



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 21, 2016 – 08:16 AM EST

PDB ID : 5F7K  
Title : Blood group antigen binding adhesin BabA of *Helicobacter pylori* strain 17875 in complex with Nanobody Nb-ER19  
Authors : Moonens, K.; Gideonsson, P.; Subedi, S.; Romao, E.; Oscarson, S.; Muyldermans, S.; Boren, T.; Remaut, H.  
Deposited on : 2015-12-08  
Resolution : 2.17 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.

---

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

MolProbity	:	4.02b-467
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20028442
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)	:	rb-20028442

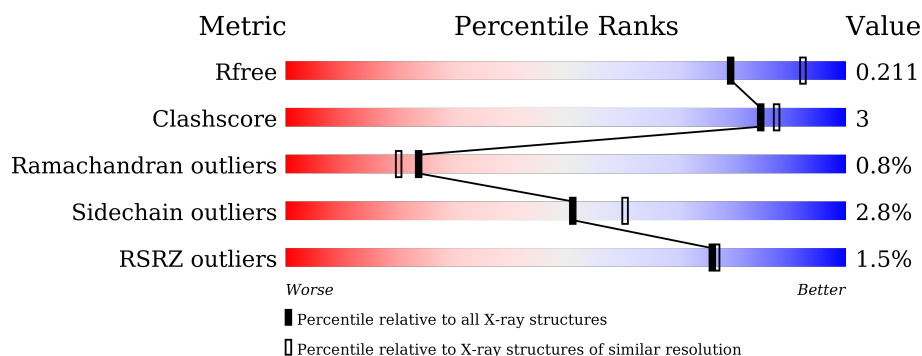
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.17 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	5130 (2.20-2.16)
Clashscore	102246	5965 (2.20-2.16)
Ramachandran outliers	100387	5863 (2.20-2.16)
Sidechain outliers	100360	5864 (2.20-2.16)
RSRZ outliers	91569	5142 (2.20-2.16)

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	466	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 82%, grey 16%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>82%</span> <span>6% • 10%</span> </div> </div>
1	B	466	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 2%, orange 1%, yellow 1%, green 83%, grey 13%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>2%</span> <span>83%</span> <span>6% • 10%</span> </div> </div>
2	C	120	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 87%, grey 10%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>87%</span> <span>7% • 6%</span> </div> </div>
2	D	120	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 87%, yellow 1%, grey 12%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span></span> <span>87%</span> <span>8% 5%</span> </div> </div>

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 8518 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 Adhesin binding fucosylated histo-blood group antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	420	Total	C	N	O	S	0	3	0
			3145	1939	541	652	13			
1	B	421	Total	C	N	O	S	0	1	0
			3146	1939	544	650	13			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3	ALA	-	expression tag	UNP O52269
A	4	SER	-	expression tag	UNP O52269
A	5	TRP	-	expression tag	UNP O52269
A	6	SER	-	expression tag	UNP O52269
A	7	HIS	-	expression tag	UNP O52269
A	8	PRO	-	expression tag	UNP O52269
A	9	GLN	-	expression tag	UNP O52269
A	10	PHE	-	expression tag	UNP O52269
A	11	GLU	-	expression tag	UNP O52269
A	12	LYS	-	expression tag	UNP O52269
A	13	SER	-	expression tag	UNP O52269
A	14	GLY	-	expression tag	UNP O52269
A	15	GLY	-	expression tag	UNP O52269
A	16	GLY	-	expression tag	UNP O52269
A	17	GLY	-	expression tag	UNP O52269
A	18	GLY	-	expression tag	UNP O52269
A	19	LEU	-	expression tag	UNP O52269
A	20	VAL	-	expression tag	UNP O52269
A	21	PRO	-	expression tag	UNP O52269
A	22	ARG	-	expression tag	UNP O52269
A	23	GLY	-	expression tag	UNP O52269
A	24	SER	-	expression tag	UNP O52269
A	461	GLY	-	expression tag	UNP O52269
A	462	SER	-	expression tag	UNP O52269
A	463	HIS	-	expression tag	UNP O52269

