



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:06 PM GMT

PDB ID : 3SYS
Title : Improved crystal structure of Pseudomonas aeruginosa OccK1 (OpdK)
Authors : van den Berg, B.; Eren, E.
Deposited on : 2011-07-18
Resolution : 1.65 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
<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 : 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

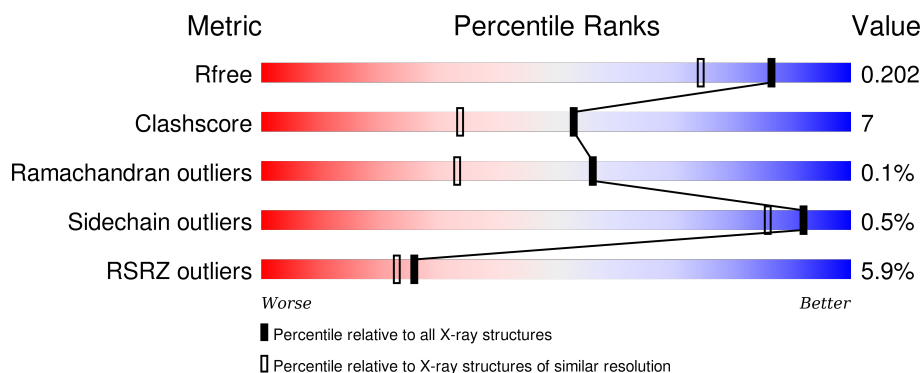
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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	1226 (1.66-1.66)
Clashscore	102246	1323 (1.66-1.66)
Ramachandran outliers	100387	1295 (1.66-1.66)
Sidechain outliers	100360	1295 (1.66-1.66)
RSRZ outliers	91569	1227 (1.66-1.66)

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 ≥ 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	398	<div> <div>6%</div> <div> <div></div> <div>85%</div> <div>9%</div> <div>6%</div> </div> </div>
1	B	398	<div> <div>5%</div> <div> <div></div> <div>86%</div> <div>8%</div> <div>6%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	EDO	B	399	-	-	-	X
2	EDO	B	400	-	-	-	X
3	C8E	A	400	-	-	-	X
3	C8E	A	401	-	-	-	X
3	C8E	A	404	-	-	-	X
3	C8E	A	405	-	-	-	X
3	C8E	A	406	-	-	-	X
3	C8E	A	407	-	-	-	X
3	C8E	A	409	-	-	-	X
3	C8E	A	413	-	-	-	X
3	C8E	B	402	-	-	-	X
3	C8E	B	403	-	-	-	X
3	C8E	B	404	-	-	-	X
3	C8E	B	405	-	-	-	X
3	C8E	B	408	-	-	-	X
3	C8E	B	409	-	-	-	X
3	C8E	B	410	-	-	-	X
3	C8E	B	411	-	-	-	X
3	C8E	B	412	-	-	-	X
3	C8E	B	414	-	-	-	X
3	C8E	B	415	-	-	-	X
4	VNL	A	415	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6853 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 Vanillate porin OpdK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	374	Total	C	N	O	S	16	2	0
			2937	1854	524	553	6			
1	B	374	Total	C	N	O	S	23	1	0
			2937	1853	526	553	5			

There are 16 discrepancies between the modelled and reference sequences:

