

# Full wwPDB X-ray Structure Validation Report (i)

#### Nov 4, 2023 – 10:58 PM EDT

PDB ID	:	3TD4
Title	:	Crystal structure of OmpA-like domain from Acinetobacter baumannii in com-
		plex with diaminopimelate
Authors	:	Park, J.S.; Lee, W.C.; Song, J.H.; Kim, H.Y.
Deposited on	:	2011-08-10
Resolution	:	1.79 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 A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) 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 (1)) 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	:	2.36
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)	:	2.36

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY\;DIFFRACTION$ 

The reported resolution of this entry is 1.79 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	Similar resolution
	$(\# { m Entries})$	$(\# { m Entries},  { m resolution}  { m range}({ m \AA}))$
$R_{free}$	130704	5950(1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 of the lower bar indicate the fraction of residues that contain outliers for >=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 <=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	А	123	80%	16%	
				10,0	
1	В	123	81%	18%	•
1	С	123	80%	16%	••••
1	D	123	86%	10%	•••
	Б	100			
	E	123	79%	18%	••



Mol	Chain	Length	Quality of chain		
1	F	123	81%	15%	•••
1	G	123	81%	15%	•••
1	Н	123	84%	11%	



## 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 8457 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.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	Δ	199	Total	С	Ν	0	$\mathbf{S}$	0	0	0
1	A	122	970	595	180	192	3	0	0	0
1	р	192	Total	С	Ν	0	S	0	0	0
1	D	123	974	597	181	193	3	0	0	0
1	С	191	Total	С	Ν	Ο	S	0	0	0
1		121	964	592	179	190	3	0	0	0
1	П	191	Total	С	Ν	0	S	0	0	0
1	D	121	964	592	179	190	3	0	0	0
1	F	120	Total	С	Ν	0	S	0	0	0
1	Ľ	120	954	586	176	189	3	0	0	0
1	Б	199	Total	С	Ν	0	S	0	0	0
1	Г	122	970	595	180	192	3	0	0	0
1	C	199	Total	С	Ν	0	$\mathbf{S}$	0	0	0
1	G	122	970	595	180	192	3	0	0	0
1	ц	191	Total	С	Ν	0	S	0	0	0
1	11		964	592	179	190	3			U

• Molecule 1 is a protein called Outer membrane protein omp38.

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	217	GLY	-	expression tag	UNP Q6RYW5
А	218	SER	-	expression tag	UNP Q6RYW5
А	219	HIS	-	expression tag	UNP Q6RYW5
А	220	MET	-	expression tag	UNP Q6RYW5
В	217	GLY	-	expression tag	UNP Q6RYW5
В	218	SER	-	expression tag	UNP Q6RYW5
В	219	HIS	-	expression tag	UNP Q6RYW5
В	220	MET	-	expression tag	UNP Q6RYW5
С	217	GLY	-	expression tag	UNP Q6RYW5
С	218	SER	-	expression tag	UNP Q6RYW5
С	219	HIS	-	expression tag	UNP Q6RYW5
С	220	MET	-	expression tag	UNP Q6RYW5
D	217	GLY	-	expression tag	UNP Q6RYW5



Chain	Residue	Modelled	Actual	Comment	Reference
D	218	SER	-	expression tag	UNP Q6RYW5
D	219	HIS	-	expression tag	UNP Q6RYW5
D	220	MET	-	expression tag	UNP Q6RYW5
E	217	GLY	-	expression tag	UNP Q6RYW5
E	218	SER	-	expression tag	UNP Q6RYW5
Е	219	HIS	-	expression tag	UNP Q6RYW5
Е	220	MET	-	expression tag	UNP Q6RYW5
F	217	GLY	-	expression tag	UNP Q6RYW5
F	218	SER	-	expression tag	UNP Q6RYW5
F	219	HIS	-	expression tag	UNP Q6RYW5
F	220	MET	-	expression tag	UNP Q6RYW5
G	217	GLY	-	expression tag	UNP Q6RYW5
G	218	SER	-	expression tag	UNP Q6RYW5
G	219	HIS	-	expression tag	UNP Q6RYW5
G	220	MET	-	expression tag	UNP Q6RYW5
Н	217	GLY	-	expression tag	UNP Q6RYW5
Н	218	SER	-	expression tag	UNP Q6RYW5
Н	219	HIS	-	expression tag	UNP Q6RYW5
Н	220	MET	-	expression tag	UNP Q6RYW5