*Continued on next page...*

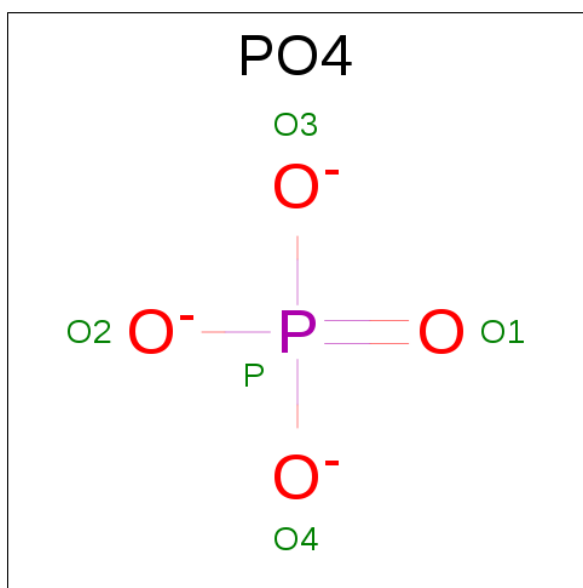
*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A	464	HIS	-	expression tag	UNP O52269
A	465	HIS	-	expression tag	UNP O52269
A	466	HIS	-	expression tag	UNP O52269
A	467	HIS	-	expression tag	UNP O52269
A	468	HIS	-	expression tag	UNP O52269
B	3	ALA	-	expression tag	UNP O52269
B	4	SER	-	expression tag	UNP O52269
B	5	TRP	-	expression tag	UNP O52269
B	6	SER	-	expression tag	UNP O52269
B	7	HIS	-	expression tag	UNP O52269
B	8	PRO	-	expression tag	UNP O52269
B	9	GLN	-	expression tag	UNP O52269
B	10	PHE	-	expression tag	UNP O52269
B	11	GLU	-	expression tag	UNP O52269
B	12	LYS	-	expression tag	UNP O52269
B	13	SER	-	expression tag	UNP O52269
B	14	GLY	-	expression tag	UNP O52269
B	15	GLY	-	expression tag	UNP O52269
B	16	GLY	-	expression tag	UNP O52269
B	17	GLY	-	expression tag	UNP O52269
B	18	GLY	-	expression tag	UNP O52269
B	19	LEU	-	expression tag	UNP O52269
B	20	VAL	-	expression tag	UNP O52269
B	21	PRO	-	expression tag	UNP O52269
B	22	ARG	-	expression tag	UNP O52269
B	23	GLY	-	expression tag	UNP O52269
B	24	SER	-	expression tag	UNP O52269
B	461	GLY	-	expression tag	UNP O52269
B	462	SER	-	expression tag	UNP O52269
B	463	HIS	-	expression tag	UNP O52269
B	464	HIS	-	expression tag	UNP O52269
B	465	HIS	-	expression tag	UNP O52269
B	466	HIS	-	expression tag	UNP O52269
B	467	HIS	-	expression tag	UNP O52269
B	468	HIS	-	expression tag	UNP O52269

- Molecule 2 is a protein called Nanobody Nb-ER19.

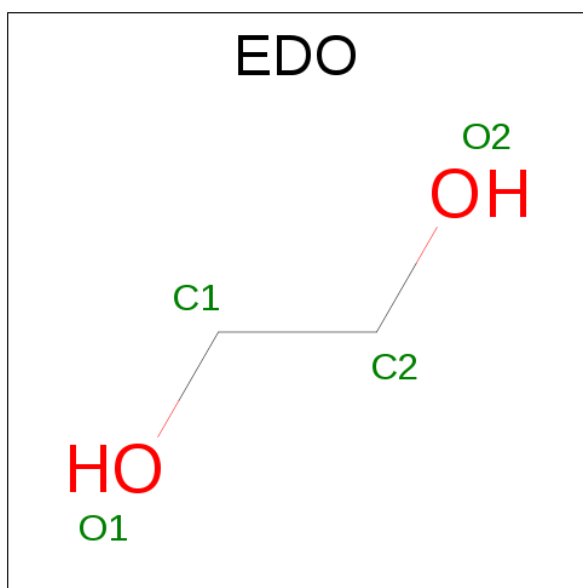
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	113	Total	C	N	O	S	0	0	0
			863	540	155	163	5			
2	D	114	Total	C	N	O	S	0	0	0
			873	546	158	164	5			

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula:  $O_4P$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	1	Total 1	Na 1	0	0

