



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:32 AM GMT

PDB ID : 2HJ9  
Title : Crystal structure of the Autoinducer-2-bound form of Vibrio harveyi LuxP complexed with the periplasmic domain of LuxQ  
Authors : Neiditch, M.B.; Hughson, F.M.  
Deposited on : 2006-06-30  
Resolution : 2.34 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

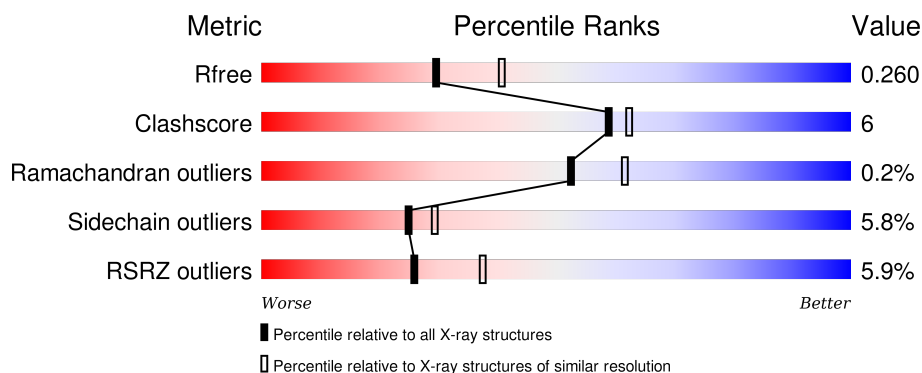
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.34 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	1406 (2.36-2.32)
Clashscore	102246	1509 (2.36-2.32)
Ramachandran outliers	100387	1490 (2.36-2.32)
Sidechain outliers	100360	1491 (2.36-2.32)
RSRZ outliers	91569	1412 (2.36-2.32)

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	339	<div> <div>6%</div> <div> <div></div> <div>84%</div> <div>14%</div> <div>•</div> </div> </div>
1	B	339	<div> <div>7%</div> <div> <div></div> <div>79%</div> <div>16%</div> <div>• •</div> </div> </div>
2	C	221	<div> <div>2%</div> <div> <div></div> <div>80%</div> <div>13%</div> <div>• 5%</div> </div> </div>
2	D	221	<div> <div>7%</div> <div> <div></div> <div>75%</div> <div>15%</div> <div>• 8%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9092 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 Autoinducer 2-binding periplasmic protein luxP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	339	Total	C	N	O	S	0	0	0
			2736	1741	462	527	6			
1	B	329	Total	C	N	O	S	0	0	0
			2659	1694	448	511	6			

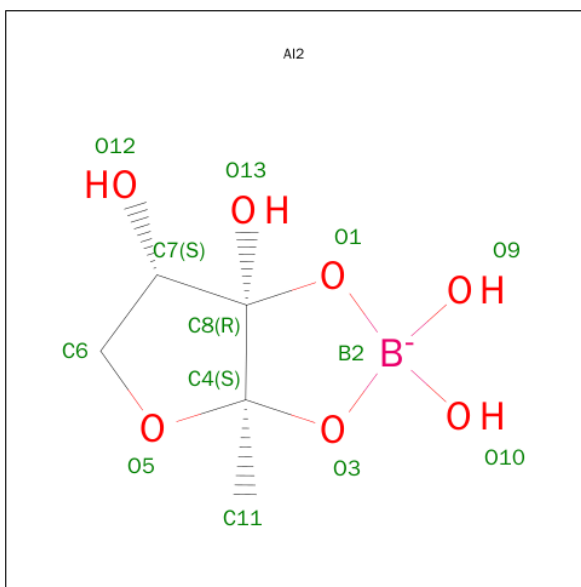
- Molecule 2 is a protein called Autoinducer 2 sensor kinase/phosphatase luxQ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	210	Total	C	N	O	S	0	0	0
			1667	1060	281	322	4			
2	D	203	Total	C	N	O	S	0	0	0
			1610	1028	268	310	4			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	51	GLY	-	SEE REMARK 999	UNP P54302
C	52	SER	-	SEE REMARK 999	UNP P54302
D	51	GLY	-	SEE REMARK 999	UNP P54302
D	52	SER	-	SEE REMARK 999	UNP P54302

