



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 04:46 AM UTC

PDB ID : 2NMP / pdb\_00002nmp  
Title : Crystal structure of human Cystathionine gamma lyase  
Authors : Karlberg, T.; Uppenberg, J.; Arrowsmith, C.; Berglund, H.; Busam, R.D.; Collins, R.; Edwards, A.; Ericsson, U.B.; Flodin, S.; Flores, A.; Graslund, S.; Hallberg, B.M.; Hammarstrom, M.; Högberg, M.; Johansson, I.; Kotenyova, T.; Magnusdottir, A.; Moche, M.; Nilsson, M.E.; Nordlund, P.; Nyman, T.; Ogg, D.; Persson, C.; Sagemark, J.; Stenmark, P.; Sundstrom, M.; Thorsell, A.G.; van-den-Berg, S.; Wallden, K.; Weigelt, J.; Holmberg-Schiavone, L.; Structural Genomics Consortium (SGC)  
Deposited on : 2006-10-23  
Resolution : 2.60 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12

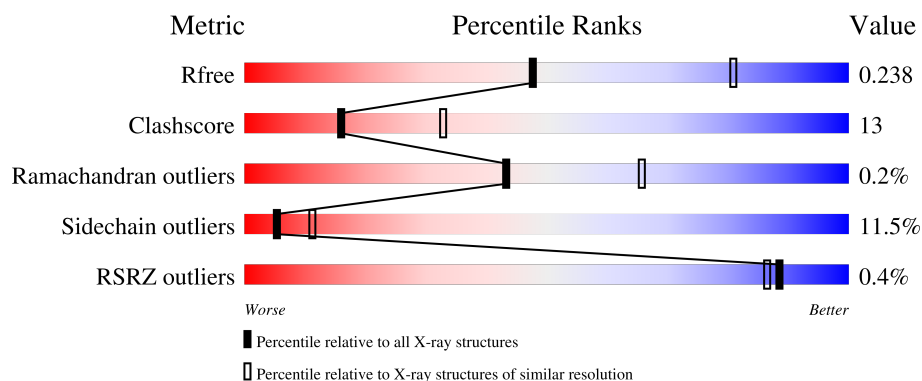
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)


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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	403	
1	B	403	
1	C	403	

*Continued on next page...*

Ideal geometry (proteins) : Engh & Huber (2001)  
 Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
 Validation Pipeline (wwPDB-VP) : 2.49

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
1	D	403	 A horizontal bar chart showing the quality of chain 1. The bar is divided into three segments: green (68%), yellow (23%), and orange (6%). The segments are labeled with their respective percentages: 68%, 23%, and 6%. The bar ends with a small black dot.

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
2	PLP	D	500	-	-	X	-

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12048 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.

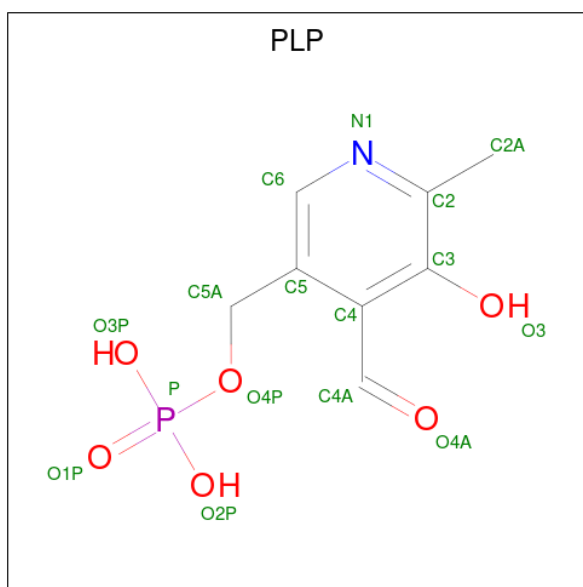
- Molecule 1 is a protein called Cystathionine gamma-lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	376	Total	C	N	O	S	0	0	0
			2914	1860	497	538	19			
1	B	376	Total	C	N	O	S	0	0	0
			2906	1856	494	538	18			
1	C	390	Total	C	N	O	S	0	0	0
			3015	1922	515	559	19			
1	D	390	Total	C	N	O	S	0	0	0
			3011	1917	515	560	19			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP P32929
B	0	SER	-	expression tag	UNP P32929
C	0	SER	-	expression tag	UNP P32929
D	0	SER	-	expression tag	UNP P32929

