

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.


Note EDS was not executed.

• Molecule 1: PROTEIN (ALANINE RACEMASE)

Chain A: 



• Molecule 1: PROTEIN (ALANINE RACEMASE)

Chain B: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	98.70 Å 90.00 Å 85.20 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.90	Depositor
% Data completeness (in resolution range)	82.9 (10.00-1.90)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.205 , 0.259	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6279	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PPI, KCX, PLP

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	0.34	0/3081	0.62	0/4188
1	B	0.35	0/3081	0.62	0/4188
All	All	0.35	0/6162	0.62	0/8376

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

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	3016	0	3002	63	0
1	B	3016	0	3003	45	0
2	A	15	0	7	0	0
2	B	15	0	7	0	0
3	A	5	0	5	0	0
3	B	5	0	5	0	0
4	A	102	0	0	0	0
4	B	105	0	0	1	0
All	All	6279	0	6029	101	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 8.

All (101) 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:231:PRO:HA	1:A:234:LYS:HE3	1.50	0.90
1:B:169:THR:HB	1:B:172:GLU:HG3	1.55	0.87
1:B:163:LEU:HD13	1:B:192:LEU:HD11	1.57	0.86
1:A:163:LEU:HD13	1:A:192:LEU:HD11	1.61	0.81
1:B:129:KCX:OQ1	1:B:136:ARG:HB3	1.83	0.78
1:A:48:VAL:HG11	1:A:76:LYS:CB	2.15	0.76
1:A:155:HIS:HD2	1:A:157:HIS:H	1.33	0.76
1:B:97:ALA:HB2	1:B:124:ILE:HG12	1.68	0.75
1:B:142:GLU:CG	1:B:146:LYS:HE3	2.19	0.72
1:A:38:VAL:HG13	1:A:38:VAL:O	1.91	0.71
1:A:48:VAL:HG11	1:A:76:LYS:HB3	1.74	0.70
1:A:61:ARG:HG2	1:A:81:PRO:HG2	1.73	0.70
1:A:230:SER:O	1:A:233:ILE:HG22	1.92	0.69
1:B:171:ASP:HB2	1:B:230:SER:HB3	1.75	0.67
1:B:155:HIS:HD2	1:B:157:HIS:H	1.42	0.67
1:B:163:LEU:HD11	1:B:189:LEU:CD2	2.26	0.66
1:A:246:SER:OG	1:A:248:HIS:HE1	1.78	0.65
1:A:293:GLN:O	1:A:294:HIS:HB2	1.96	0.65
1:A:231:PRO:HA	1:A:234:LYS:CE	2.25	0.64
1:A:38:VAL:O	1:A:38:VAL:CG1	2.46	0.62
1:A:163:LEU:HD11	1:A:189:LEU:HD23	1.81	0.62
1:A:350:GLU:HB2	1:B:291:ARG:NH2	2.16	0.60
1:B:98:GLN:HG3	1:B:122:PHE:CE2	2.38	0.59
1:B:163:LEU:HD11	1:B:189:LEU:HD23	1.86	0.57
1:A:262:LYS:HD3	1:A:267:ALA:HB1	1.86	0.57
1:A:184:ARG:O	1:A:188:MET:HG3	2.03	0.57
1:A:39:LYS:HE3	1:B:313:ASP:OD2	2.04	0.56
1:A:48:VAL:HG11	1:A:76:LYS:HB2	1.87	0.56
1:B:142:GLU:HG2	1:B:146:LYS:HE3	1.86	0.56
1:A:299:VAL:O	1:A:299:VAL:HG13	2.04	0.56
1:A:291:ARG:NH2	1:B:349:LEU:O	2.40	0.55
1:A:48:VAL:CG1	1:A:76:LYS:HD3	2.36	0.55
1:A:350:GLU:HB2	1:B:291:ARG:HH22	1.71	0.55
1:B:209:ARG:HG3	1:B:233:ILE:HD11	1.90	0.54
1:A:293:GLN:O	1:A:294:HIS:CB	2.56	0.54
1:A:155:HIS:CD2	1:A:157:HIS:H	2.21	0.54
1:A:234:LYS:HA	1:A:237:LEU:HD22	1.89	0.54
1:B:291:ARG:HH11	1:B:291:ARG:HB2	1.73	0.53
1:A:246:SER:OG	1:A:248:HIS:CE1	2.61	0.53
1:A:66:PHE:HZ	1:B:363:ARG:HG2	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:291:ARG:HB2	1:B:291:ARG:NH1	2.24	0.52