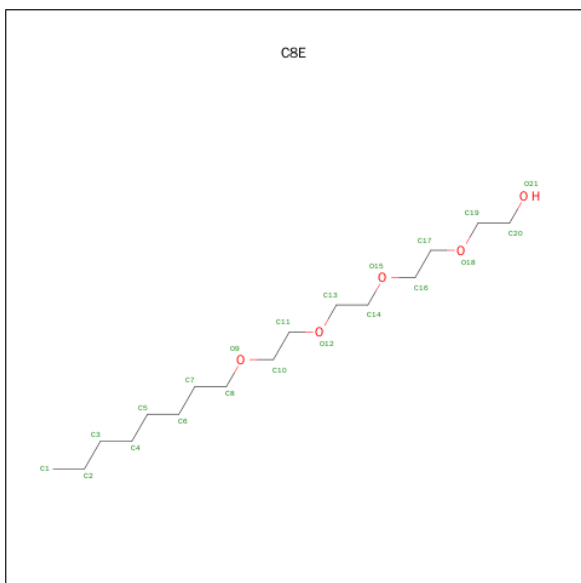
Chain	Residue	Modelled	Actual	Comment	Reference
A	391	GLY	-	EXPRESSION TAG	UNP Q9HUR5
A	392	GLY	-	EXPRESSION TAG	UNP Q9HUR5
A	393	HIS	-	EXPRESSION TAG	UNP Q9HUR5
A	394	HIS	-	EXPRESSION TAG	UNP Q9HUR5
A	395	HIS	-	EXPRESSION TAG	UNP Q9HUR5
A	396	HIS	-	EXPRESSION TAG	UNP Q9HUR5
A	397	HIS	-	EXPRESSION TAG	UNP Q9HUR5
A	398	HIS	-	EXPRESSION TAG	UNP Q9HUR5
B	391	GLY	-	EXPRESSION TAG	UNP Q9HUR5
B	392	GLY	-	EXPRESSION TAG	UNP Q9HUR5
B	393	HIS	-	EXPRESSION TAG	UNP Q9HUR5
B	394	HIS	-	EXPRESSION TAG	UNP Q9HUR5
B	395	HIS	-	EXPRESSION TAG	UNP Q9HUR5
B	396	HIS	-	EXPRESSION TAG	UNP Q9HUR5
B	397	HIS	-	EXPRESSION TAG	UNP Q9HUR5
B	398	HIS	-	EXPRESSION TAG	UNP Q9HUR5

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

- Molecule 3 is (HYDROXYETHYLOXY)TRI(ETHYLOXY)OCTANE (three-letter code: C8E) (formula: $C_{16}H_{34}O_5$).



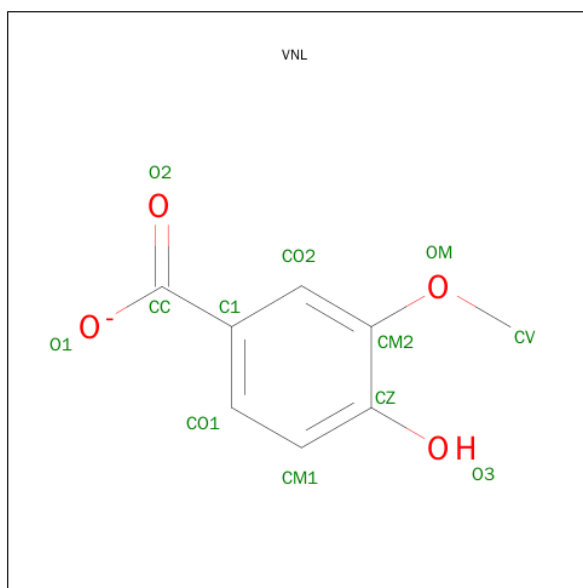
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 9 8 1	0	0
3	A	1	Total C 7 7	0	0
3	A	1	Total C 6 6	0	0
3	A	1	Total C O 9 6 3	0	0
3	A	1	Total C O 14 12 2	0	0
3	A	1	Total C O 16 12 4	0	0
3	A	1	Total C O 5 3 2	0	0
3	A	1	Total C O 9 8 1	0	0
3	A	1	Total C O 7 4 3	0	0
3	A	1	Total C O 9 6 3	0	0
3	A	1	Total C O 6 4 2	0	0
3	A	1	Total C O 9 6 3	0	0
3	A	1	Total C O 9 8 1	0	0
3	A	1	Total C O 15 10 5	0	0
3	B	1	Total C 7 7	0	0
3	B	1	Total C 5 5	0	0
3	B	1	Total C O 11 9 2	0	0
3	B	1	Total C 6 6	0	0
3	B	1	Total C O 12 8 4	0	0
3	B	1	Total C O 8 5 3	0	0
3	B	1	Total C 7 7	0	0
3	B	1	Total C O 10 6 4	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 11 10 1	0	0
3	B	1	Total C 6 6	0	0
3	B	1	Total C O 14 12 2	0	0
3	B	1	Total C O 5 3 2	0	0
3	B	1	Total C 4 4	0	0
3	B	1	Total C 7 7	0	0
3	B	1	Total C 5 5	0	0

- Molecule 4 is 4-HYDROXY-3-METHOXYBENZOATE (three-letter code: VNL) (formula: $C_8H_7O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 12 8 4	0	0
4	A	1	Total C O 12 8 4	0	0
4	B	1	Total C O 12 8 4	0	0
4	B	1	Total C O 12 8 4	0	0