• Molecule 2 is 2,6-DIAMINOPIMELIC ACID (three-letter code: API) (formula:  $C_7H_{14}N_2O_4$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	Total         C         N         O           13         7         2         4	0	0
2	В	1	Total         C         N         O           13         7         2         4	0	0



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	С	1	Total C N O	0	0
	U	T	13  7  2  4	0	0
2	Л	1	Total C N O	0	0
	D	I	13  7  2  4	0	0
2	E	1	Total C N O	0	0
	Ľ	I	13  7  2  4	0	0
2	F	1	Total C N O	0	0
2	Ľ	I	13  7  2  4	0	0
2	G	1	Total C N O	0	0
	ŭ	Ĩ	13  7  2  4	0	0
2	н	1	Total C N O	0	0
	11	1	13 7 2 4	0	

• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	92	Total         O           92         92	0	0
3	В	69	Total         O           69         69	0	0
3	С	72	Total         O           72         72	0	0
3	D	58	$\begin{array}{cc} \text{Total} & \text{O} \\ 58 & 58 \end{array}$	0	0
3	Ε	85	Total O 85 85	0	0
3	F	85	Total O 85 85	0	0
3	G	88	Total         O           88         88	0	0
3	Н	74	$\begin{array}{cc} \text{Total} & \text{O} \\ 74 & 74 \end{array}$	0	0



Chain F:

# 3 Residue-property plots (i)

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.

Chain A: 80% 16% • Molecule 1: Outer membrane protein omp38 Chain B: 81% 18% • Molecule 1: Outer membrane protein omp38 Chain C: 80% 16% • Molecule 1: Outer membrane protein omp38 Chain D: 86% 10% • Molecule 1: Outer membrane protein omp38 Chain E: 79% 18% • Molecule 1: Outer membrane protein omp38

81%

15%

• Molecule 1: Outer membrane protein omp38

#### 

 $\bullet$  Molecule 1: Outer membrane protein omp38







## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	57.87Å 98.22Å 98.44Å	Deperitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $105.51^{\circ}$ $90.00^{\circ}$	Depositor
$\mathbf{P}_{\text{acclution}}(\hat{\mathbf{A}})$	94.86 - 1.79	Depositor
Resolution (A)	47.43 - 1.79	EDS
% Data completeness	99.1 (94.86-1.79)	Depositor
(in resolution range)	99.2(47.43-1.79)	EDS
R <sub>merge</sub>	(Not available)	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.17 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
D D	0.179 , $0.214$	Depositor
$\Pi, \Pi_{free}$	0.178 , $0.215$	DCC
$R_{free}$ test set	4939 reflections $(4.99%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	16.7	Xtriage
Anisotropy	0.164	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.42, $50.6$	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.023 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8457	wwPDB-VP
Average B, all atoms $(Å^2)$	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.68% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: API

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).

Mal	Chain	Bo	nd lengths	Bond angles	
	Unain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	1.44	4/984~(0.4%)	1.29	6/1324~(0.5%)
1	В	1.39	5/988~(0.5%)	1.28	8/1329~(0.6%)
1	С	1.36	3/978~(0.3%)	1.16	3/1316~(0.2%)
1	D	1.23	2/978~(0.2%)	1.18	6/1316~(0.5%)
1	Е	1.32	3/967~(0.3%)	1.24	6/1301~(0.5%)
1	F	1.43	5/984~(0.5%)	1.32	7/1324~(0.5%)
1	G	1.47	8/984~(0.8%)	1.35	11/1324~(0.8%)
1	Н	1.38	3/978~(0.3%)	1.26	4/1316~(0.3%)
All	All	1.38	33/7841~(0.4%)	1.26	$51/1055\overline{0}\ (0.5\%)$

