



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:28 PM GMT

PDB ID : 3RCH  
Title : Crystal structure of Human aromatic L-amino acid decarboxylase (AADC) in the open conformation with LLP and PLP bound to Chain-A and Chain-B respectively  
Authors : Giardina, G.; Montioli, R.; Gianni, S.; Cellini, B.; Paiardini, A.; Borri Voltattorni, C.; Cutruzzola, F.  
Deposited on : 2011-03-31  
Resolution : 2.80 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.

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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

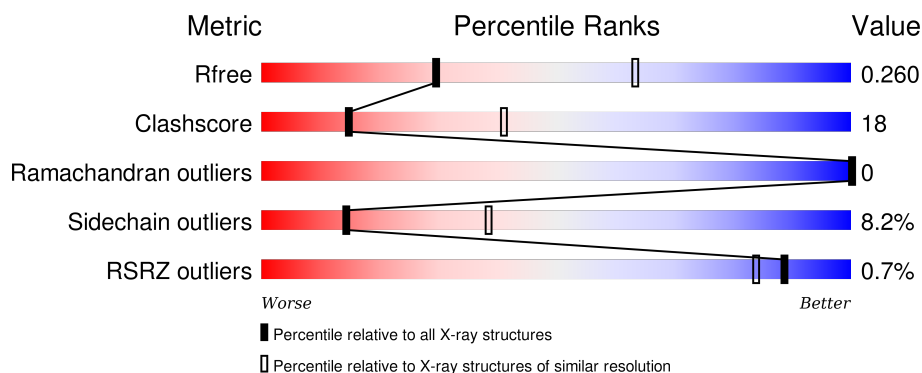
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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	480	 67% 24% • 7%
2	B	480	 63% 27% • 8%

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
3	PLP	B	481	-	-	X	X

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7018 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.

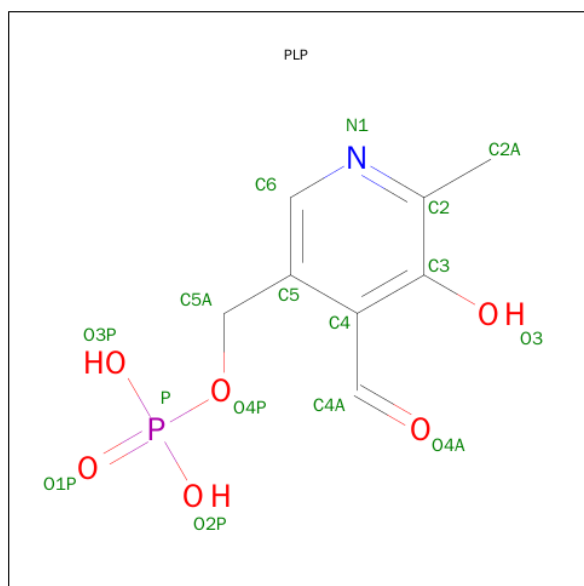
- Molecule 1 is a protein called aromatic L-amino acid decarboxylase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	446	3519	2252	604	634	1	28	0	2	0

- Molecule 2 is a protein called aromatic L-amino acid decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	440	3455	2212	597	620	26	0	0	0

- Molecule 3 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C<sub>8</sub>H<sub>10</sub>NO<sub>6</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	B	1	16	8	1	6	1	0	0

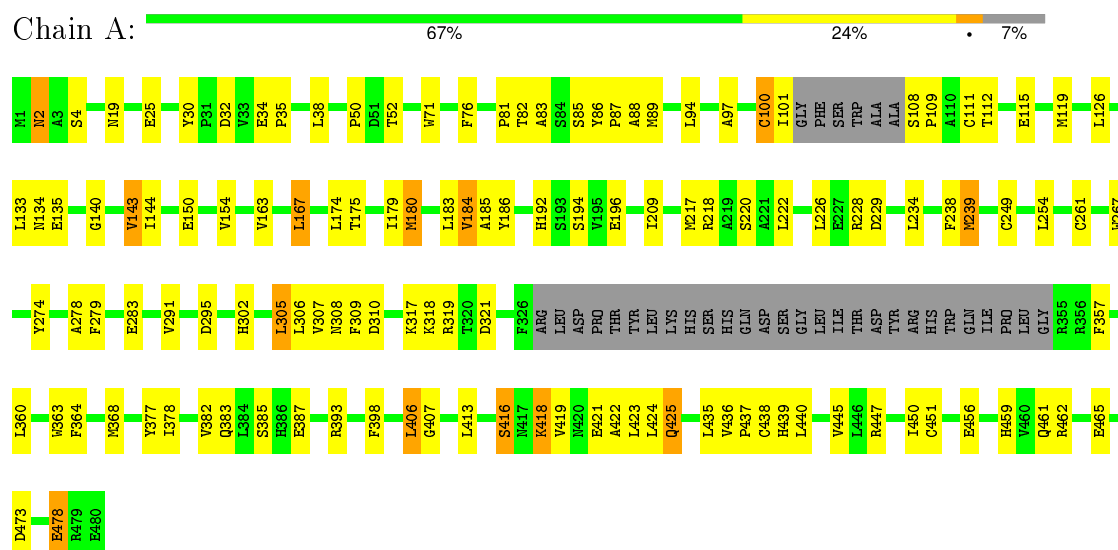
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	14	Total 14	O 14	0	0
4	B	14	Total 14	O 14	0	0