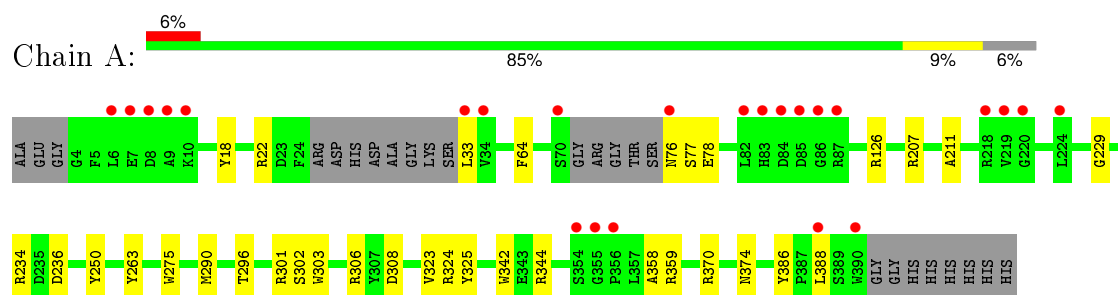
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	345	Total 345	O 345	0	0
5	B	322	Total 322	O 322	0	0

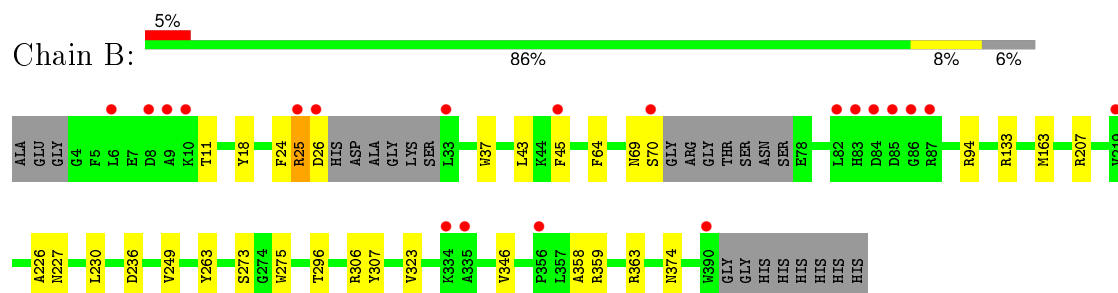
3 Residue-property plots [i](#)

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: Vanillate porin OpdK



• Molecule 1: Vanillate porin OpdK



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	82.14Å 96.84Å 121.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.91 – 1.65 37.81 – 1.65	Depositor EDS
% Data completeness (in resolution range)	96.7 (19.91-1.65) 96.2 (37.81-1.65)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.87 (at 1.65Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.181 , 0.201 0.179 , 0.202	Depositor DCC
R_{free} test set	1999 reflections (1.81%)	DCC
Wilson B-factor (Å ²)	18.6	Xtriage
Anisotropy	0.221	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 65.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 116677 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6853	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 34.39 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 6.8729e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical 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: VNL, C8E, 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	0.33	0/3011	0.53	0/4072
1	B	0.33	0/3008	0.53	0/4068
All	All	0.33	0/6019	0.53	0/8140