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
1	F	248	GLU	CD-OE2	9.68	1.36	1.25
1	С	221	GLU	CG-CD	7.83	1.63	1.51
1	В	331	VAL	CB-CG1	7.45	1.68	1.52
1	А	330	ARG	CZ-NH2	7.33	1.42	1.33
1	В	248	GLU	CD-OE1	7.16	1.33	1.25
1	G	323	GLU	CB-CG	6.68	1.64	1.52
1	D	311	ALA	CA-CB	6.62	1.66	1.52
1	А	234	PHE	CD1-CE1	6.50	1.52	1.39
1	Ε	323	GLU	CG-CD	6.41	1.61	1.51
1	G	252	VAL	CB-CG2	6.24	1.66	1.52
1	D	229	GLU	CB-CG	6.16	1.63	1.52
1	G	287	ALA	CA-CB	6.12	1.65	1.52
1	А	271	ASP	CB-CG	6.11	1.64	1.51
1	В	298	TYR	CD1-CE1	6.03	1.48	1.39
1	Н	331	VAL	CB-CG1	6.01	1.65	1.52
1	F	234	PHE	CE1-CZ	6.01	1.48	1.37
1	F	298	TYR	CD1-CE1	6.00	1.48	1.39
1	F	298	TYR	CE2-CZ	5.93	1.46	1.38



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	311	ALA	CA-CB	5.89	1.64	1.52
1	В	295	VAL	CB-CG1	5.82	1.65	1.52
1	А	228	MET	CG-SD	5.78	1.96	1.81
1	G	224	GLU	CG-CD	-5.78	1.43	1.51
1	Н	289	SER	CA-CB	5.71	1.61	1.52
1	Н	248	GLU	CB-CG	-5.60	1.41	1.52
1	С	312	TRP	CE3-CZ3	5.51	1.47	1.38
1	G	239	SER	CA-CB	5.50	1.61	1.52
1	С	323	GLU	CB-CG	5.46	1.62	1.52
1	G	234	PHE	CD1-CE1	5.41	1.50	1.39
1	Ε	248	GLU	CD-OE1	5.24	1.31	1.25
1	G	302	ALA	CA-CB	5.24	1.63	1.52
1	Ε	234	PHE	CE1-CZ	5.22	1.47	1.37
1	G	265	ARG	CG-CD	5.20	1.65	1.51
1	В	267	GLU	CB-CG	5.12	1.61	1.52

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	Н	330	ARG	NE-CZ-NH2	-11.75	114.42	120.30
1	G	327	MET	CG-SD-CE	-11.08	82.47	100.20
1	G	301	ASP	CB-CG-OD1	10.13	127.41	118.30
1	D	276	ARG	NE-CZ-NH2	9.46	125.03	120.30
1	А	231	ARG	NE-CZ-NH2	9.39	124.99	120.30
1	А	286	ARG	NE-CZ-NH2	-9.31	115.64	120.30
1	F	286	ARG	NE-CZ-NH1	8.99	124.80	120.30
1	F	330	ARG	NE-CZ-NH2	-8.98	115.81	120.30
1	В	330	ARG	NE-CZ-NH2	-8.88	115.86	120.30
1	Н	228	MET	CG-SD-CE	8.74	114.18	100.20
1	F	286	ARG	NE-CZ-NH2	-8.66	115.97	120.30
1	В	286	ARG	NE-CZ-NH1	8.65	124.63	120.30
1	В	286	ARG	NE-CZ-NH2	-8.21	116.19	120.30
1	D	276	ARG	NE-CZ-NH1	-8.04	116.28	120.30
1	G	330	ARG	NE-CZ-NH2	-7.98	116.31	120.30
1	А	220	MET	CG-SD-CE	-7.66	87.95	100.20
1	G	220	MET	CG-SD-CE	-7.60	88.03	100.20
1	В	228	MET	CG-SD-CE	7.27	111.83	100.20
1	Е	304	ARG	NE-CZ-NH2	-7.26	116.67	120.30
1	А	330	ARG	NE-CZ-NH1	-7.22	116.69	120.30
1	В	330	ARG	NE-CZ-NH1	6.92	123.76	120.30
1	D	327	MET	CG-SD-CE	-6.91	89.14	100.20
1	G	286	ARG	NE-CZ-NH2	-6.78	116.91	120.30