- Molecule 3 is 3A-METHYL-5,6-DIHYDRO-FURO[2,3-D][1,3,2]DIOXABOROLE-2,2,6,6A-TETRAOL (three-letter code: AI2) (formula: C<sub>5</sub>H<sub>10</sub>BO<sub>7</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	B	C	O	0	0
			13	1	5	7		
3	B	1	Total	B	C	O	0	0
			13	1	5	7		

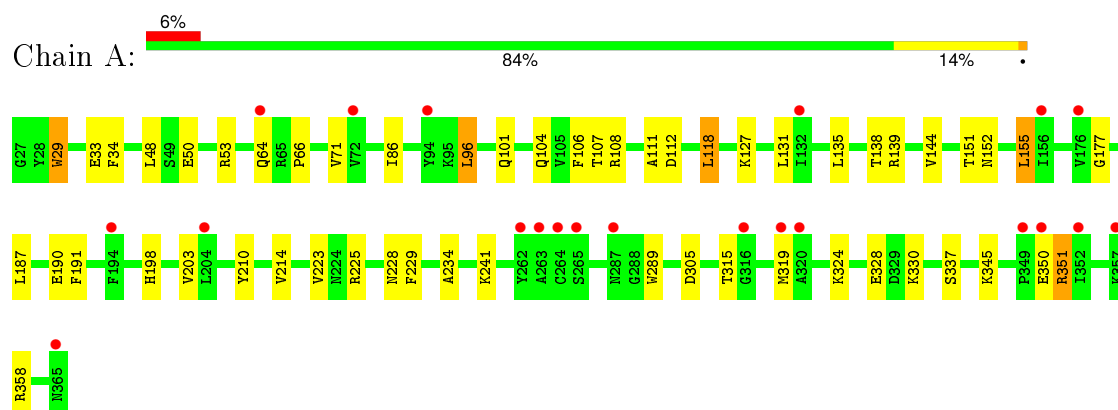
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	139	Total	O	0	0
			139	139		
4	B	105	Total	O	0	0
			105	105		
4	C	95	Total	O	0	0
			95	95		
4	D	55	Total	O	0	0
			55	55		

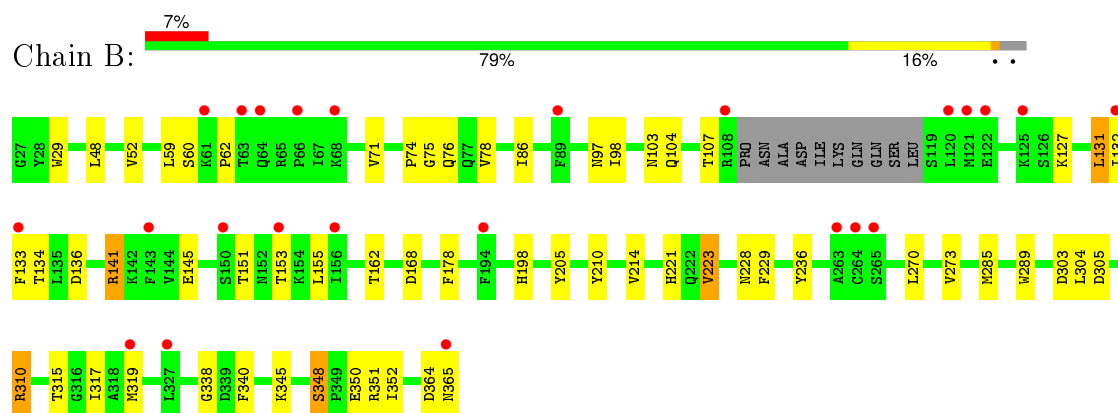
### 3 Residue-property plots [i](#)

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.

