



# Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 03:29 am BST

PDB ID : 3N0T  
Title : Human dipeptidil peptidase DPP7 complexed with inhibitor GSK237826A  
Authors : Dobrovetsky, E.; Khutoreskaya, G.; Seitova, A.; Crombet, L.; Cossar, D.; Pagannon, S.; Arrowsmith, C.H.; Bountra, C.; Weigelt, J.; Edwards, A.M.; Hassell, A.; Shewchuk, L.; Haffner, C.; Bochkarev, A.; Structural Genomics Consortium (SGC)  
Deposited on : 2010-05-14  
Resolution : 2.45 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

<https://www.wwpdb.org/validation/2017/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	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

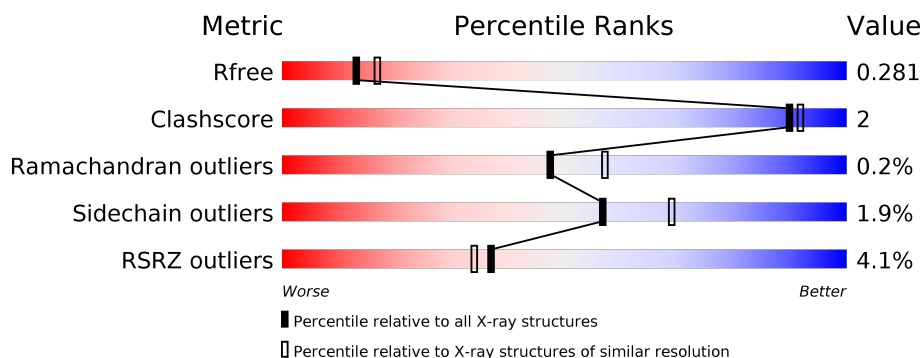
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.45 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))
$R_{free}$	130704	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

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 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	469	<div> <div>%</div> <div> <div></div> <div>91%</div> <div>5%</div> <div>.</div> </div> </div>
1	B	469	<div> <div>2%</div> <div> <div></div> <div>92%</div> <div>.</div> <div>.</div> </div> </div>
1	C	469	<div> <div>6%</div> <div> <div></div> <div>90%</div> <div>6%</div> <div>.</div> </div> </div>
1	D	469	<div> <div>7%</div> <div> <div></div> <div>90%</div> <div>6%</div> <div>.</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14133 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.

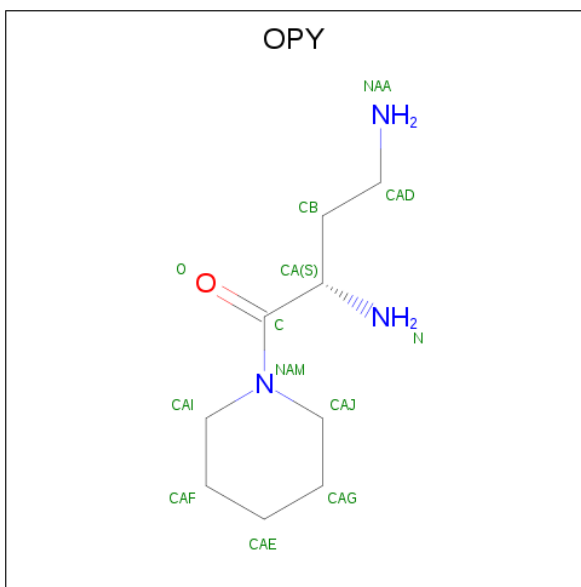
- Molecule 1 is a protein called Dipeptidyl peptidase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	452	Total	C	N	O	S	0	0	0
			3486	2230	601	641	14			
1	B	452	Total	C	N	O	S	0	0	0
			3476	2227	597	638	14			
1	C	451	Total	C	N	O	S	0	0	0
			3449	2210	592	633	14			
1	D	449	Total	C	N	O	S	0	0	0
			3422	2194	586	628	14			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	24	GLY	-	EXPRESSION TAG	UNP Q9UHL4
A	25	ALA	-	EXPRESSION TAG	UNP Q9UHL4
A	26	MET	-	EXPRESSION TAG	UNP Q9UHL4
A	27	ASP	-	EXPRESSION TAG	UNP Q9UHL4
B	24	GLY	-	EXPRESSION TAG	UNP Q9UHL4
B	25	ALA	-	EXPRESSION TAG	UNP Q9UHL4
B	26	MET	-	EXPRESSION TAG	UNP Q9UHL4
B	27	ASP	-	EXPRESSION TAG	UNP Q9UHL4
C	24	GLY	-	EXPRESSION TAG	UNP Q9UHL4
C	25	ALA	-	EXPRESSION TAG	UNP Q9UHL4
C	26	MET	-	EXPRESSION TAG	UNP Q9UHL4
C	27	ASP	-	EXPRESSION TAG	UNP Q9UHL4
D	24	GLY	-	EXPRESSION TAG	UNP Q9UHL4
D	25	ALA	-	EXPRESSION TAG	UNP Q9UHL4
D	26	MET	-	EXPRESSION TAG	UNP Q9UHL4
D	27	ASP	-	EXPRESSION TAG	UNP Q9UHL4