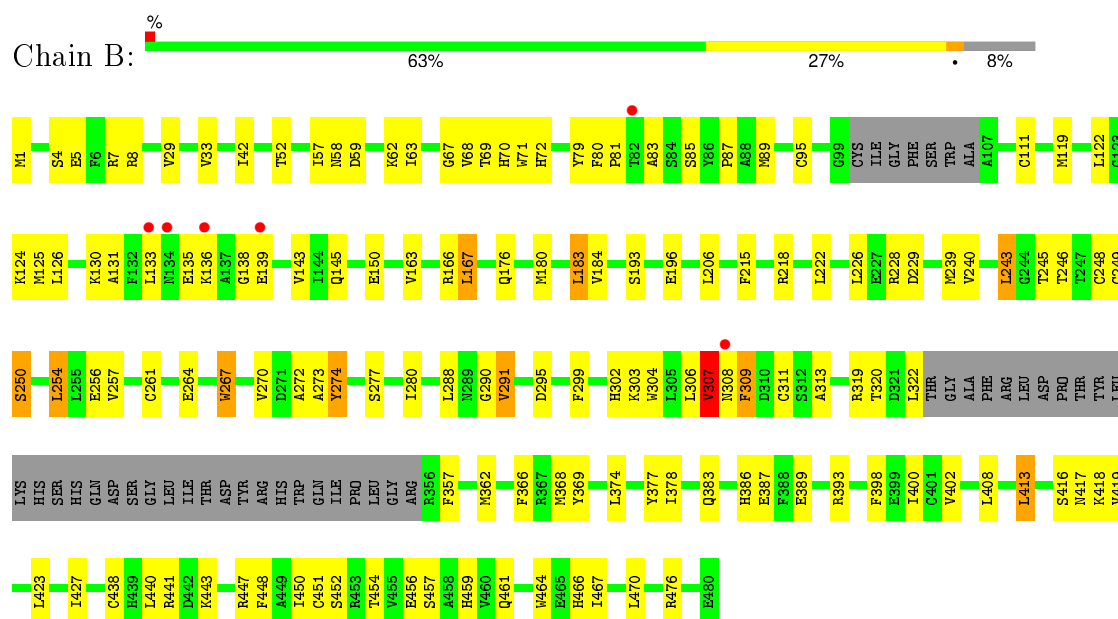
### 3 Residue-property plots

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 L-amino acid decarboxylase



- Molecule 2: aromatic L-amino acid decarboxylase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	177.00 Å   177.00 Å   74.83 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	30.00 – 2.80 49.09 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (30.00-2.80) 99.9 (49.09-2.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.13	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.06 (at 2.81 Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.201   ,   0.259 0.214   ,   0.260	Depositor DCC
$R_{free}$ test set	1514 reflections (5.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	46.1	Xtriage
Anisotropy	0.236	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 51.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 29858 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	7018	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.86% 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: LLP, 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	0.56	0/3580	0.65	0/4841
2	B	0.57	1/3534 (0.0%)	0.66	1/4779 (0.0%)
All	All	0.56	1/7114 (0.0%)	0.65	1/9620 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	249	CYS	CB-SG	-5.71	1.72	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	307	VAL	CB-CA-C	5.40	121.66	111.40

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	3519	0	3498	104	5
2	B	3455	0	3446	150	5
3	B	16	0	8	6	0
4	A	14	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	14	0	0	3	0
All	All	7018	0	6952	246	5

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 18.