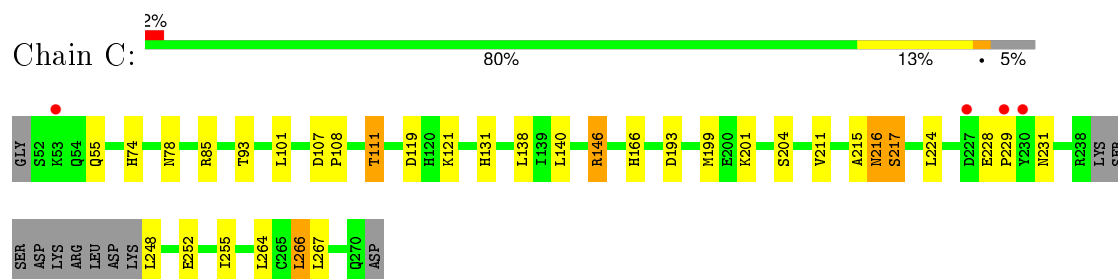
- Molecule 1: Autoinducer 2-binding periplasmic protein luxP



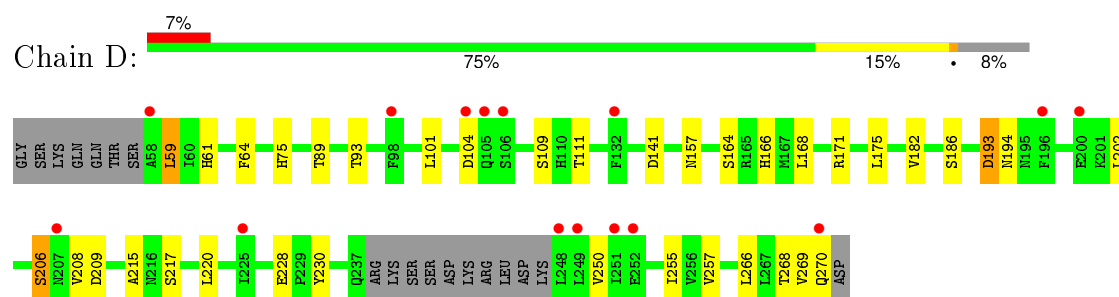
- Molecule 1: Autoinducer 2-binding periplasmic protein luxP



- Molecule 2: Autoinducer 2 sensor kinase/phosphatase luxQ



- Molecule 2: Autoinducer 2 sensor kinase/phosphatase luxQ



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.92Å 83.92Å 365.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.70 – 2.34 29.67 – 2.34	Depositor EDS
% Data completeness (in resolution range)	98.4 (29.70-2.34) 98.4 (29.67-2.34)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.41 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.207 , 0.262 0.205 , 0.260	Depositor DCC
$R_{free}$ test set	2827 reflections (5.36%)	DCC
Wilson B-factor (Å <sup>2</sup> )	52.5	Xtriage
Anisotropy	0.003	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 38.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 55555 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	9092	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.18% 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: AI2

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	0.64	0/2801	0.69	0/3796
1	B	0.61	0/2722	0.69	2/3687 (0.1%)
2	C	0.65	0/1702	0.74	0/2320
2	D	0.58	0/1645	0.66	0/2245
All	All	0.62	0/8870	0.70	2/12048 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	310	ARG	NE-CZ-NH2	-5.53	117.53	120.30
1	B	168	ASP	CB-CG-OD1	5.07	122.86	118.30

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	2736	0	2654	32	0
1	B	2659	0	2575	30	0
2	C	1667	0	1620	22	0
2	D	1610	0	1561	18	0
3	A	13	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	13	0	10	0	0
4	A	139	0	0	8	0
4	B	105	0	0	3	0
4	C	95	0	0	6	0
4	D	55	0	0	2	0
All	All	9092	0	8430	100	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 6.