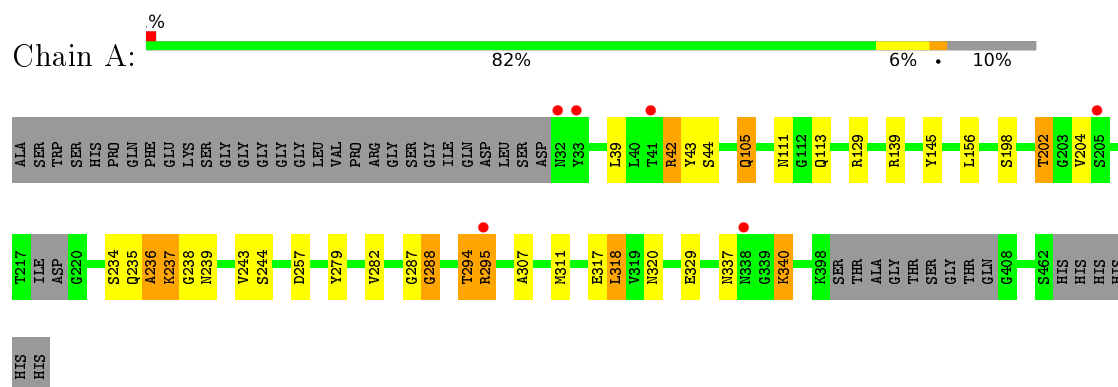
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	176	Total 176	O 176	0	0
6	C	54	Total 54	O 54	0	0
6	B	158	Total 158	O 158	0	0
6	D	93	Total 93	O 93	0	0

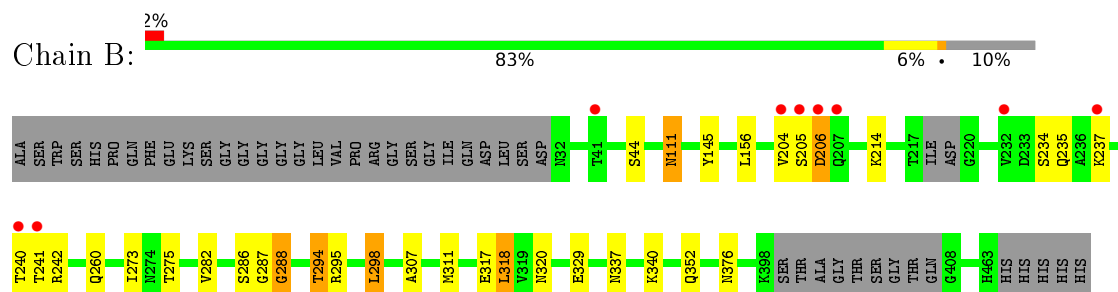
### 3 Residue-property plots [i](#)

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

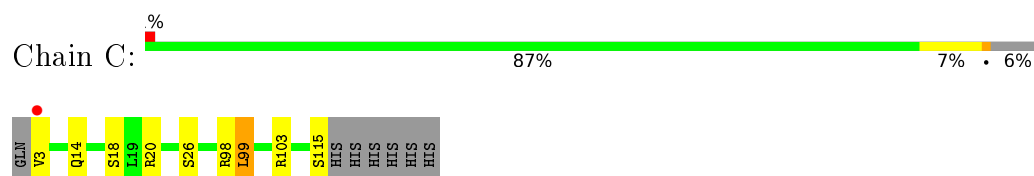
- Molecule 1: Adhesin binding fucosylated histo-blood group antigen



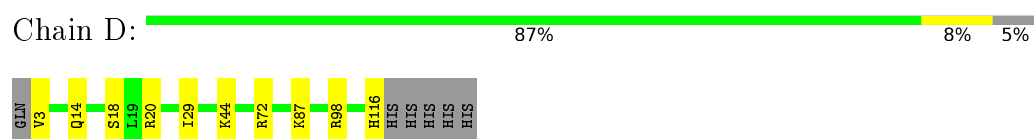
- Molecule 1: Adhesin binding fucosylated histo-blood group antigen



- Molecule 2: Nanobody Nb-ER19



- Molecule 2: Nanobody Nb-ER19



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	50.99Å 131.66Å 123.46Å 90.00° 94.77° 90.00°	Depositor
Resolution (Å)	58.04 – 2.17 58.04 – 2.17	Depositor EDS
% Data completeness (in resolution range)	99.4 (58.04-2.17) 99.4 (58.04-2.17)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.17 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, $R_{free}$	0.171 , 0.207 0.178 , 0.211	Depositor DCC
$R_{free}$ test set	4261 reflections (5.27%)	DCC
Wilson B-factor (Å <sup>2</sup> )	46.1	Xtriage
Anisotropy	0.109	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 48.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	8518	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.53% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, PO4, EDO

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	0.94	3/3197 (0.1%)	0.88	5/4344 (0.1%)
1	B	0.88	0/3193	0.86	2/4338 (0.0%)
2	C	0.94	1/882 (0.1%)	1.01	4/1195 (0.3%)
2	D	1.09	2/893 (0.2%)	1.00	2/1210 (0.2%)
All	All	0.94	6/8165 (0.1%)	0.90	13/11087 (0.1%)