- Molecule 2 is (3S)-4-oxo-4-piperidin-1-ylbutane-1,3-diamine (three-letter code: OPY) (formula: C<sub>9</sub>H<sub>19</sub>N<sub>3</sub>O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			13	9	3	1		
2	B	1	Total	C	N	O	0	0
			13	9	3	1		
2	C	1	Total	C	N	O	0	0
			13	9	3	1		
2	D	1	Total	C	N	O	0	0
			13	9	3	1		

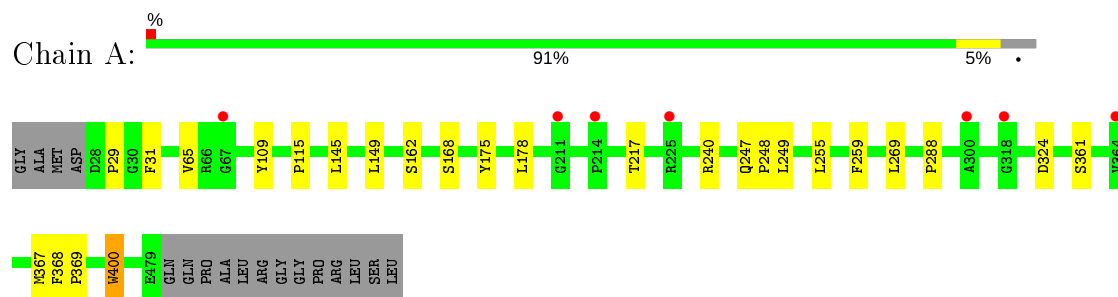
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	89	Total	O	0	0
			89	89		
3	B	87	Total	O	0	0
			87	87		
3	C	41	Total	O	0	0
			41	41		
3	D	31	Total	O	0	0
			31	31		

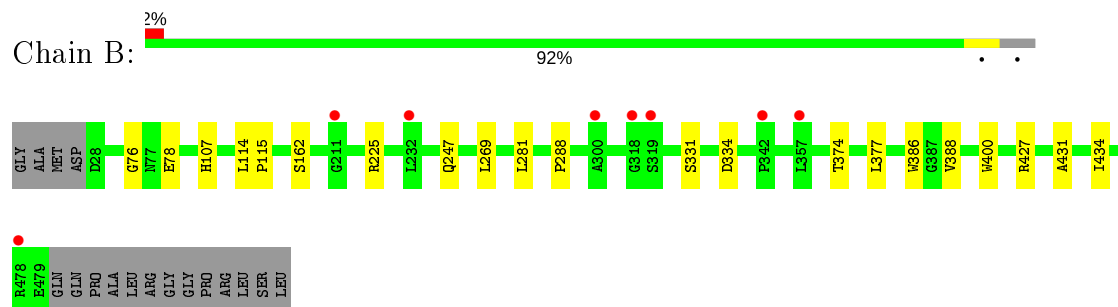
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