All (246) 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)
2:B:302:HIS:CD2	2:B:307:VAL:O	1.79	1.36
2:B:302:HIS:HD2	2:B:307:VAL:O	0.93	1.23
1:A:71:TRP:CZ3	1:A:82:THR:HB	1.78	1.19
2:B:308:ASN:O	2:B:309:PHE:HD2	1.29	1.14
2:B:308:ASN:O	2:B:309:PHE:CD2	2.05	1.08
1:A:108:SER:HB3	1:A:109:PRO:HD3	1.36	1.05
1:A:108:SER:CB	1:A:109:PRO:HD3	1.90	1.02
1:A:81:PRO:HG3	1:A:451:CYS:HA	1.38	1.01
1:A:71:TRP:CH2	1:A:82:THR:CG2	2.46	0.99
1:A:456:GLU:H	1:A:459:HIS:HD2	1.13	0.96
1:A:71:TRP:CH2	1:A:82:THR:HG22	2.03	0.92
2:B:130:LYS:O	2:B:133:LEU:HD13	1.70	0.91
2:B:307:VAL:HG23	2:B:308:ASN:H	1.34	0.89
2:B:456:GLU:H	2:B:459:HIS:HD2	1.16	0.89
2:B:306:LEU:HD21	2:B:377:TYR:CE2	2.09	0.88
2:B:304:TRP:HB3	2:B:378:ILE:HD11	1.55	0.88
1:A:71:TRP:HH2	1:A:82:THR:HG22	1.39	0.87
1:A:71:TRP:CZ3	1:A:82:THR:CB	2.59	0.85
2:B:304:TRP:HB3	2:B:378:ILE:CD1	2.08	0.84
1:A:456:GLU:H	1:A:459:HIS:CD2	1.96	0.84
2:B:273:ALA:HB2	3:B:481:PLP:H2A2	1.60	0.83
1:A:100:CYS:HB2	4:A:482:HOH:O	1.78	0.82
2:B:387:GLU:OE2	2:B:457:SER:HB2	1.80	0.80
1:A:19:ASN:ND2	2:B:7:ARG:HH22	1.82	0.77
1:A:108:SER:CB	1:A:109:PRO:CD	2.62	0.77
2:B:246:THR:HG1	3:B:481:PLP:HO3	1.31	0.76
2:B:246:THR:HG22	2:B:246:THR:O	1.86	0.75
1:A:81:PRO:HB3	1:A:451:CYS:O	1.87	0.75
1:A:418:LYS:HE3	1:A:421:GLU:OE1	1.87	0.74
2:B:274:TYR:HB2	2:B:303:LYS:HD2	1.67	0.74
2:B:307:VAL:CG2	2:B:308:ASN:H	2.00	0.74
2:B:239:MET:CE	2:B:261:CYS:SG	2.76	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:72:HIS:HE1	2:B:83:ALA:HA	1.53	0.73
1:A:108:SER:HB3	1:A:109:PRO:CD	2.18	0.73
2:B:398:PHE:CE2	2:B:413:LEU:HD13	2.24	0.71
1:A:71:TRP:HZ3	1:A:82:THR:HB	1.49	0.71
1:A:25:GLU:OE1	1:A:459:HIS:HE1	1.72	0.71
2:B:196:GLU:HA	2:B:206:LEU:HD22	1.73	0.70
2:B:456:GLU:N	2:B:459:HIS:HD2	1.89	0.69
1:A:71:TRP:CH2	1:A:82:THR:HG21	2.27	0.69
2:B:130:LYS:C	2:B:133:LEU:HD13	2.13	0.69
1:A:81:PRO:CG	1:A:451:CYS:HA	2.21	0.68
2:B:133:LEU:N	2:B:133:LEU:HD12	2.09	0.68
2:B:307:VAL:CG2	2:B:308:ASN:N	2.57	0.67
2:B:306:LEU:HD21	2:B:377:TYR:CZ	2.29	0.67
2:B:163:VAL:HG22	2:B:167:LEU:HD22	1.76	0.67
2:B:288:LEU:O	2:B:291:VAL:HG22	1.94	0.67
1:A:424:LEU:HD21	1:A:437:PRO:HD3	1.76	0.67
2:B:302:HIS:HD2	2:B:307:VAL:C	1.90	0.66
2:B:456:GLU:H	2:B:459:HIS:CD2	2.07	0.66
1:A:413:LEU:HD22	1:A:423:LEU:HD22	1.76	0.66
1:A:249:CYS:SG	1:A:406:LEU:HD21	2.36	0.66
1:A:134:ASN:HB3	1:A:140:GLY:O	1.94	0.66
1:A:108:SER:HB2	1:A:109:PRO:HD3	1.76	0.65
2:B:274:TYR:HB2	2:B:303:LYS:CD	2.26	0.65
2:B:83:ALA:O	2:B:302:HIS:NE2	2.25	0.64
1:A:249:CYS:SG	1:A:406:LEU:CD2	2.85	0.64
2:B:58:ASN:HB3	2:B:62:LYS:NZ	2.13	0.64
1:A:126:LEU:HD23	1:A:279:PHE:HB2	1.80	0.64
1:A:425:GLN:NE2	1:A:425:GLN:HA	2.12	0.63
2:B:79:TYR:CZ	2:B:303:LYS:HD3	2.35	0.62