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	B	0	1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	18	SER	CB-OG	-5.79	1.34	1.42
1	A	105	GLN	CG-CD	5.74	1.64	1.51
2	C	18	SER	CB-OG	-5.34	1.35	1.42
2	D	98	ARG	CZ-NH2	-5.27	1.26	1.33
1	A	317[A]	GLU	CD-OE2	5.25	1.31	1.25
1	A	317[B]	GLU	CD-OE2	5.25	1.31	1.25

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	318	LEU	CA-CB-CG	7.89	133.45	115.30
1	B	318	LEU	CA-CB-CG	7.88	133.42	115.30
2	C	99	LEU	CA-CB-CG	6.82	130.98	115.30

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	44	LYS	CB-CA-C	-5.78	98.84	110.40
2	C	99	LEU	CB-CG-CD2	5.66	120.63	111.00
2	C	20	ARG	NE-CZ-NH2	-5.64	117.48	120.30
1	A	317[A]	GLU	CA-CB-CG	5.54	125.60	113.40
1	A	317[B]	GLU	CA-CB-CG	5.54	125.60	113.40
1	B	295	ARG	CA-CB-CG	5.37	125.20	113.40
2	C	98	ARG	NE-CZ-NH1	5.27	122.94	120.30
1	A	139	ARG	NE-CZ-NH2	-5.24	117.68	120.30
2	D	72	ARG	NE-CZ-NH1	5.20	122.90	120.30
1	A	257	ASP	CB-CG-OD2	-5.16	113.66	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	286	SER	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	3145	0	3067	24	0
1	B	3146	0	3063	15	0
2	C	863	0	845	3	0
2	D	873	0	852	4	0
3	A	5	0	0	0	0
4	A	4	0	6	0	0
5	C	1	0	0	0	0
6	A	176	0	0	1	0
6	B	158	0	0	5	0
6	C	54	0	0	1	0
6	D	93	0	0	2	0
All	All	8518	0	7833	46	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 3.

All (46) 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:B:317:GLU:HG2	6:B:644:HOH:O	1.47	1.12
1:A:202:THR:HG22	1:A:204:VAL:H	1.43	0.82
1:A:129:ARG:NH1	6:A:602:HOH:O	2.15	0.80
1:A:198:SER:O	1:A:202:THR:HB	1.87	0.75
1:A:243:VAL:HG12	1:A:244:SER:H	1.53	0.72
1:A:234:SER:CB	1:A:243:VAL:HA	2.25	0.67
2:D:20:ARG:NH1	6:D:201:HOH:O	2.21	0.65
1:B:234:SER:OG	6:B:501:HOH:O	2.14	0.64
1:B:352[A]:GLN:HG3	6:B:548:HOH:O	1.99	0.63
2:C:103:ARG:HG2	6:C:353:HOH:O	1.98	0.62
2:C:3:VAL:N	2:C:26:SER:HG	1.98	0.60
2:D:14:GLN:OE1	2:D:116:HIS:HB3	2.01	0.60
1:A:243:VAL:CG1	1:A:244:SER:H	2.16	0.58
1:B:204:VAL:HG12	1:B:206:ASP:O	2.05	0.57
1:A:235:GLN:O	1:A:236:ALA:O	2.22	0.57
1:A:39:LEU:HD13	1:A:39:LEU:C	2.25	0.56
1:B:273:ILE:HG23	1:B:298:LEU:HD23	1.88	0.55
1:A:42:ARG:NH1	1:A:43:TYR:OH	2.34	0.55
1:A:105:GLN:OE1	1:A:279:TYR:CD2	2.60	0.54
1:B:275:THR:OG1	6:B:502:HOH:O	2.19	0.53
1:A:234:SER:HB2	1:A:243:VAL:HA	1.89	0.53
1:A:235:GLN:O	1:A:236:ALA:C	2.49	0.51
1:A:287:GLY:O	1:A:288:GLY:O	2.30	0.51
1:B:287:GLY:O	1:B:288:GLY:O	2.29	0.50
1:B:307:ALA:C	1:B:311:MET:HE2	2.31	0.50
2:D:87:LYS:HE3	6:D:253:HOH:O	2.10	0.50
1:A:202:THR:HG23	1:A:204:VAL:HG23	1.94	0.49
1:A:111:ASN:OD1	1:A:113:GLN:HB2	2.12	0.48
1:B:307:ALA:O	1:B:311:MET:HE2	2.12	0.48
2:D:3:VAL:HG13	2:D:29:ILE:HG13	1.95	0.48
1:B:156:LEU:HD23	1:B:156:LEU:C	2.34	0.48
1:A:307:ALA:O	1:A:311:MET:HE3	2.14	0.47
1:B:376:ASN:HB3	6:B:551:HOH:O	2.15	0.47
1:A:279:TYR:CE1	1:A:295:ARG:HG3	2.50	0.46
1:B:111:ASN:OD1	1:B:111:ASN:N	2.46	0.46
1:A:307:ALA:C	1:A:311:MET:HE3	2.36	0.45
1:A:156:LEU:HD23	1:A:156:LEU:C	2.39	0.43
1:B:240:THR:O	1:B:242:ARG:N	2.52	0.43
1:A:282:VAL:HG22	1:A:294:THR:HA	2.01	0.43
1:A:337:ASN:O	1:A:340:LYS:CG	2.67	0.43
1:A:237:LYS:O	1:A:239:ASN:N	2.53	0.41