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: PLP) (formula: C<sub>8</sub>H<sub>10</sub>NO<sub>6</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	C	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	D	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

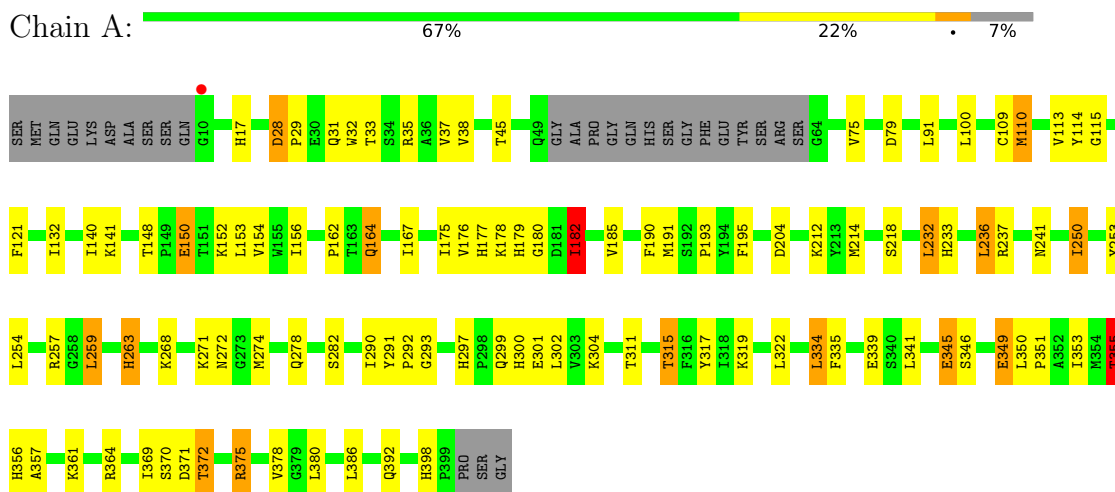
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	42	Total	O	0	0
			42	42		
3	B	28	Total	O	0	0
			28	28		
3	C	42	Total	O	0	0
			42	42		
3	D	45	Total	O	0	0
			45	45		

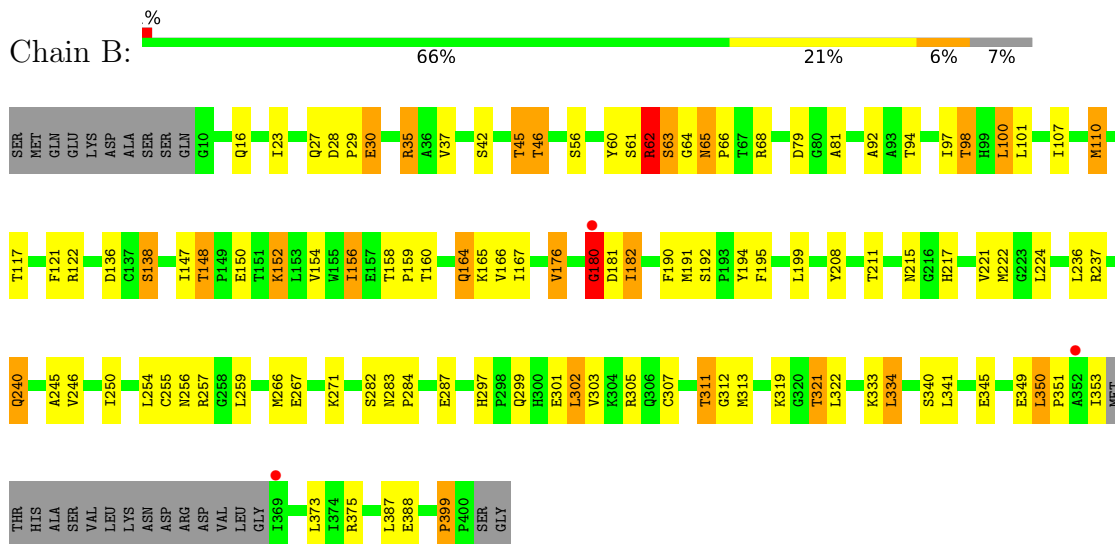
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: Cystathionine gamma-lyase