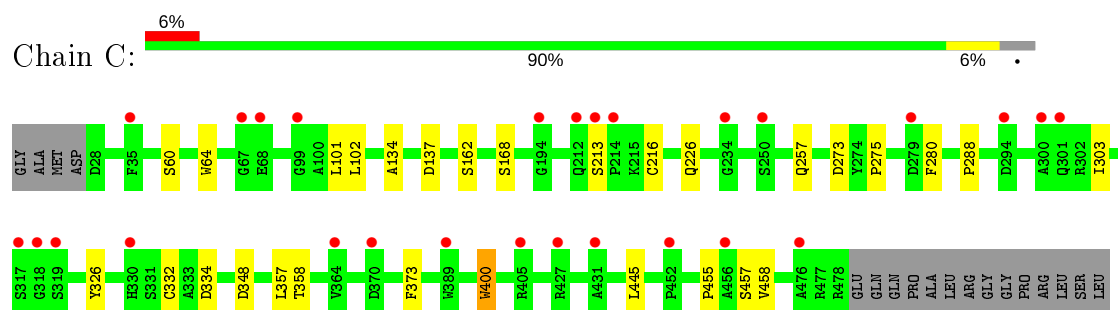
#### • Molecule 1: Dipeptidyl peptidase 2



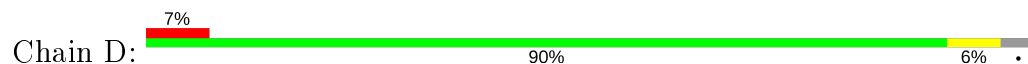
#### • Molecule 1: Dipeptidyl peptidase 2

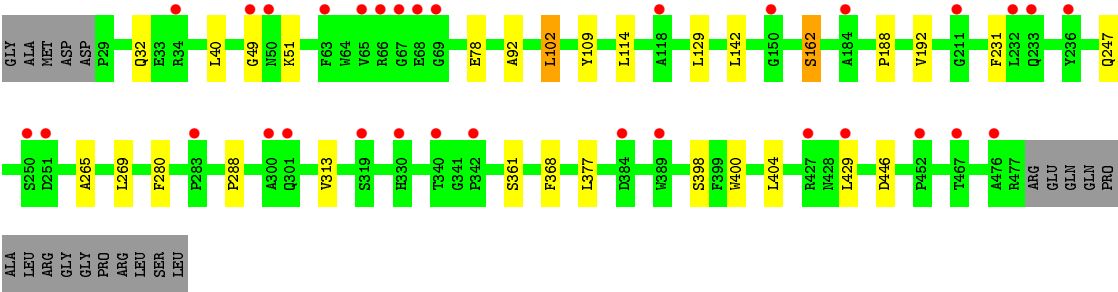


#### • Molecule 1: Dipeptidyl peptidase 2



#### • Molecule 1: Dipeptidyl peptidase 2





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.55Å 130.50Å 125.08Å 90.00° 102.28° 90.00°	Depositor
Resolution (Å)	20.01 – 2.45 20.01 – 2.45	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.01-2.45) 99.4 (20.01-2.45)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.35 (at 2.47Å)	Xtriage
Refinement program	BUSTER-TNT, BUSTER 2.8.0	Depositor
R, $R_{free}$	0.218 , 0.260 0.231 , 0.281	Depositor DCC
$R_{free}$ test set	4609 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	37.4	Xtriage
Anisotropy	0.176	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 59.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	14133	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.95% 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: OPY