Mol	Chain	$\operatorname{Res}$	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	G	286	ARG	NE-CZ-NH1	6.73	123.66	120.30
1	D	222	LEU	CA-CB-CG	6.57	130.41	115.30
1	В	329	ARG	NE-CZ-NH1	6.41	123.50	120.30
1	С	282	LEU	CB-CG-CD2	-6.34	100.22	111.00
1	Е	286	ARG	NE-CZ-NH2	-6.33	117.14	120.30
1	G	301	ASP	CB-CG-OD2	-6.22	112.70	118.30
1	Е	286	ARG	NE-CZ-NH1	6.17	123.39	120.30
1	F	281	ARG	NE-CZ-NH2	-6.16	117.22	120.30
1	Е	332	PHE	CB-CG-CD2	-6.15	116.50	120.80
1	А	224	GLU	OE1-CD-OE2	-5.89	116.23	123.30
1	А	222	LEU	CB-CG-CD1	-5.86	101.05	111.00
1	Н	228	MET	CA-CB-CG	5.85	123.24	113.30
1	F	222	LEU	CA-CB-CG	5.58	128.14	115.30
1	С	226	LEU	CB-CG-CD2	-5.41	101.81	111.00
1	G	231	ARG	NE-CZ-NH1	-5.36	117.62	120.30
1	F	313	ASP	CB-CG-OD2	-5.26	113.57	118.30
1	D	327	MET	CB-CG-SD	-5.12	97.05	112.40
1	F	307	THR	CA-CB-OG1	5.11	119.72	109.00
1	В	222	LEU	CB-CG-CD1	-5.10	102.33	111.00
1	Н	289	SER	CB-CA-C	5.09	119.77	110.10
1	G	265	ARG	NE-CZ-NH1	5.09	122.84	120.30
1	Е	265	ARG	NE-CZ-NH1	-5.08	117.76	120.30
1	С	242	LYS	CD-CE-NZ	-5.08	100.02	111.70
1	D	246	LYS	CD-CE-NZ	-5.08	100.03	111.70
1	Е	238	LYS	CD-CE-NZ	-5.05	100.08	111.70
1	G	231	ARG	NE-CZ-NH2	5.03	122.81	120.30
1	В	325	ARG	NE-CZ-NH1	5.01	122.81	120.30
1	G	228	MET	CG-SD-CE	5.01	108.22	100.20

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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	А	970	0	957	31	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	В	974	0	960	11	0
1	С	964	0	952	30	0
1	D	964	0	952	10	0
1	Е	954	0	945	14	0
1	F	970	0	957	15	0
1	G	970	0	957	12	0
1	Н	964	0	952	19	0
2	А	13	0	7	0	0
2	В	13	0	7	1	0
2	С	13	0	7	0	0
2	D	13	0	7	0	0
2	Е	13	0	7	0	0
2	F	13	0	7	0	0
2	G	13	0	7	0	0
2	Н	13	0	7	0	0
3	А	92	0	0	3	0
3	В	69	0	0	3	0
3	С	72	0	0	3	0
3	D	58	0	0	0	0
3	Е	85	0	0	1	0
3	F	85	0	0	4	0
3	G	88	0	0	3	0
3	Н	74	0	0	1	0
All	All	8457	0	7688	107	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 7.

All (107) 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:299:ASN:HB2	3:B:521:HOH:O	1.40	1.20
1:F:246:LYS:HE2	3:F:116:HOH:O	1.45	1.11
1:A:231:ARG:NH1	1:C:219:HIS:CB	2.24	1.01
1:H:229:GLU:HG3	1:H:332:PHE:CE1	2.02	0.94
1:A:231:ARG:NH1	1:C:219:HIS:HB2	1.83	0.93
1:D:276:ARG:HD2	1:D:280:GLU:OE2	1.75	0.86
1:A:231:ARG:NH1	1:C:219:HIS:HB3	1.89	0.84
1:B:217:GLY:N	1:E:263:THR:HG1	1.76	0.84
1:A:221:GLU:HG2	1:C:231:ARG:NH2	1.94	0.82
1:A:248:GLU:HG2	1:C:220:MET:HB2	1.63	0.79