All (100) 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:71:VAL:HG11	1:A:86:ILE:HD11	1.43	0.97
2:D:59:LEU:HB3	4:D:281:HOH:O	1.72	0.88
2:C:255:ILE:HD11	2:C:266:LEU:CD2	2.10	0.82
1:B:132:ILE:HD13	1:B:319:MET:HE1	1.61	0.82
1:B:348:SER:HB2	1:B:350:GLU:HG2	1.64	0.79
2:D:202:LEU:O	2:D:206:SER:OG	2.02	0.78
1:B:75:GLY:HA2	4:B:598:HOH:O	1.84	0.77
1:A:138:THR:HG21	2:C:111:THR:HG21	1.68	0.73
2:C:255:ILE:HD11	2:C:266:LEU:HD23	1.69	0.73
2:C:107:ASP:O	2:C:111:THR:HG22	1.89	0.73
1:A:139:ARG:NE	4:A:594:HOH:O	2.21	0.72
1:B:223:VAL:HG13	1:B:229:PHE:HB2	1.72	0.71
1:A:223:VAL:HG13	1:A:229:PHE:HB2	1.72	0.70
2:C:252:GLU:HG2	2:C:267:LEU:CD2	2.22	0.69
2:D:75:HIS:HE1	2:D:186:SER:OG	1.76	0.68
2:D:93:THR:HG22	4:D:308:HOH:O	1.95	0.66
1:B:315:THR:O	1:B:319:MET:HG3	1.95	0.66
2:D:166:HIS:HD2	2:D:193:ASP:OD1	1.79	0.65
1:A:139:ARG:NH2	4:A:594:HOH:O	2.29	0.64
1:A:144:VAL:HG13	1:A:155:LEU:HD11	1.80	0.63
1:B:52:VAL:HG22	1:B:317:ILE:HG22	1.81	0.62
2:D:250:VAL:HG22	2:D:269:VAL:HG22	1.83	0.61
1:B:86:ILE:HG21	1:B:104:GLN:HE22	1.67	0.60
2:C:255:ILE:HD11	2:C:266:LEU:HD22	1.82	0.59
2:D:157:ASN:ND2	2:D:166:HIS:CE1	2.71	0.59
1:A:118:LEU:HD13	2:C:131:HIS:HB3	1.84	0.59
1:A:71:VAL:HG11	1:A:86:ILE:CD1	2.28	0.58
1:A:210:TYR:O	1:A:214:VAL:HG22	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:64:PHE:CD1	2:D:266:LEU:HD11	2.39	0.57
2:C:74:HIS:CE1	2:C:78:ASN:HD21	2.23	0.57
2:D:59:LEU:HD22	2:D:61:HIS:H	1.70	0.56
1:B:178:PHE:CD2	1:B:310:ARG:HB2	2.41	0.55
2:C:85:ARG:HD2	4:C:348:HOH:O	2.07	0.55
1:A:104:GLN:NE2	4:A:638:HOH:O	2.39	0.54
2:C:228:GLU:HB2	2:C:229:PRO:HD2	1.88	0.54
1:B:141:ARG:HG2	4:B:530:HOH:O	2.07	0.54
1:B:141:ARG:O	1:B:145:GLU:HG3	2.07	0.54
1:A:139:ARG:CZ	4:A:594:HOH:O	2.55	0.54
1:A:29:TRP:HD1	1:A:33:GLU:HG2	1.74	0.53
1:A:107:THR:HB	1:A:112:ASP:HB2	1.91	0.53
2:D:250:VAL:HA	2:D:268:THR:O	2.09	0.53
2:C:166:HIS:HD2	2:C:193:ASP:OD1	1.92	0.52
2:C:74:HIS:HD2	4:C:360:HOH:O	1.92	0.52
1:A:96:LEU:HG	1:A:324:LYS:HD3	1.91	0.52
2:D:215:ALA:HB2	2:D:220:LEU:CD2	2.40	0.52
2:D:208:VAL:HA	2:D:270:GLN:HE21	1.75	0.51
1:B:71:VAL:HG11	1:B:86:ILE:HD11	1.93	0.51
1:B:210:TYR:O	1:B:214:VAL:HG22	2.10	0.51
2:C:215:ALA:O	2:C:217:SER:N	2.44	0.50
1:A:351:ARG:HG2	1:A:351:ARG:HH11	1.77	0.50
1:A:50:GLU:HG3	4:A:640:HOH:O	2.12	0.50
1:B:60:SER:O	1:B:62:PRO:HD3	2.11	0.50
1:A:198:HIS:HA	1:A:228:ASN:O	2.12	0.50