2:B:308:ASN:O	2:B:309:PHE:CB	2.48	0.61
1:A:438:CYS:HB3	1:A:447:ARG:HH21	1.65	0.61
2:B:295:ASP:CG	4:B:492:HOH:O	2.38	0.61
1:A:309:PHE:CG	1:A:310:ASP:N	2.68	0.61
2:B:274:TYR:CE1	2:B:304:TRP:NE1	2.68	0.60
1:A:306:LEU:HD21	1:A:377:TYR:CE1	2.37	0.60
2:B:254:LEU:HB3	2:B:290:GLY:HA3	1.83	0.60
2:B:307:VAL:HG23	2:B:308:ASN:N	2.11	0.59
1:A:228:ARG:HD2	1:A:229:ASP:OD1	2.03	0.59
2:B:122:LEU:HD22	2:B:362:MET:HE1	1.83	0.59
1:A:25:GLU:OE1	1:A:459:HIS:CE1	2.54	0.59
2:B:226:LEU:HD13	2:B:264:GLU:HG3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:246:THR:CG2	2:B:246:THR:O	2.50	0.58
1:A:71:TRP:CZ3	1:A:82:THR:CG2	2.85	0.58
2:B:398:PHE:CD2	2:B:413:LEU:HD13	2.38	0.58
1:A:302:HIS:HB2	1:A:309:PHE:HA	1.85	0.58
2:B:85:SER:HB3	2:B:306:LEU:HD12	1.84	0.58
2:B:119:MET:HE1	2:B:313:ALA:HB1	1.85	0.58
2:B:389:GLU:HG3	2:B:400:ILE:HD13	1.85	0.58
2:B:245:THR:OG1	2:B:250:SER:HB2	2.03	0.58
2:B:139:GLU:C	2:B:139:GLU:OE1	2.42	0.58
1:A:364:PHE:CD2	1:A:368:MET:HE2	2.39	0.57
2:B:29:VAL:O	2:B:69:THR:O	2.22	0.57
2:B:274:TYR:HA	2:B:303:LYS:HG3	1.87	0.57
2:B:239:MET:HE2	2:B:261:CYS:SG	2.43	0.57
2:B:130:LYS:HA	2:B:133:LEU:HD13	1.86	0.57
1:A:478:GLU:HA	1:A:478:GLU:OE2	2.05	0.57
2:B:386:HIS:HD2	2:B:389:GLU:OE1	1.87	0.57
2:B:306:LEU:CD2	2:B:377:TYR:CE2	2.87	0.57
2:B:423:LEU:O	2:B:427:ILE:HG13	2.05	0.56
1:A:465:GLU:HA	1:A:465:GLU:OE1	2.04	0.56
1:A:150:GLU:O	1:A:154:VAL:HG23	2.05	0.56
2:B:79:TYR:OH	2:B:302:HIS:ND1	2.32	0.56
1:A:97:ALA:O	2:B:72:HIS:CD2	2.58	0.56
1:A:364:PHE:CD2	1:A:368:MET:CE	2.89	0.56
1:A:19:ASN:ND2	2:B:7:ARG:HH12	2.04	0.56
1:A:438:CYS:HB3	1:A:447:ARG:HE	1.69	0.56
2:B:131:ALA:HA	2:B:139:GLU:OE2	2.05	0.56
1:A:97:ALA:O	2:B:72:HIS:HD2	1.89	0.55
2:B:408:LEU:HD11	2:B:447:ARG:HB3	1.88	0.55
2:B:125:MET:HB3	2:B:280:ILE:HG22	1.87	0.55
2:B:133:LEU:CD1	2:B:133:LEU:H	2.20	0.55
2:B:246:THR:OG1	3:B:481:PLP:O3	2.08	0.55
2:B:145:GLN:NE2	2:B:150:GLU:OE1	2.40	0.55
1:A:383:GLN:OE1	1:A:387:GLU:HG3	2.06	0.54
1:A:85:SER:O	1:A:89:MET:HG3	2.07	0.54
2:B:277:SER:HB2	2:B:304:TRP:HB2	1.90	0.54
2:B:413:LEU:HD22	2:B:423:LEU:HD22	1.89	0.54
2:B:386:HIS:HE1	4:B:482:HOH:O	1.90	0.53
2:B:389:GLU:OE2	2:B:393:ARG:NH1	2.41	0.53
2:B:362:MET:CE	2:B:366:PHE:CE1	2.91	0.53
2:B:416:SER:HB3	2:B:419:VAL:HG23	1.90	0.53
2:B:133:LEU:CD1	2:B:133:LEU:N	2.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:457:SER:O	2:B:461:GLN:HG2	2.07	0.53
2:B:59:ASP:O	2:B:63:ILE:HB	2.08	0.53
2:B:440:LEU:O	2:B:441:ARG:HB2	2.08	0.53
2:B:133:LEU:H	2:B:133:LEU:HD12	1.73	0.53
2:B:126:LEU:HD11	2:B:299:PHE:CE2	2.44	0.53
1:A:456:GLU:N	1:A:459:HIS:HD2	1.96	0.53
2:B:138:GLY:O	2:B:319:ARG:NH2	2.42	0.52
1:A:2:ASN:ND2	1:A:2:ASN:H	2.07	0.52