1:A:288:TRP:CE2	1:A:331:LEU:HD23	2.45	0.52
1:A:370:ARG:O	1:A:371:HIS:HB2	2.10	0.51
1:B:299:VAL:HG13	1:B:299:VAL:O	2.11	0.51
1:B:118:TYR:OH	1:B:122:PHE:O	2.20	0.49
1:A:233:ILE:O	1:A:237:LEU:HD13	2.13	0.49
1:B:26:ARG:HG3	1:B:26:ARG:HH11	1.77	0.49
1:A:209:ARG:HG3	1:A:233:ILE:HD11	1.95	0.49
1:B:142:GLU:HG3	1:B:146:LYS:HE3	1.93	0.49
1:A:29:PRO:HG2	1:A:32:THR:OG1	2.13	0.48
1:A:80:ALA:HB1	1:A:81:PRO:HD2	1.95	0.48
1:A:29:PRO:HB2	1:A:31:ASP:OD2	2.14	0.47
1:A:363:ARG:HG2	1:B:66:PHE:HZ	1.80	0.47
1:A:106:PHE:CD2	1:A:107:ARG:HG3	2.50	0.47
1:B:299:VAL:O	1:B:299:VAL:CG1	2.62	0.47
1:A:200:HIS:HB3	1:A:217:MET:HB3	1.96	0.47
1:B:239:TYR:HB2	1:B:240:PRO:HD2	1.97	0.47
1:B:220:PHE:CE1	1:B:223:ALA:HB3	2.50	0.47
1:B:142:GLU:HG2	1:B:146:LYS:CE	2.43	0.47
1:A:98:GLN:HB3	1:A:98:GLN:HE21	1.49	0.46
1:A:231:PRO:CA	1:A:234:LYS:HE3	2.34	0.46
1:A:164:TYR:HB2	1:A:200:HIS:O	2.15	0.46
1:B:142:GLU:HG2	1:B:146:LYS:NZ	2.30	0.46
1:A:163:LEU:HD11	1:A:189:LEU:CD2	2.44	0.45
1:A:231:PRO:HB3	1:A:234:LYS:NZ	2.31	0.45
1:B:230:SER:O	1:B:233:ILE:HG22	2.16	0.45
1:A:48:VAL:HG13	1:A:76:LYS:HD3	1.98	0.45
1:B:139:VAL:HG23	1:B:144:GLU:HG2	1.98	0.45
1:A:331:LEU:HD12	1:A:331:LEU:N	2.31	0.45
1:A:120:GLY:HA3	1:A:157:HIS:CE1	2.52	0.44
1:A:362:TYR:OH	1:B:41:ASN:HB2	2.17	0.44
1:A:222:ILE:HG13	1:A:227:LEU:HB2	2.00	0.44
1:B:306:ILE:HA	1:B:317:ILE:HG22	1.98	0.44
1:A:234:LYS:N	1:A:235:PRO:HD2	2.32	0.44
1:B:3:ASP:N	1:B:3:ASP:OD1	2.51	0.43
1:A:252:VAL:HG11	1:A:281:PRO:HG3	2.00	0.43
1:B:182:TYR:CE2	1:B:186:LEU:HD11	2.53	0.43
1:A:288:TRP:CZ2	1:A:331:LEU:HD23	2.54	0.43
1:A:200:HIS:N	1:A:200:HIS:CD2	2.87	0.43
1:A:362:TYR:O	1:A:380:ALA:HB3	2.18	0.43
1:B:106:PHE:CD2	1:B:107:ARG:HG3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:262:LYS:HA	1:B:269:TYR:O	2.19	0.42
1:A:155:HIS:HB3	1:A:158:PHE:HB2	2.00	0.42
1:A:139:VAL:CG2	1:A:144:GLU:HB3	2.50	0.42
1:B:237:LEU:HD12	1:B:237:LEU:HA	1.93	0.42
1:B:347:ARG:HH21	1:B:348:HIS:CE1	2.37	0.42
1:A:257:LEU:HG	1:A:277:ILE:HG13	2.01	0.42
1:B:347:ARG:HH21	1:B:348:HIS:HE1	1.68	0.42
1:B:66:PHE:CE2	1:B:68:ASP:HB2	2.55	0.41
1:A:259:PRO:HA	1:A:271:ALA:O	2.19	0.41
1:B:264:SER:HB3	4:B:569:HOH:O	2.20	0.41
1:A:48:VAL:CG1	1:A:76:LYS:HB2	2.51	0.41
1:A:356:VAL:HB	1:A:357:PRO:HD3	2.01	0.41
1:A:231:PRO:HB3	1:A:234:LYS:HZ2	1.85	0.41
1:B:79:GLU:HA	1:B:79:GLU:OE1	2.19	0.41
1:A:171:ASP:HA	1:A:233:ILE:HD12	2.03	0.41
1:A:172:GLU:O	1:A:209:ARG:NH2	2.50	0.41
1:B:164:TYR:HB2	1:B:200:HIS:O	2.21	0.41
1:B:142:GLU:CG	1:B:146:LYS:CE	2.96	0.40
1:A:47:ASP:OD1	1:A:48:VAL:N	2.54	0.40
1:A:210:PHE:O	1:A:214:THR:HG23	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	376/388 (97%)	362 (96%)	14 (4%)	0	100	100
1	B	376/388 (97%)	366 (97%)	10 (3%)	0	100	100
All	All	752/776 (97%)	728 (97%)	24 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	316/322 (98%)	299 (95%)	17 (5%)	27	15
1	B	316/322 (98%)	298 (94%)	18 (6%)	25	13
All	All	632/644 (98%)	597 (94%)	35 (6%)	27	14