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:3:VAL:HB	2:C:26:SER:HB3	2.01	0.41
1:B:337:ASN:O	1:B:340:LYS:HG2	2.21	0.41
1:B:282:VAL:HG22	1:B:294:THR:HA	2.01	0.41
1:A:236:ALA:O	1:A:237:LYS:O	2.39	0.40
1:A:111:ASN:CG	1:A:113:GLN:HG2	2.42	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	417/466 (90%)	399 (96%)	14 (3%)	4 (1%)	19	15
1	B	416/466 (89%)	396 (95%)	16 (4%)	4 (1%)	19	15
2	C	111/120 (92%)	107 (96%)	4 (4%)	0	100	100
2	D	112/120 (93%)	110 (98%)	2 (2%)	0	100	100
All	All	1056/1172 (90%)	1012 (96%)	36 (3%)	8 (1%)	24	20

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	237	LYS
1	B	288	GLY
1	A	236	ALA
1	A	288	GLY
1	B	241	THR
1	B	237	LYS
1	A	238	GLY
1	B	205	SER

### 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	349/381 (92%)	339 (97%)	10 (3%)	50	59
1	B	348/381 (91%)	336 (97%)	12 (3%)	44	52
2	C	92/99 (93%)	89 (97%)	3 (3%)	45	53
2	D	93/99 (94%)	93 (100%)	0	100	100
All	All	882/960 (92%)	857 (97%)	25 (3%)	51	60

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	ARG
1	A	44	SER
1	A	145	TYR
1	A	202	THR
1	A	294	THR
1	A	295	ARG
1	A	318	LEU
1	A	320	ASN
1	A	329	GLU
1	A	340	LYS
2	C	14	GLN
2	C	99	LEU
2	C	115	SER
1	B	44	SER
1	B	111	ASN
1	B	145	TYR
1	B	206	ASP
1	B	214	LYS
1	B	235	GLN
1	B	260	GLN
1	B	294	THR
1	B	298	LEU
1	B	318	LEU
1	B	320	ASN
1	B	329	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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	PO4	A	501	-	4,4,4	0.34	0	6,6,6	0.35	0
4	EDO	A	502	-	3,3,3	0.56	0	2,2,2	0.68	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
3	PO4	A	501	-	-	0/0/0/0	0/0/0/0
4	EDO	A	502	-	-	0/1/1/1	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	420/466 (90%)	0.11	6 (1%) 78 78	36, 48, 95, 128	0
1	B	421/466 (90%)	0.17	9 (2%) 67 68	35, 52, 98, 128	0
2	C	113/120 (94%)	-0.14	1 (0%) 85 86	39, 49, 66, 85	0
2	D	114/120 (95%)	0.02	0 100 100	32, 42, 57, 80	0
All	All	1068/1172 (91%)	0.10	16 (1%) 76 77	32, 49, 95, 128	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	241	THR	4.2
1	A	41	THR	3.6
1	B	204	VAL	3.5
1	B	232	VAL	3.4
1	B	207	GLN	3.3
1	A	32	ASN	2.6
2	C	3	VAL	2.6
1	B	205	SER	2.5
1	A	33	TYR	2.5
1	A	338	ASN	2.4
1	A	205	SER	2.3
1	A	295	ARG	2.2
1	B	206	ASP	2.2
1	B	41	THR	2.2
1	B	237	LYS	2.1
1	B	240	THR	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. 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	PO4	A	501	5/5	0.92	0.17	1.19	73,79,97,108	0
4	EDO	A	502	4/4	0.90	0.11	-0.97	33,39,46,46	0
5	NA	C	201	1/1	0.93	0.18	-	48,48,48,48	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.