	page	Interatomic	Clash
Atom-1	Atom-2	distance $(Å)$	overlap (Å)
1:A:231:ARG:HH12	1:C:219:HIS:CB	1.97	0.77
1:H:229:GLU:CD	1:H:332:PHE:HE1	1.92	0.72
1:A:231:ARG:HH12	1:C:219:HIS:HB2	1.53	0.72
$1 \cdot F \cdot 240 \cdot ASN \cdot HD22$	1.F.240:ASN·H	1.38	0.72
1:H:229:GLU:CG	1:H:332:PHE:HE1	2.04	0.71
1:F:255:LYS:HE2	1:G:222:LEU:HD21	1.73	0.70
1:H:229:GLU:HG3	1:H:332:PHE:HE1	1.55	0.69
1:H:229:GLU:CG	1:H:332:PHE:CE1	2.73	0.69
1:B:235:ASP:HB2	1:B:238:LYS:HD2	1.74	0.68
1:E:278:LEU:HD12	3:E:427:HOH:O	1.94	0.67
1:E:231:ABG:NH2	1:H:221:GLU:OE1	2.28	0.66
1:D:319:ASN:ND2	1:D:328:ASN:HD22	1.93	0.66
1:C:231:ARG:HG2	1:C:332:PHE:CE1	2.31	0.65
1:D:276:ARG:HD3	1:D:280:GLU:HG3	1.79	0.64
1:H:231:ARG:HB2	3:H:620:HOH:O	1.99	0.62
1:C:222:LEU:HD12	1:C:222:LEU:C	2.20	0.62
1:A:220:MET:HE1	1:C:252:VAL:HG23	1.82	0.61
1:B:225:ASP:OD1	1:B:338:SEB:OG	2.18	0.61
1:A:219:HIS:HB2	1:C:248:GLU:OE1	1.99	0.61
1:A:219:HIS:CD2	1:C:245:TYR:HE1	2.19	0.61
1:F:218:SER:CB	3:F:211:HOH:O	2.47	0.60
1:G:229:GLU:OE1	3:G:486:HOH:O	2.16	0.60
1:C:243:ASP:HA	1:C:246:LYS:HD3	1.84	0.59
1:A:219:HIS:HB3	1:C:231:ARG:O	2.03	0.59
1:A:221:GLU:HG2	1:C:231:ARG:HH22	1.67	0.59
1:A:221:GLU:CG	1:C:231:ARG:NH2	2.64	0.58
1:B:222:LEU:HD13	1:D:228:MET:HG2	1.86	0.57
1:C:222:LEU:HD11	3:C:540:HOH:O	2.04	0.57
1:A:218:SER:HB3	1:F:336:THR:OG1	2.04	0.57
1:E:225:ASP:OD1	1:E:338:SER:OG	2.15	0.57
1:A:228:MET:HE1	1:A:255:LYS:HB2	1.86	0.56
1:B:299:ASN:CB	3:B:521:HOH:O	2.19	0.55
1:B:217:GLY:HA2	1:E:336:THR:OG1	2.07	0.55
1:A:219:HIS:CD2	1:C:245:TYR:CE1	2.95	0.54
1:C:231:ARG:HG2	1:C:332:PHE:CD1	2.41	0.54
1:D:276:ARG:CD	1:D:280:GLU:OE2	2.50	0.54
1:F:243:ASP:HA	1:F:246:LYS:HD2	1.88	0.54
1:A:222:LEU:HD13	1:C:228:MET:HG2	1.90	0.53
1:C:219:HIS:N	3:C:580:HOH:O	2.42	0.52
1:D:265:ARG:HD3	1:D:267:GLU:OE2	2.08	0.52
1:E:248:GLU:HG2	1:H:220:MET:HB2	1.92	0.52