2:D:168:LEU:HD21	2:D:257:VAL:HG21	1.94	0.49
2:C:201:LYS:HE2	4:C:310:HOH:O	2.13	0.49
2:C:231:ASN:HB2	4:C:312:HOH:O	2.11	0.49
1:A:152:ASN:HB2	4:A:616:HOH:O	2.12	0.49
2:C:216:ASN:ND2	4:C:342:HOH:O	2.45	0.49
1:A:108:ARG:HB2	1:A:111:ALA:HB3	1.95	0.48
2:C:255:ILE:HB	2:C:264:LEU:HB2	1.95	0.48
1:A:187:LEU:O	1:A:191:PHE:HD1	1.97	0.48
1:A:29:TRP:HB3	1:A:34:PHE:HB2	1.96	0.47
1:B:221:HIS:HB2	4:B:529:HOH:O	2.13	0.47
1:B:133:PHE:CG	1:B:134:THR:N	2.82	0.47
1:A:144:VAL:HG13	1:A:155:LEU:CD1	2.44	0.47
1:A:177:GLY:O	1:A:337:SER:HA	2.15	0.47
2:D:255:ILE:HD11	2:D:266:LEU:HD12	1.96	0.46
1:B:364:ASP:O	1:B:365:ASN:HB2	2.15	0.46
1:B:59:LEU:HD22	1:B:98:ILE:HD13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:146:ARG:HH11	2:C:146:ARG:HB2	1.80	0.45
1:B:178:PHE:CE2	1:B:338:GLY:HA3	2.53	0.45
1:B:348:SER:CB	1:B:350:GLU:HG2	2.41	0.44
2:C:119:ASP:HB2	4:C:353:HOH:O	2.17	0.44
2:C:252:GLU:HG2	2:C:267:LEU:HD21	1.98	0.44
1:B:75:GLY:O	1:B:76:GLN:HB2	2.17	0.44
1:A:223:VAL:CG1	1:A:229:PHE:HB2	2.47	0.44
2:C:199:MET:HE3	2:C:211:VAL:HG23	2.01	0.43
1:A:53:ARG:HG3	4:A:602:HOH:O	2.17	0.43
1:B:205:TYR:HB2	1:B:236:TYR:HA	2.01	0.43
1:B:178:PHE:HB3	1:B:340:PHE:CZ	2.53	0.43
1:A:350:GLU:HA	4:A:604:HOH:O	2.19	0.42
1:B:136:ASP:HA	1:B:210:TYR:HB3	2.01	0.42
1:A:86:ILE:HD12	1:A:106:PHE:CZ	2.54	0.42
1:A:315:THR:O	1:A:319:MET:HG3	2.18	0.42
1:B:348:SER:O	1:B:352:ILE:HG12	2.19	0.42
1:A:305:ASP:OD1	1:A:345:LYS:HE3	2.20	0.41
1:A:203:VAL:O	1:A:234:ALA:HA	2.20	0.41
1:B:285:MET:HE2	1:B:305:ASP:HB3	2.03	0.41
1:A:66:PRO:HG2	1:A:101:GLN:HE21	1.85	0.41
1:B:131:LEU:HB2	1:B:153:THR:HG21	2.02	0.41
1:B:29:TRP:O	1:B:162:THR:HB	2.21	0.41
2:D:171:ARG:HA	2:D:186:SER:O	2.21	0.41
1:B:273:VAL:HG11	1:B:303:ASP:HB3	2.03	0.41
2:D:175:LEU:CD2	2:D:182:VAL:HG22	2.51	0.41
2:C:108:PRO:O	2:C:111:THR:HG23	2.21	0.40
1:B:198:HIS:HA	1:B:228:ASN:O	2.22	0.40
2:D:104:ASP:HA	2:D:111:THR:HG21	2.02	0.40
2:D:228:GLU:C	2:D:230:TYR:H	2.24	0.40
1:A:328:GLU:OE1	1:A:330:LYS:NZ	2.43	0.40
1:B:78:VAL:HG11	1:B:270:LEU:HD12	2.03	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	337/339 (99%)	326 (97%)	11 (3%)	0	100	100
1	B	325/339 (96%)	311 (96%)	13 (4%)	1 (0%)	46	54
2	C	206/221 (93%)	202 (98%)	3 (2%)	1 (0%)	34	37
2	D	199/221 (90%)	192 (96%)	7 (4%)	0	100	100
All	All	1067/1120 (95%)	1031 (97%)	34 (3%)	2 (0%)	52	61