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	0.51	0/3584	0.69	0/4879
1	B	0.52	0/3574	0.69	0/4867
1	C	0.50	0/3547	0.67	0/4834
1	D	0.49	0/3520	0.67	0/4800
All	All	0.50	0/14225	0.68	0/19380

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	3486	0	3272	14	0
1	B	3476	0	3256	8	0
1	C	3449	0	3216	16	0
1	D	3422	0	3183	9	0
2	A	13	0	19	2	0
2	B	13	0	19	2	0
2	C	13	0	19	2	0
2	D	13	0	19	1	0
3	A	89	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	87	0	0	0	0
3	C	41	0	0	0	0
3	D	31	0	0	0	0
All	All	14133	0	13003	47	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 (47) 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:C:162:SER:OG	2:C:1001:OPY:HAI	1.99	0.62
1:D:92:ALA:HA	1:D:102:LEU:HD21	1.84	0.60
1:A:145:LEU:O	1:A:149:LEU:HB2	2.06	0.56
1:D:109:TYR:HB2	1:D:129:LEU:HD13	1.89	0.55
1:C:273:ASP:HA	1:C:288:PRO:HD2	1.91	0.53
1:A:162:SER:OG	2:A:1001:OPY:HAI	2.11	0.51
1:C:257:GLN:HE21	1:C:326:TYR:HA	1.75	0.51
1:C:332:CYS:HB2	1:C:348:ASP:OD1	2.11	0.51
1:A:247:GLN:NE2	1:A:324:ASP:OD1	2.44	0.50
1:D:404:LEU:HB2	1:D:429:LEU:HD13	1.94	0.49
1:A:255:LEU:HD11	1:A:259:PHE:CZ	2.48	0.49
1:C:162:SER:HG	2:C:1001:OPY:HAI	1.78	0.48
1:C:358:THR:HA	1:C:373:PHE:HD2	1.79	0.48
1:D:269:LEU:HD22	1:D:288:PRO:HB2	1.95	0.48
1:C:134:ALA:O	1:C:137:ASP:HB2	2.13	0.47
1:D:162:SER:OG	2:D:1001:OPY:HAI	2.15	0.47
1:B:162:SER:OG	2:B:1001:OPY:HAI	2.15	0.47
1:B:269:LEU:HD22	1:B:288:PRO:HB2	1.97	0.47
1:A:109:TYR:CE2	1:A:115:PRO:HG2	2.50	0.46
1:C:334:ASP:CG	1:C:357:LEU:HD13	2.36	0.46
1:B:386:TRP:HB2	1:B:388:VAL:HG22	1.97	0.46
1:A:217:THR:HG22	1:A:367:MET:SD	2.57	0.45
1:C:400:TRP:N	1:C:400:TRP:CD1	2.83	0.45
1:A:29:PRO:HG2	1:A:31:PHE:CE2	2.52	0.44
1:B:374:THR:H	1:B:377:LEU:HD12	1.82	0.44
1:A:269:LEU:HD22	1:A:288:PRO:HB2	1.99	0.44
1:D:361:SER:HB2	1:D:368:PHE:HB2	2.00	0.43
1:B:431:ALA:O	1:B:434:ILE:HD11	2.19	0.43
1:A:400:TRP:N	1:A:400:TRP:CD1	2.86	0.43
1:C:60:SER:HB3	1:C:102:LEU:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:446:ASP:N	1:D:446:ASP:OD1	2.52	0.42
1:C:213:SER:HB3	1:C:216:CYS:HB2	2.01	0.42
1:C:358:THR:HA	1:C:373:PHE:CD2	2.54	0.42
1:B:114:LEU:HA	1:B:115:PRO:HD3	1.94	0.42
1:B:334:ASP:OD2	2:B:1001:OPY:HA	2.18	0.42
1:C:445:LEU:HG	1:C:458:VAL:HG21	2.00	0.42
1:A:259:PHE:CG	1:A:369:PRO:HG2	2.55	0.41
1:C:226:GLN:HB3	1:C:303:ILE:HD11	2.02	0.41
1:B:76:GLY:O	1:B:107:HIS:HB2	2.20	0.41
1:C:275:PRO:HG3	1:C:455:PRO:HD3	2.02	0.41
1:A:175:TYR:HB3	1:A:178:LEU:HD12	2.03	0.41
1:D:265:ALA:HA	1:D:313:VAL:HG21	2.03	0.41
1:D:188:PRO:O	1:D:192:VAL:HG22	2.21	0.41
1:A:361:SER:HB2	1:A:368:PHE:HB2	2.03	0.41
1:C:64:TRP:CG	1:C:101:LEU:HB2	2.56	0.41
1:A:162:SER:HG	2:A:1001:OPY:HAI	1.86	0.40
1:A:240:ARG:HD2	1:A:248:PRO:HA	2.04	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	450/469 (96%)	427 (95%)	23 (5%)	0	100	100
1	B	450/469 (96%)	431 (96%)	18 (4%)	1 (0%)	47	57
1	C	449/469 (96%)	419 (93%)	30 (7%)	0	100	100
1	D	447/469 (95%)	421 (94%)	23 (5%)	3 (1%)	22	25
All	All	1796/1876 (96%)	1698 (94%)	94 (5%)	4 (0%)	47	57