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:221:GLU:CG	1:C:231:ARG:HH22	2.21	0.52
1:G:231:ARG:HG2	1:G:332:PHE:CD2	2.45	0.52
1:H:229:GLU:CD	1:H:332:PHE:CE1	2.80	0.52
1:B:244:GLN:HA	3:B:430:HOH:O	2.10	0.52
1:F:240:ASN:H	1:F:240:ASN:ND2	2.05	0.52
1:G:231:ARG:HG2	1:G:332:PHE:CE2	2.46	0.51
1:G:319:ASN:ND2	1:G:328:ASN:HD22	2.08	0.51
1:G:332:PHE:CD1	3:G:415:HOH:O	2.54	0.51
1:A:231:ARG:HH11	1:C:219:HIS:HB3	1.73	0.49
1:E:222:LEU:HD13	1:H:228:MET:HG2	1.94	0.49
1:A:319:ASN:HD22	1:A:325:ARG:HG2	1.77	0.49
1:E:220:MET:HB2	1:H:248:GLU:HG3	1.95	0.48
1:A:231:ARG:CZ	1:C:219:HIS:HB2	2.41	0.48
1:A:336:THR:OG1	1:F:218:SER:HB3	2.12	0.48
1:F:218:SER:HB2	1:G:248:GLU:OE2	2.14	0.48
1:A:218:SER:CB	3:A:83:HOH:O	2.62	0.47
1:E:231:ARG:HH22	1:H:221:GLU:CD	2.16	0.47
1:D:270:THR:HG23	1:D:283:SER:HB3	1.96	0.47
1:C:318:ASP:OD1	1:C:320:LYS:HE3	2.15	0.46
1:C:321:THR:HB	1:C:323:GLU:OE2	2.16	0.46
1:E:319:ASN:ND2	1:E:328:ASN:HD22	2.13	0.46
1:H:228:MET:HB2	1:H:335:ILE:HB	1.98	0.46
1:D:276:ARG:HD3	1:D:280:GLU:CG	2.46	0.46
1:A:236:THR:HG22	1:A:329:ARG:CZ	2.46	0.46
1:A:218:SER:HB2	3:A:83:HOH:O	2.15	0.46
1:H:220:MET:HE1	1:H:222:LEU:HD12	1.98	0.46
1:F:319:ASN:HD22	1:F:325:ARG:HG2	1.81	0.46
1:F:280:GLU:HG2	3:F:596:HOH:O	2.16	0.45
1:H:319:ASN:ND2	1:H:328:ASN:HD22	2.15	0.45
1:B:235:ASP:OD2	1:B:242:LYS:NZ	2.49	0.45
1:G:330:ARG:HD2	1:G:332:PHE:CE2	2.52	0.45
1:B:237:ASN:ND2	2:B:401:API:CA	2.80	0.45
1:F:319:ASN:ND2	1:F:328:ASN:HD22	2.15	0.44
1:G:229:GLU:OE2	1:G:231:ARG:NH2	2.49	0.44
1:H:230:LEU:HB3	1:H:333:ALA:HB3	2.00	0.44
1:A:229:GLU:O	1:C:220:MET:HA	2.18	0.43
1:H:320:LYS:HB2	1:H:320:LYS:HE2	1.71	0.43
1:F:238:LYS:HB3	1:F:240:ASN:ND2	2.33	0.43
1:C:251:LYS:CE	3:C:374:HOH:O	2.65	0.43
1:B:219:HIS:HB3	1:D:231:ARG:O	2.18	0.42
1:E:243:ASP:HA	1:E:246:LYS:HG2	2.01	0.42



Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:E:319:ASN:HD22	1:E:325:ARG:HG2	1.83	0.42
1:A:243:ASP:HA	1:A:246:LYS:HE2	2.01	0.42
1:E:322:LYS:HG2	1:E:325:ARG:NH2	2.35	0.42
1:A:221:GLU:HG2	1:C:231:ARG:HH21	1.81	0.41
1:E:271:ASP:HB2	1:E:319:ASN:ND2	2.35	0.41
1:A:231:ARG:NE	3:A:358:HOH:O	2.30	0.41
1:G:319:ASN:HD22	1:G:325:ARG:HG2	1.86	0.41
1:H:220:MET:C	1:H:220:MET:HE3	2.41	0.41
1:F:219:HIS:HB2	1:G:248:GLU:OE1	2.20	0.41
1:A:259:TYR:CE1	1:A:339:ARG:HG2	2.56	0.41
1:F:218:SER:HB2	3:F:211:HOH:O	2.16	0.41
1:D:319:ASN:HD21	1:D:328:ASN:HD22	1.66	0.41
1:G:248:GLU:HG3	3:G:541:HOH:O	2.21	0.40
1:H:237:ASN:HD22	1:H:237:ASN:HA	1.69	0.40
1:A:221:GLU:CD	1:C:231:ARG:HH22	2.25	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	А	120/123~(98%)	119 (99%)	1 (1%)	0	100	100
1	В	121/123~(98%)	119 (98%)	2(2%)	0	100	100
1	С	119/123~(97%)	118 (99%)	1 (1%)	0	100	100
1	D	119/123~(97%)	118 (99%)	1 (1%)	0	100	100
1	Е	118/123~(96%)	117 (99%)	1 (1%)	0	100	100
1	F	120/123~(98%)	119 (99%)	1 (1%)	0	100	100
1	G	120/123~(98%)	119 (99%)	1 (1%)	0	100	100
1	Н	119/123~(97%)	118 (99%)	1 (1%)	0	100	100



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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
All	All	956/984~(97%)	947~(99%)	9~(1%)	0	100	100

There are no Ramachandran outliers to report.