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	216	ASN
1	B	74	PRO

### 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	294/294 (100%)	278 (95%)	16 (5%)	27	33
1	B	285/294 (97%)	270 (95%)	15 (5%)	28	34
2	C	192/202 (95%)	179 (93%)	13 (7%)	20	22
2	D	185/202 (92%)	174 (94%)	11 (6%)	24	28
All	All	956/992 (96%)	901 (94%)	55 (6%)	25	29

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	TRP
1	A	48	LEU
1	A	64	GLN
1	A	96	LEU
1	A	118	LEU
1	A	127	LYS

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Mol	Chain	Res	Type
1	A	131	LEU
1	A	135	LEU
1	A	151	THR
1	A	155	LEU
1	A	190	GLU
1	A	225	ARG
1	A	241	LYS
1	A	289	TRP
1	A	351	ARG
1	A	358	ARG
1	B	48	LEU
1	B	97	ASN
1	B	103	ASN
1	B	107	THR
1	B	127	LYS
1	B	131	LEU
1	B	141	ARG
1	B	151	THR
1	B	155	LEU
1	B	223	VAL
1	B	289	TRP
1	B	304	LEU
1	B	345	LYS
1	B	348	SER
1	B	351	ARG
2	C	55	GLN
2	C	93	THR
2	C	101	LEU
2	C	111	THR
2	C	121	LYS
2	C	138	LEU
2	C	140	LEU
2	C	146	ARG
2	C	204	SER
2	C	217	SER
2	C	224	LEU
2	C	248	LEU
2	C	266	LEU
2	D	59	LEU
2	D	89	THR
2	D	101	LEU
2	D	109	SER

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Mol	Chain	Res	Type
2	D	141	ASP
2	D	164	SER
2	D	193	ASP
2	D	194	ASN
2	D	206	SER
2	D	209	ASP
2	D	217	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	101	GLN
1	A	115	GLN
1	A	224	ASN
1	A	242	GLN
1	A	300	GLN
1	B	104	GLN
1	B	224	ASN
1	B	255	HIS
2	C	55	GLN
2	C	74	HIS
2	C	78	ASN
2	C	166	HIS
2	D	74	HIS
2	D	75	HIS
2	D	166	HIS
2	D	258	ASN
2	D	270	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	AI2	A	501	-	9,14,14	2.21	3 (33%)	8,25,25	1.21	1 (12%)
3	AI2	B	502	-	9,14,14	2.14	3 (33%)	8,25,25	1.38	1 (12%)