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	51	LYS
1	B	78	GLU
1	D	49	GLY
1	D	78	GLU

### 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	343/371 (92%)	339 (99%)	4 (1%)	71	81
1	B	339/371 (91%)	333 (98%)	6 (2%)	59	71
1	C	335/371 (90%)	331 (99%)	4 (1%)	71	81
1	D	332/371 (90%)	320 (96%)	12 (4%)	35	46
All	All	1349/1484 (91%)	1323 (98%)	26 (2%)	57	69

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	VAL
1	A	168	SER
1	A	249	LEU
1	A	400	TRP
1	B	225	ARG
1	B	247	GLN
1	B	281	LEU
1	B	331	SER
1	B	400	TRP
1	B	427	ARG
1	C	168	SER
1	C	280	PHE
1	C	400	TRP
1	C	457	SER
1	D	32	GLN
1	D	40	LEU
1	D	102	LEU
1	D	114	LEU

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Mol	Chain	Res	Type
1	D	142	LEU
1	D	162	SER
1	D	231	PHE
1	D	247	GLN
1	D	280	PHE
1	D	377	LEU
1	D	398	SER
1	D	400	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	38	GLN
1	D	247	GLN
1	D	330	HIS

### 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 [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
2	OPY	C	1001	-	13,13,13	0.83	0	15,16,16	1.42	2 (13%)
2	OPY	B	1001	-	13,13,13	0.72	0	15,16,16	1.32	2 (13%)
2	OPY	D	1001	-	13,13,13	0.75	0	15,16,16	1.36	2 (13%)
2	OPY	A	1001	-	13,13,13	0.73	0	15,16,16	1.30	3 (20%)

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	OPY	C	1001	-	-	0/11/19/19	0/1/1/1
2	OPY	B	1001	-	-	2/11/19/19	0/1/1/1
2	OPY	D	1001	-	-	0/11/19/19	0/1/1/1
2	OPY	A	1001	-	-	0/11/19/19	0/1/1/1

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1001	OPY	CAJ-NAM-CAI	4.10	120.51	112.62
2	C	1001	OPY	CAJ-NAM-CAI	3.68	119.70	112.62
2	B	1001	OPY	CAJ-NAM-CAI	3.47	119.31	112.62
2	A	1001	OPY	CAJ-NAM-CAI	2.92	118.24	112.62
2	A	1001	OPY	CA-C-NAM	2.59	122.78	118.87
2	A	1001	OPY	O-C-NAM	-2.49	118.75	121.67
2	C	1001	OPY	O-C-NAM	-2.37	118.90	121.67
2	B	1001	OPY	CA-C-NAM	2.17	122.14	118.87
2	D	1001	OPY	O-C-NAM	-2.03	119.29	121.67