2:B:308:ASN:O	2:B:309:PHE:HB3	2.09	0.52
1:A:184:VAL:CG2	1:A:234:LEU:HB3	2.40	0.52
2:B:130:LYS:CA	2:B:133:LEU:HD13	2.39	0.52
2:B:72:HIS:CE1	2:B:80:PHE:HE2	2.28	0.52
2:B:248:CYS:HB3	2:B:402:VAL:HG21	1.91	0.51
1:A:2:ASN:H	1:A:2:ASN:HD22	1.58	0.51
2:B:176:GLN:O	2:B:180:MET:HG3	2.10	0.51
2:B:273:ALA:HB2	3:B:481:PLP:C2A	2.37	0.51
2:B:308:ASN:O	2:B:309:PHE:CG	2.58	0.51
1:A:94:LEU:HD23	1:A:360:LEU:HD21	1.92	0.51
2:B:438:CYS:SG	2:B:447:ARG:HD2	2.50	0.51
2:B:71:TRP:HB2	2:B:80:PHE:CD2	2.45	0.51
2:B:288:LEU:O	2:B:288:LEU:HG	2.10	0.51
1:A:278:ALA:HA	1:A:378:ILE:HD13	1.93	0.51
1:A:364:PHE:O	1:A:368:MET:HG3	2.12	0.50
1:A:385:SER:HB2	1:A:407:GLY:HA2	1.93	0.50
2:B:79:TYR:CZ	2:B:81:PRO:HA	2.46	0.50
2:B:464:TRP:HA	2:B:467:ILE:HD12	1.94	0.50
2:B:272:ALA:HB3	2:B:299:PHE:HB3	1.94	0.49
1:A:83:ALA:HB3	1:A:307:VAL:O	2.12	0.49
2:B:81:PRO:O	2:B:302:HIS:CE1	2.66	0.49
1:A:115:GLU:HG3	1:A:144:ILE:HD12	1.94	0.49
2:B:180:MET:HA	2:B:183:LEU:HD22	1.94	0.49
2:B:111:CYS:SG	2:B:357:PHE:CD2	3.03	0.49
2:B:87:PRO:HG2	2:B:369:TYR:HE1	1.78	0.49
2:B:277:SER:CB	2:B:304:TRP:HB2	2.43	0.49
1:A:85:SER:HB2	1:A:87:PRO:HD2	1.95	0.49
1:A:302:HIS:HA	1:A:307:VAL:O	2.13	0.48
1:A:81:PRO:HG3	1:A:450:ILE:O	2.13	0.48
2:B:139:GLU:O	2:B:139:GLU:OE1	2.30	0.48
1:A:398:PHE:CE2	1:A:413:LEU:HD13	2.48	0.48
1:A:30:TYR:HH	1:A:76:PHE:HE1	1.59	0.48
2:B:69:THR:O	2:B:70:HIS:HB2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:363:TRP:CZ2	2:B:42:ILE:HD11	2.49	0.48
2:B:239:MET:HG2	2:B:240:VAL:N	2.28	0.48
2:B:288:LEU:HD23	4:B:487:HOH:O	2.12	0.48
2:B:85:SER:O	2:B:89:MET:HG3	2.14	0.48
2:B:309:PHE:C	2:B:311:CYS:N	2.66	0.47
1:A:179:ILE:O	1:A:183:LEU:HD13	2.13	0.47
1:A:267:TRP:HA	1:A:295:ASP:OD2	2.14	0.47
1:A:30:TYR:OH	1:A:76:PHE:HE1	1.96	0.47
1:A:317:LYS:HE3	4:A:494:HOH:O	2.12	0.47
2:B:1:MET:HE3	2:B:5:GLU:HB3	1.97	0.47
1:A:109:PRO:HD2	2:B:67:GLY:O	2.13	0.47
2:B:362:MET:HE3	2:B:366:PHE:CZ	2.49	0.47
2:B:362:MET:HE2	2:B:366:PHE:HE1	1.78	0.47
2:B:239:MET:HE1	2:B:257:VAL:HG13	1.96	0.47
1:A:192:HIS:CD2	1:A:194:SER:H	2.32	0.47
2:B:239:MET:CG	2:B:240:VAL:N	2.78	0.46
2:B:362:MET:HE2	2:B:366:PHE:CE1	2.51	0.46
1:A:111[A]:CYS:HA	1:A:357:PHE:CE1	2.50	0.46
2:B:274:TYR:HB2	2:B:303:LYS:CG	2.44	0.46
2:B:248:CYS:CB	2:B:402:VAL:HG21	2.46	0.46
1:A:111[B]:CYS:HA	1:A:357:PHE:CE1	2.50	0.46
2:B:139:GLU:O	2:B:139:GLU:CD	2.54	0.46
1:A:19:ASN:ND2	2:B:7:ARG:NH2	2.59	0.46
2:B:29:VAL:O	2:B:29:VAL:HG12	2.15	0.46
1:A:192:HIS:CD2	1:A:194:SER:HB3	2.51	0.46
2:B:466:HIS:NE2	2:B:470:LEU:HD11	2.30	0.46
2:B:303:LYS:HZ3	3:B:481:PLP:H4A	1.81	0.45
2:B:72:HIS:CE1	2:B:83:ALA:HA	2.42	0.45
2:B:267:TRP:C	2:B:267:TRP:CD1	2.90	0.45
2:B:417:ASN:O	2:B:418:LYS:C	2.55	0.45