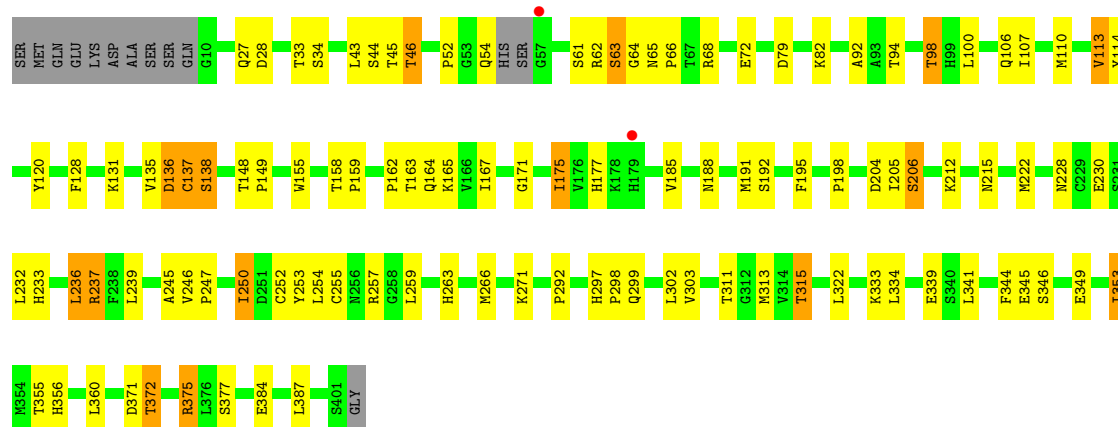


#### • Molecule 1: Cystathionine gamma-lyase



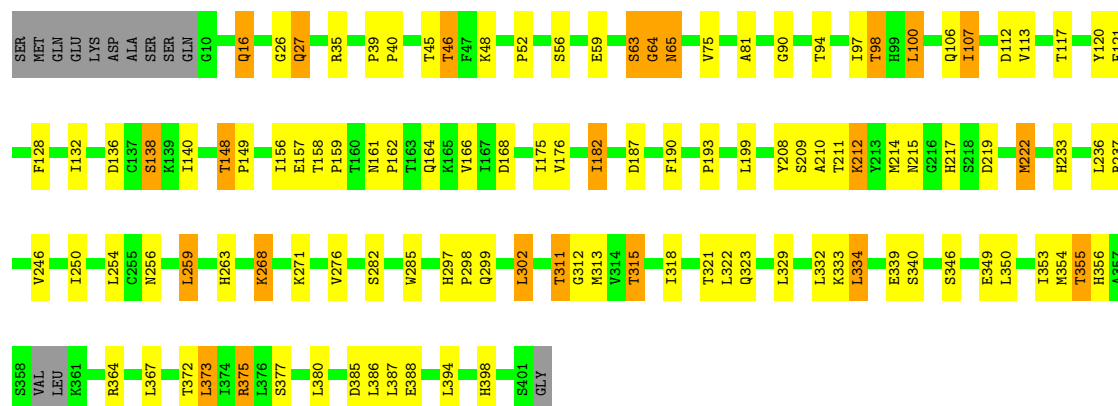
#### • Molecule 1: Cystathionine gamma-lyase





● Molecule 1: Cystathionine gamma-lyase

Chain D: 68% 23% 6%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	105.78Å 107.57Å 153.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.93 – 2.60 19.93 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.93-2.60) 99.7 (19.93-2.60)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	0.23	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.73 (at 2.59Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.177 , 0.245 0.172 , 0.238	Depositor DCC
$R_{free}$ test set	2718 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	29.3	Xtriage
Anisotropy	0.573	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 31.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.049 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	12048	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.80% 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, 0.333 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: 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	0.85	1/2978 (0.0%)	1.04	7/4041 (0.2%)
1	B	0.83	0/2973	1.05	7/4035 (0.2%)
1	C	0.84	0/3083	1.06	7/4183 (0.2%)
1	D	0.86	0/3079	1.08	8/4177 (0.2%)
All	All	0.84	1/12113 (0.0%)	1.06	29/16436 (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	1
1	B	0	3
1	C	0	1
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	182	ILE	CA-CB	5.90	1.62	1.54

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	65	ASN	N-CA-C	11.32	122.72	108.11
1	D	16	GLN	N-CA-C	10.70	122.52	111.07
1	B	65	ASN	N-CA-C	10.63	117.78	108.22
1	A	180	GLY	N-CA-C	8.43	123.01	112.14
1	C	138	SER	N-CA-C	-8.23	102.80	113.17

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	179	HIS	Peptide
1	B	180	GLY	Peptide
1	B	399	PRO	Peptide
1	B	62	ARG	Peptide
1	C	136	ASP	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	2914	0	2921	73	0
1	B	2906	0	2895	83	0
1	C	3015	0	3009	86	0
1	D	3011	0	2996	93	0
2	A	15	0	6	2	0
2	C	15	0	6	2	0
2	D	15	0	6	6	0
3	A	42	0	0	2	0
3	B	28	0	0	2	0
3	C	42	0	0	0	0
3	D	45	0	0	1	0
All	All	12048	0	11839	310	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 13.