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	AI2	A	501	-	-	0/0/33/33	0/2/2/2
3	AI2	B	502	-	-	0/0/33/33	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	502	AI2	B2-O1	2.52	1.50	1.45
3	A	501	AI2	B2-O1	2.61	1.50	1.45
3	B	502	AI2	O13-C8	2.81	1.44	1.39
3	A	501	AI2	O13-C8	2.86	1.44	1.39
3	B	502	AI2	B2-O3	4.49	1.54	1.45
3	A	501	AI2	B2-O3	5.17	1.55	1.45

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	502	AI2	O3-B2-O1	-3.40	97.74	104.21
3	A	501	AI2	O3-B2-O1	-3.19	98.13	104.21

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 ⓘ

### 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	339/339 (100%)	0.32	21 (6%)	24 35	37, 51, 70, 77	0
1	B	329/339 (97%)	0.45	24 (7%)	18 27	39, 55, 85, 107	0
2	C	210/221 (95%)	-0.06	4 (1%)	70 80	36, 48, 65, 84	0
2	D	203/221 (91%)	0.22	15 (7%)	17 26	45, 62, 78, 88	0
All	All	1081/1120 (96%)	0.27	64 (5%)	26 37	36, 53, 76, 107	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	64	GLN	5.4
1	B	121	MET	4.7
1	A	352	ILE	4.6
2	C	53	LYS	4.6
1	A	365	ASN	4.5
2	D	248	LEU	4.4
2	D	58	ALA	4.4
1	B	122	GLU	4.0
2	D	225	ILE	3.9
1	B	264	CYS	3.6
1	B	120	LEU	3.5
1	A	94	TYR	3.5
2	D	105	GLN	3.4
1	A	349	PRO	3.3
2	D	249	LEU	3.2
1	B	365	ASN	3.2
1	A	264	CYS	3.1
1	A	176	VAL	3.1
1	B	108	ARG	3.1
1	B	263	ALA	3.0
1	B	132	ILE	3.0

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Mol	Chain	Res	Type	RSRZ
2	D	207	ASN	2.9
2	D	132	PHE	2.9
1	B	143	PHE	2.8
1	B	133	PHE	2.7
2	D	196	PHE	2.7
2	C	227	ASP	2.7
1	B	61	LYS	2.7
1	A	320	ALA	2.7
1	B	194	PHE	2.6
2	C	229	PRO	2.6
1	B	265	SER	2.6
1	A	132	ILE	2.6
1	B	64	GLN	2.6
1	B	66	PRO	2.6
1	B	125	LYS	2.5
1	A	287	ASN	2.5
1	A	262	TYR	2.5
1	A	194	PHE	2.5
2	C	230	TYR	2.4
2	D	106	SER	2.4
2	D	104	ASP	2.4
1	A	265	SER	2.3
1	A	357	LYS	2.3
1	B	319	MET	2.3
1	A	204	LEU	2.3
1	B	150	SER	2.3
1	B	156	ILE	2.2
2	D	251	ILE	2.2
1	A	72	VAL	2.2
2	D	200	GLU	2.2
1	A	316	GLY	2.2
1	B	89	PHE	2.2
1	B	63	THR	2.2
1	A	319	MET	2.1
1	B	327	LEU	2.1
1	A	156	ILE	2.1
1	A	263	ALA	2.1
2	D	98	PHE	2.1
2	D	252	GLU	2.1
1	B	153	THR	2.1
1	A	350	GLU	2.1
1	B	68	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
2	D	270	GLN	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(Å <sup>2</sup> )	Q<0.9
3	AI2	B	502	13/13	0.97	0.25	1.14	45,47,49,50	0
3	AI2	A	501	13/13	0.98	0.15	-0.40	36,39,41,42	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.