1:A:406:LEU:O	1:A:406:LEU:CG	2.64	0.45
1:A:302:HIS:CB	1:A:309:PHE:HA	2.46	0.45
2:B:320:THR:C	2:B:322:LEU:H	2.19	0.45
2:B:443:LYS:HB3	2:B:443:LYS:HE2	1.86	0.45
2:B:303:LYS:NZ	3:B:481:PLP:H4A	2.31	0.45
2:B:135:GLU:O	2:B:135:GLU:HG2	2.16	0.45
1:A:119:MET:CE	1:A:143:VAL:H	2.30	0.45
1:A:378:ILE:O	1:A:382:VAL:HG23	2.17	0.44
2:B:448:PHE:CE2	2:B:450:ILE:HD11	2.52	0.44
2:B:277:SER:O	2:B:280:ILE:HG12	2.17	0.44
2:B:306:LEU:N	2:B:306:LEU:HD22	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:448:PHE:HE2	2:B:450:ILE:HD11	1.83	0.44
1:A:184:VAL:HG22	1:A:234:LEU:HB3	1.99	0.44
1:A:192:HIS:HD2	1:A:194:SER:HB3	1.83	0.44
2:B:124:LYS:HE2	2:B:135:GLU:OE1	2.17	0.44
2:B:222:LEU:O	2:B:226:LEU:HG	2.18	0.44
1:A:318:LYS:O	1:A:321:ASP:HB2	2.18	0.44
1:A:416:SER:OG	1:A:419:VAL:HG23	2.17	0.43
1:A:86:TYR:N	1:A:87:PRO:CD	2.82	0.43
2:B:309:PHE:C	2:B:309:PHE:CD2	2.86	0.43
1:A:88:ALA:HB3	1:A:308:ASN:OD1	2.18	0.43
2:B:303:LYS:H	2:B:303:LYS:HG2	1.47	0.42
1:A:305:LEU:HD23	1:A:305:LEU:HA	1.82	0.42
2:B:228:ARG:HD2	2:B:229:ASP:OD1	2.20	0.42
1:A:108:SER:HB2	1:A:109:PRO:CD	2.41	0.42
1:A:186:TYR:CD2	1:A:209:ILE:HD11	2.55	0.42
2:B:309:PHE:C	2:B:311:CYS:H	2.16	0.42
2:B:79:TYR:CE2	2:B:303:LYS:HD3	2.55	0.42
1:A:239:MET:HG2	1:A:261:CYS:SG	2.60	0.42
1:A:419:VAL:O	1:A:422:ALA:HB3	2.19	0.42
1:A:50:PRO:HB3	2:B:368:MET:O	2.19	0.42
2:B:306:LEU:HD13	2:B:306:LEU:HA	1.83	0.42
2:B:239:MET:HE1	2:B:261:CYS:SG	2.58	0.41
1:A:163:VAL:HG22	1:A:167:LEU:HD22	2.01	0.41
2:B:71:TRP:HB2	2:B:80:PHE:CE2	2.55	0.41
2:B:80:PHE:HA	2:B:81:PRO:HD3	1.92	0.41
1:A:406:LEU:O	1:A:406:LEU:HD23	2.20	0.41
1:A:436:VAL:O	1:A:447:ARG:HB2	2.20	0.41
2:B:111:CYS:SG	2:B:357:PHE:CG	2.98	0.41
1:A:81:PRO:HD2	1:A:274:TYR:CE1	2.55	0.41
2:B:163:VAL:HG23	2:B:166:ARG:HH12	1.86	0.41
1:A:406:LEU:HG	1:A:406:LEU:O	2.21	0.41
2:B:87:PRO:HG2	2:B:369:TYR:CE1	2.55	0.41
1:A:185:ALA:HA	1:A:238:PHE:O	2.21	0.41
1:A:217:MET:SD	1:A:239:MET:HE1	2.60	0.41
1:A:254:LEU:HA	1:A:254:LEU:HD12	1.78	0.41
1:A:126:LEU:CD2	1:A:279:PHE:HB2	2.48	0.41
2:B:215:PHE:HB2	2:B:250:SER:OG	2.21	0.41
1:A:192:HIS:HD2	1:A:194:SER:CB	2.34	0.41
1:A:222:LEU:O	1:A:226:LEU:HG	2.21	0.41
2:B:218:ARG:HD2	2:B:256:GLU:OE1	2.21	0.41
1:A:81:PRO:HD2	1:A:274:TYR:HE1	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:34:GLU:O	1:A:35:PRO:C	2.60	0.40
1:A:180:MET:HB3	1:A:180:MET:HE3	1.67	0.40
1:A:100:CYS:O	1:A:101:ILE:HG13	2.22	0.40
2:B:226:LEU:CD1	2:B:264:GLU:HG3	2.51	0.40
1:A:440:LEU:HD12	1:A:445:VAL:HG21	2.02	0.40
2:B:288:LEU:HG	2:B:291:VAL:HG22	2.04	0.40
2:B:58:ASN:HB3	2:B:62:LYS:HZ2	1.86	0.40
2:B:362:MET:HE2	2:B:362:MET:HB3	1.98	0.40
2:B:243:LEU:HD22	2:B:270:VAL:HG11	2.02	0.40