The worst 5 of 310 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:212:LYS:HZ2	2:A:500:PLP:C4A	1.51	1.18
1:A:355:THR:HG23	1:A:356:HIS:CD2	1.79	1.18
1:D:176:VAL:HG13	1:D:182:ILE:CD1	1.76	1.14
1:D:375:ARG:HH11	1:D:375:ARG:HG2	1.14	1.12
1:A:176:VAL:CG1	1:A:182:ILE:HD12	1.78	1.11

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	372/403 (92%)	357 (96%)	14 (4%)	1 (0%)	36	58
1	B	372/403 (92%)	350 (94%)	22 (6%)	0	100	100
1	C	386/403 (96%)	363 (94%)	23 (6%)	0	100	100
1	D	386/403 (96%)	363 (94%)	21 (5%)	2 (0%)	24	46
All	All	1516/1612 (94%)	1433 (94%)	80 (5%)	3 (0%)	43	66

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	211	THR
1	A	355	THR
1	D	64	GLY

#### 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	321/342 (94%)	285 (89%)	36 (11%)	6	12
1	B	318/342 (93%)	276 (87%)	42 (13%)	4	8
1	C	331/342 (97%)	299 (90%)	32 (10%)	8	17
1	D	330/342 (96%)	290 (88%)	40 (12%)	5	10

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1300/1368 (95%)	1150 (88%)	150 (12%)	5 11

5 of 150 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	59	GLU
1	D	334	LEU
1	D	106	GLN
1	D	222	MET
1	B	110	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	174	HIS
1	C	241	ASN
1	D	398	HIS
1	C	177	HIS
1	C	228	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

3 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	PLP	D	500	1	15,15,16	1.27	2 (13%)	21,22,23	1.42	3 (14%)
2	PLP	C	500	1	15,15,16	1.26	1 (6%)	21,22,23	1.40	2 (9%)
2	PLP	A	500	1	15,15,16	1.64	2 (13%)	21,22,23	1.25	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
2	PLP	D	500	1	-	2/6/6/8	0/1/1/1
2	PLP	C	500	1	-	0/6/6/8	0/1/1/1
2	PLP	A	500	1	-	0/6/6/8	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	PLP	C2A-C2	4.52	1.57	1.50
2	A	500	PLP	P-O2P	2.63	1.64	1.54
2	D	500	PLP	C2A-C2	2.57	1.54	1.50
2	C	500	PLP	P-O3P	2.48	1.64	1.54
2	D	500	PLP	P-O3P	2.39	1.63	1.54

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	500	PLP	O4P-P-O1P	3.52	115.96	106.44
2	D	500	PLP	O2P-P-O4P	-2.99	98.88	106.67
2	A	500	PLP	C2A-C2-N1	2.57	122.48	117.64
2	C	500	PLP	C4A-C4-C5	-2.53	118.33	120.94
2	C	500	PLP	C6-C5-C4	-2.34	116.18	118.10

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	500	PLP	C4-C5-C5A-O4P
2	D	500	PLP	C6-C5-C5A-O4P

There are no ring outliers.

3 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	500	PLP	6	0
2	C	500	PLP	2	0
2	A	500	PLP	2	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, 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	376/403 (93%)	-0.45	1 (0%) 90 88	15, 23, 37, 54	0
1	B	376/403 (93%)	-0.45	3 (0%) 82 80	12, 23, 38, 44	0
1	C	390/403 (96%)	-0.58	2 (0%) 87 85	13, 23, 36, 48	0
1	D	390/403 (96%)	-0.58	0 100 100	12, 23, 37, 51	0
All	All	1532/1612 (95%)	-0.52	6 (0%) 88 86	12, 23, 37, 54	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	179	HIS	2.7
1	B	180	GLY	2.5
1	B	369	ILE	2.3
1	C	57	GLY	2.2
1	A	10	GLY	2.2

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PLP	D	500	15/16	0.94	0.09	37,43,44,44	0
2	PLP	A	500	15/16	0.95	0.11	25,27,29,29	0
2	PLP	C	500	15/16	0.98	0.09	19,23,25,25	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.