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1001	OPY	O-C-CA-N
2	B	1001	OPY	O-C-CA-CB

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1001	OPY	2	0
2	B	1001	OPY	2	0
2	D	1001	OPY	1	0
2	A	1001	OPY	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 ⓘ

### 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	452/469 (96%)	-0.11	7 (1%) 73 71	22, 33, 52, 66	0
1	B	452/469 (96%)	-0.06	8 (1%) 68 65	23, 33, 49, 79	0
1	C	451/469 (96%)	0.28	27 (5%) 21 18	31, 46, 64, 79	0
1	D	449/469 (95%)	0.35	32 (7%) 16 12	30, 47, 65, 77	0
All	All	1804/1876 (96%)	0.11	74 (4%) 37 34	22, 41, 60, 79	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	67	GLY	5.9
1	C	389	TRP	4.4
1	C	431	ALA	3.8
1	D	118	ALA	3.6
1	B	478	ARG	3.5
1	A	67	GLY	3.4
1	C	318	GLY	3.4
1	C	364	VAL	3.4
1	D	67	GLY	3.3
1	D	211	GLY	3.2
1	D	429	LEU	3.1
1	D	384	ASP	3.1
1	D	476	ALA	3.0
1	D	319	SER	3.0
1	C	300	ALA	3.0
1	D	301	GLN	2.9
1	C	317	SER	2.9
1	D	342	PRO	2.8
1	C	213	SER	2.8
1	D	236	TYR	2.8
1	D	330	HIS	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	68	GLU	2.8
1	D	250	SER	2.8
1	C	212	GLN	2.8
1	C	476	ALA	2.8
1	B	319	SER	2.7
1	D	34	ARG	2.7
1	C	370	ASP	2.7
1	C	301	GLN	2.7
1	C	330	HIS	2.7
1	D	389	TRP	2.7
1	A	364	VAL	2.6
1	C	319	SER	2.6
1	B	342	PRO	2.6
1	D	49	GLY	2.6
1	A	211	GLY	2.6
1	D	150	GLY	2.6
1	D	427	ARG	2.6
1	D	232	LEU	2.5
1	D	283	PRO	2.5
1	D	63	PHE	2.5
1	D	467	THR	2.5
1	B	232	LEU	2.5
1	C	452	PRO	2.5
1	A	318	GLY	2.5
1	D	452	PRO	2.4
1	D	50	ASN	2.4
1	D	300	ALA	2.4
1	C	456	ALA	2.3
1	D	65	VAL	2.3
1	B	318	GLY	2.3
1	D	340	THR	2.3
1	C	214	PRO	2.2
1	C	194	GLY	2.2
1	D	251	ASP	2.2
1	C	68	GLU	2.2
1	D	184	ALA	2.2
1	B	211	GLY	2.2
1	C	35	PHE	2.2
1	D	233	GLN	2.1
1	D	66	ARG	2.1
1	A	214	PRO	2.1
1	C	234	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	69	GLY	2.1
1	B	357	LEU	2.1
1	C	405	ARG	2.1
1	A	300	ALA	2.1
1	C	250	SER	2.1
1	B	300	ALA	2.1
1	A	225	ARG	2.1
1	C	427	ARG	2.1
1	C	294	ASP	2.0
1	C	99	GLY	2.0
1	C	279	ASP	2.0

## 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 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. 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	OPY	A	1001	13/13	0.95	0.16	20,25,43,43	0
2	OPY	D	1001	13/13	0.96	0.12	24,32,66,76	0
2	OPY	C	1001	13/13	0.96	0.13	19,38,71,78	0
2	OPY	B	1001	13/13	0.97	0.13	9,26,42,42	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.