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	ARG
1	A	27	LEU
1	A	38	VAL
1	A	75	GLU
1	A	95	LEU
1	A	98	GLN
1	A	117	LEU
1	A	139	VAL
1	A	140	LYS
1	A	153	GLU
1	A	163	LEU
1	A	184	ARG
1	A	212	ASP
1	A	213	ARG
1	A	237	LEU
1	A	257	LEU
1	A	335	GLN
1	B	3	ASP
1	B	27	LEU
1	B	30	ASP
1	B	115	SER
1	B	143	GLU
1	B	154	ARG
1	B	163	LEU
1	B	172	GLU
1	B	184	ARG
1	B	213	ARG

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Mol	Chain	Res	Type
1	B	237	LEU
1	B	272	GLN
1	B	275	GLU
1	B	313	ASP
1	B	334	ARG
1	B	335	GLN
1	B	339	VAL
1	B	376	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	HIS
1	A	33	HIS
1	A	98	GLN
1	A	155	HIS
1	A	248	HIS
1	A	294	HIS
1	A	348	HIS
1	B	5	HIS
1	B	155	HIS
1	B	248	HIS
1	B	314	GLN
1	B	348	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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	KCX	A	129	1	7,11,12	0.73	0	7,12,14	1.10	0
1	KCX	B	129	1	7,11,12	0.98	0	7,12,14	1.37	2 (28%)

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	KCX	A	129	1	-	0/6/10/12	0/0/0/0
1	KCX	B	129	1	-	0/6/10/12	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	129	KCX	CE-NZ-CX	-2.06	121.16	123.49
1	B	129	KCX	CD-CE-NZ	2.06	117.03	111.46

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	129	KCX	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

4 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	$\# Z > 2$
3	PPI	A	400	-	1,4,4	0.42	0	0,4,4	0.00	-
2	PLP	A	500	1	15,15,16	1.36	1 (6%)	21,22,23	1.97	6 (28%)
3	PPI	B	400	-	1,4,4	0.42	0	0,4,4	0.00	-
2	PLP	B	500	1	15,15,16	1.82	7 (46%)	21,22,23	1.79	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 Torsions and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PPI	A	400	-	-	0/0/2/2	0/0/0/0
2	PLP	A	500	1	-	0/6/6/8	0/1/1/1
3	PPI	B	400	-	-	0/0/2/2	0/0/0/0
2	PLP	B	500	1	-	0/6/6/8	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	PLP	C5-C4	-2.80	1.37	1.40
2	B	500	PLP	C5A-C5	-2.68	1.43	1.50
2	B	500	PLP	C3-C2	-2.46	1.39	1.40
2	B	500	PLP	P-O2P	-2.36	1.46	1.54
2	B	500	PLP	P-O3P	-2.08	1.47	1.54
2	B	500	PLP	O3-C3	2.22	1.42	1.37
2	B	500	PLP	C6-N1	2.27	1.39	1.34
2	B	500	PLP	C2A-C2	3.15	1.56	1.50

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	PLP	C5A-C5-C6	-3.61	112.46	119.28
2	B	500	PLP	C4A-C4-C3	-3.20	114.56	120.36
2	A	500	PLP	C3-C4-C5	-2.53	116.02	118.78
2	B	500	PLP	O2P-P-O4P	-2.12	100.47	106.56
2	A	500	PLP	O2P-P-O4P	-2.07	100.60	106.56
2	B	500	PLP	O3P-P-O2P	2.55	117.11	107.38
2	A	500	PLP	C5A-C5-C4	2.59	125.08	121.65

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	500	PLP	C4A-C4-C5	2.78	123.78	120.88
2	A	500	PLP	C6-C5-C4	4.95	122.35	118.15
2	B	500	PLP	C4A-C4-C5	5.72	126.84	120.88

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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](#)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.