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:421:GLU:OE2	2:B:136:LYS:NZ[7_555]	1.47	0.73
1:A:439:HIS:NE2	2:B:136:LYS:CD[7_555]	1.82	0.38
1:A:439:HIS:NE2	2:B:136:LYS:CB[7_555]	1.88	0.32
1:A:439:HIS:CE1	2:B:136:LYS:CD[7_555]	2.14	0.06
1:A:439:HIS:NE2	2:B:136:LYS:CG[7_555]	2.16	0.04

## 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	441/480 (92%)	410 (93%)	31 (7%)	0	100	100
2	B	434/480 (90%)	406 (94%)	28 (6%)	0	100	100
All	All	875/960 (91%)	816 (93%)	59 (7%)	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	369/398 (93%)	336 (91%)	33 (9%)	12	34
2	B	364/399 (91%)	337 (93%)	27 (7%)	17	43
All	All	733/797 (92%)	673 (92%)	60 (8%)	14	38

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ASN
1	A	4	SER
1	A	32	ASP
1	A	38	LEU
1	A	52	THR
1	A	100	CYS
1	A	112	THR
1	A	133	LEU
1	A	135	GLU
1	A	143	VAL
1	A	167	LEU
1	A	174	LEU
1	A	175	THR
1	A	180	MET
1	A	184	VAL
1	A	196	GLU
1	A	218	ARG
1	A	220	SER
1	A	239	MET
1	A	283	GLU
1	A	291	VAL
1	A	305	LEU
1	A	319	ARG
1	A	393	ARG
1	A	406	LEU
1	A	416	SER
1	A	418	LYS