#### 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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	А	105/105~(100%)	105 (100%)	0	100	100
1	В	105/105~(100%)	103~(98%)	2(2%)	57	46
1	С	104/105~(99%)	101~(97%)	3(3%)	42	29
1	D	104/105~(99%)	102~(98%)	2(2%)	57	46
1	Е	103/105~(98%)	103 (100%)	0	100	100
1	F	105/105~(100%)	102~(97%)	3(3%)	42	29
1	G	105/105~(100%)	104 (99%)	1 (1%)	76	71
1	Н	104/105~(99%)	100 (96%)	4 (4%)	33	18
All	All	835/840 (99%)	820 (98%)	15 (2%)	59	48

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	221	GLU
1	В	246	LYS
1	С	219	HIS
1	С	229	GLU
1	С	323	GLU
1	D	222	LEU
1	D	265	ARG
1	F	222	LEU
1	F	240	ASN
1	F	246	LYS
1	G	222	LEU
1	Н	220	MET



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Mol	Chain	Res	Type
1	Н	222	LEU
1	Н	237	ASN
1	Н	248	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	219	HIS
1	А	314	GLN
1	А	319	ASN
1	В	319	ASN
1	С	308	GLN
1	С	314	GLN
1	D	288	ASN
1	D	308	GLN
1	D	314	GLN
1	D	319	ASN
1	Е	319	ASN
1	F	240	ASN
1	F	319	ASN
1	G	308	GLN
1	G	319	ASN
1	Н	219	HIS
1	Н	237	ASN
1	Н	308	GLN
1	Н	319	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 monosaccharides in this entry.



## 5.6 Ligand geometry (i)

8 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).

Mal	Turne	Chain	Dec	Tink	Bo	ond leng	$\mathbf{ths}$	Bond angles		
MIOI	туре	Unam	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2
2	API	В	401	-	10,12,12	1.29	2 (20%)	$13,\!15,\!15$	1.43	2 (15%)
2	API	Е	401	-	10,12,12	1.21	1 (10%)	$13,\!15,\!15$	1.64	4 (30%)
2	API	А	401	-	10,12,12	1.24	1 (10%)	13,15,15	1.52	1 (7%)
2	API	D	401	-	10,12,12	0.91	1 (10%)	13,15,15	1.28	2 (15%)
2	API	С	401	-	10,12,12	1.13	1 (10%)	13,15,15	1.79	3 (23%)
2	API	G	401	-	10,12,12	1.57	2 (20%)	13,15,15	2.78	2 (15%)
2	API	Н	401	-	10,12,12	1.32	1 (10%)	13,15,15	<mark>3.09</mark>	6 (46%)
2	API	F	401	-	10,12,12	1.37	1 (10%)	13,15,15	1.81	6 (46%)

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	$\mathbf{Res}$	Link	Chirals	Torsions	Rings
2	API	В	401	-	-	4/14/14/14	-
2	API	Е	401	-	-	1/14/14/14	-
2	API	А	401	-	-	4/14/14/14	-
2	API	D	401	-	-	3/14/14/14	-
2	API	С	401	-	-	4/14/14/14	-
2	API	G	401	-	-	2/14/14/14	-
2	API	Н	401	-	-	3/14/14/14	-
2	API	F	401	-	_	2/14/14/14	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
2	Н	401	API	C3-CA	3.14	1.59	1.53



Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
2	F	401	API	O3-C7	3.09	1.31	1.22
2	G	401	API	O4-C7	-3.07	1.20	1.30
2	Е	401	API	O4-C7	-2.66	1.21	1.30
2	G	401	API	C3-CA	2.61	1.58	1.53
2	В	401	API	O3-C7	2.42	1.29	1.22
2	D	401	API	OXT-C	-2.24	1.23	1.30
2	А	401	API	C3-CA	2.14	1.57	1.53
2	В	401	API	OXT-C	-2.14	1.23	1.30
2	С	401	API	C3-CA	2.03	1.57	1.53