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Mol	Chain	Res	Type
1	A	425	GLN
1	A	435	LEU
1	A	461	GLN
1	A	462	ARG
1	A	473	ASP
1	A	478	GLU
2	B	4	SER
2	B	8	ARG
2	B	33	VAL
2	B	52	THR
2	B	57	ILE
2	B	68	VAL
2	B	95	CYS
2	B	143	VAL
2	B	167	LEU
2	B	183	LEU
2	B	184	VAL
2	B	193	SER
2	B	243	LEU
2	B	250	SER
2	B	254	LEU
2	B	267	TRP
2	B	274	TYR
2	B	291	VAL
2	B	307	VAL
2	B	309	PHE
2	B	374	LEU
2	B	383	GLN
2	B	413	LEU
2	B	451	CYS
2	B	452	SER
2	B	454	THR
2	B	476	ARG

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	2	ASN
1	A	19	ASN
1	A	192	HIS
1	A	375	GLN
1	A	425	GLN

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Mol	Chain	Res	Type
1	A	459	HIS
2	B	72	HIS
2	B	145	GLN
2	B	262	ASN
2	B	375	GLN
2	B	386	HIS
2	B	459	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	LLP	A	303	1	23,24,25	1.62	3 (13%)	28,32,34	1.42	4 (14%)

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	LLP	A	303	1	-	0/15/17/19	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	303	LLP	C2-N1	2.35	1.39	1.34
1	A	303	LLP	C4-C4'	2.55	1.51	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	303	LLP	C4'-NZ	5.67	1.44	1.27

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	303	LLP	C3-C4-C4'	-4.17	114.76	120.16
1	A	303	LLP	C4-C4'-NZ	2.20	137.29	125.06
1	A	303	LLP	O3-C3-C2	2.47	121.96	117.66
1	A	303	LLP	CE-NZ-C4'	2.88	127.29	118.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

1 ligand is 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	PLP	B	481	-	16,16,16	1.19	1 (6%)	21,23,23	1.28	3 (14%)

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
3	PLP	B	481	-	-	0/8/8/8	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	481	PLP	C4-C5	-2.37	1.38	1.42

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	481	PLP	C5-C6-N1	-2.53	119.47	123.86
3	B	481	PLP	O4A-C4A-C4	-2.03	121.01	125.11
3	B	481	PLP	O3-C3-C2	2.58	122.15	117.66

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	481	PLP	6	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	445/480 (92%)	-0.35	0	100   100	19, 48, 96, 157	2 (0%)
2	B	440/480 (91%)	-0.14	6 (1%)	78   69	21, 56, 103, 161	8 (1%)
All	All	885/960 (92%)	-0.25	6 (0%)	89   84	19, 52, 100, 161	10 (1%)

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	139	GLU	3.5
2	B	134	ASN	3.4
2	B	136	LYS	3.4
2	B	82	THR	2.4
2	B	308	ASN	2.3
2	B	133	LEU	2.0

### 6.2 Non-standard residues in protein, DNA, RNA chains

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
1	LLP	A	303	24/25	0.97	0.13	-	33,40,43,45	0

### 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, 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( $\text{\AA}^2$ )	Q<0.9
3	PLP	B	481	16/16	0.89	0.25	2.57	32,33,39,41	16

## 6.5 Other polymers [i](#)

There are no such residues in this entry.