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	G	401	API	C3-CA-C	-7.74	91.89	110.30
2	Н	401	API	C3-CA-C	-7.02	93.59	110.30
2	Н	401	API	C3-CA-N	6.51	127.23	110.17
2	G	401	API	C3-CA-N	5.07	123.46	110.17
2	С	401	API	C3-CA-C	-3.53	101.89	110.30
2	А	401	API	O4-C7-C6	3.42	125.02	113.38
2	Е	401	API	OXT-C-CA	2.94	123.41	113.38
2	Е	401	API	C3-CA-N	-2.90	102.58	110.17
2	F	401	API	O3-C7-C6	-2.88	111.99	122.14
2	В	401	API	C3-CA-C	-2.71	103.85	110.30
2	Н	401	API	OXT-C-O	2.59	129.97	124.09
2	F	401	API	O4-C7-C6	2.58	122.16	113.38
2	D	401	API	O3-C7-C6	-2.49	113.35	122.14
2	С	401	API	O4-C7-C6	2.48	121.83	113.38
2	Е	401	API	O-C-CA	-2.47	113.43	122.14
2	F	401	API	O-C-CA	-2.46	113.45	122.14
2	С	401	API	O-C-CA	-2.44	113.51	122.14
2	D	401	API	O4-C7-C6	2.38	121.51	113.38
2	В	401	API	O-C-CA	-2.35	113.83	122.14
2	Н	401	API	C5-C6-C7	-2.31	104.80	110.30
2	F	401	API	OXT-C-CA	2.30	121.21	113.38
2	Н	401	API	O-C-CA	-2.28	114.08	122.14
2	Е	401	API	C5-C4-C3	-2.20	103.11	113.24
2	Н	401	API	C4-C5-C6	2.19	120.40	113.35
2	F	401	API	C3-CA-C	-2.08	105.35	110.30
2	F	401	API	C5-C6-N6	-2.00	104.92	110.17

There are no chirality outliers.

All (23) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
2	F	401	API	C4-C3-CA-C
2	F	401	API	C4-C3-CA-N
2	G	401	API	C4-C3-CA-N
2	Н	401	API	C4-C3-CA-N
2	С	401	API	OXT-C-CA-N
2	Н	401	API	C3-C4-C5-C6
2	В	401	API	OXT-C-CA-N
2	С	401	API	C3-C4-C5-C6
2	D	401	API	CA-C3-C4-C5
2	С	401	API	CA-C3-C4-C5
2	В	401	API	CA-C3-C4-C5
2	В	401	API	O-C-CA-N
2	С	401	API	O-C-CA-N
2	D	401	API	O-C-CA-N
2	А	401	API	C3-C4-C5-C6
2	G	401	API	C4-C3-CA-C
2	Н	401	API	C4-C3-CA-C
2	D	401	API	OXT-C-CA-N
2	Е	401	API	C4-C3-CA-N
2	А	401	API	CA-C3-C4-C5
2	А	401	API	OXT-C-CA-N
2	В	401	API	C3-C4-C5-C6
2	А	401	API	O-C-CA-N

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	401	API	1	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,  $95^{th}$  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	< <b>RSRZ</b> >	#RSRZ>2	$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q<0.9
1	А	122/123~(99%)	-0.28	0 100 100	7, 13, 28, 36	0
1	В	123/123~(100%)	-0.38	0 100 100	9,16,26,35	0
1	С	121/123~(98%)	-0.31	2 (1%) 70 66	9,15,29,43	0
1	D	121/123~(98%)	-0.23	0 100 100	11, 19, 30, 39	0
1	Е	120/123~(97%)	-0.28	0 100 100	7,15,27,31	0
1	F	122/123~(99%)	-0.37	0 100 100	8,15,24,32	0
1	G	122/123~(99%)	-0.29	0 100 100	6, 14, 24, 36	0
1	Н	121/123~(98%)	-0.31	0 100 100	6, 14, 26, 34	0
All	All	972/984~(98%)	-0.31	2 (0%) 95 93	6, 15, 28, 43	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	С	318	ASP	3.2
1	С	219	HIS	2.1

### 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 monosaccharides 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,  $95^{th}$  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	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q<0.9
2	API	А	401	13/13	0.93	0.12	6,14,40,43	0
2	API	С	401	13/13	0.93	0.14	14,18,41,43	0
2	API	F	401	13/13	0.93	0.13	8,14,46,47	0
2	API	Н	401	13/13	0.93	0.12	6,14,39,40	0
2	API	G	401	13/13	0.94	0.14	9,13,41,44	0
2	API	Е	401	13/13	0.94	0.14	11,15,38,39	0
2	API	В	401	13/13	0.95	0.12	13,17,42,47	0
2	API	D	401	13/13	0.95	0.12	15,19,49,49	0

### 6.5 Other polymers (i)

There are no such residues in this entry.