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	2937	0	2812	45	0
1	B	2937	0	2809	32	0
2	A	4	0	6	0	0
2	B	12	0	18	1	0
3	A	130	0	183	18	0
3	B	118	0	179	11	0
4	A	24	0	14	0	0
4	B	24	0	13	0	0
5	A	345	0	0	5	0
5	B	322	0	0	6	0
All	All	6853	0	6034	80	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 (80) 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:303:TRP:HD1	3:A:413:C8E:H201	1.21	1.04
1:A:303:TRP:CD1	3:A:413:C8E:H201	2.04	0.93
1:A:301:ARG:HD3	3:A:413:C8E:H161	1.55	0.89
1:A:301:ARG:HG2	3:A:413:C8E:H191	1.54	0.88
1:A:76:ASN:ND2	1:A:126:ARG:HH21	1.75	0.85
1:A:76:ASN:HB3	1:A:77:SER:HA	1.65	0.79
1:B:163:MET:HB2	3:B:413:C8E:H202	1.65	0.75
1:A:76:ASN:HD21	1:A:126:ARG:HH21	1.34	0.74
1:B:64:PHE:HB2	3:B:404:C8E:H81	1.71	0.72
1:A:22:ARG:CZ	1:A:76:ASN:HD22	2.06	0.68
1:B:26:ASP:HB3	5:B:598:HOH:O	1.94	0.67
3:A:402:C8E:H11	3:A:412:C8E:H52	1.76	0.67
1:A:76:ASN:HD21	1:A:126:ARG:NH2	1.94	0.65
1:A:22:ARG:NH2	1:A:76:ASN:HD22	1.95	0.65
1:A:358:ALA:O	1:A:359:ARG:HB2	1.98	0.63
1:B:273:SER:N	5:B:762:HOH:O	2.04	0.62
1:A:207:ARG:HD3	1:A:234:ARG:NH2	2.14	0.62
1:B:230:LEU:HD13	1:B:249:VAL:HG12	1.81	0.61
1:B:94:ARG:HH12	3:B:413:C8E:H191	1.67	0.60
1:A:344:ARG:CD	3:A:412:C8E:H51	2.31	0.59
1:B:374:ASN:O	5:B:474:HOH:O	2.17	0.59
1:A:22:ARG:NH2	1:A:76:ASN:ND2	2.51	0.59
1:A:301:ARG:CD	3:A:413:C8E:H161	2.32	0.58
1:B:94:ARG:HH22	3:B:413:C8E:C17	2.16	0.58
1:A:33:LEU:N	5:A:603:HOH:O	2.38	0.56
1:B:323[A]:VAL:HG13	1:B:346:VAL:HG22	1.87	0.56
1:B:43:LEU:HD21	1:B:45:PHE:CZ	2.40	0.56
1:B:11:THR:HG23	1:B:45:PHE:CE1	2.41	0.56
1:B:275:TRP:HB3	1:B:296:THR:HB	1.87	0.56
1:A:207:ARG:HD3	1:A:234:ARG:HH22	1.70	0.55
1:A:302:SER:HA	3:A:413:C8E:H202	1.87	0.55
1:A:301:ARG:CG	3:A:413:C8E:H191	2.32	0.54
1:A:76:ASN:ND2	1:A:126:ARG:NH2	2.52	0.54
1:A:76:ASN:HA	1:A:78:GLU:HG3	1.91	0.53
1:B:363:ARG:HD3	5:B:604:HOH:O	2.09	0.53
1:A:344:ARG:HD3	3:A:412:C8E:H51	1.89	0.52
1:B:133:ARG:NH1	5:B:689:HOH:O	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:TRP:CZ2	1:A:370:ARG:HG3	2.45	0.52
1:B:24:PHE:O	1:B:25:ARG:HB2	2.10	0.52
1:A:207:ARG:HD3	1:A:234:ARG:NH1	2.25	0.52
1:A:275:TRP:HB3	1:A:296:THR:HB	1.92	0.52
1:B:307:TYR:CE2	3:B:410:C8E:H82	2.44	0.52
1:A:386:TYR:HE1	1:A:388:LEU:HD21	1.74	0.51
3:A:402:C8E:H11	3:A:412:C8E:C5	2.39	0.51
1:A:344:ARG:HD2	3:A:412:C8E:H51	1.92	0.51
1:B:227:ASN:HB2	2:B:399:EDO:H12	1.92	0.51
1:A:207:ARG:HD3	1:A:234:ARG:CZ	2.42	0.50
1:B:26:ASP:OD1	1:B:26:ASP:O	2.29	0.50
1:B:163:MET:H	3:B:413:C8E:C20	2.24	0.50
1:A:207:ARG:HG3	1:A:236:ASP:HB2	1.94	0.49
1:B:263:TYR:HB2	1:B:306:ARG:HB3	1.95	0.49
1:B:163:MET:H	3:B:413:C8E:H202	1.78	0.49
1:B:358:ALA:O	1:B:359:ARG:HB2	2.12	0.49
1:A:211:ALA:HB1	3:A:400:C8E:H13	1.97	0.47
1:A:263:TYR:HB2	1:A:306:ARG:HB3	1.96	0.47
1:B:37:TRP:HB3	1:B:69:ASN:HB3	1.97	0.47
1:A:76:ASN:CB	1:A:77:SER:HA	2.42	0.46
1:B:226:ALA:HB2	3:B:415:C8E:H52	1.96	0.46
1:A:76:ASN:CG	1:A:126:ARG:HH21	2.18	0.46
1:B:307:TYR:CZ	3:B:410:C8E:H61	2.51	0.45
3:B:407:C8E:H192	5:B:781:HOH:O	2.16	0.45
1:B:11:THR:HG23	1:B:45:PHE:HE1	1.82	0.44
1:B:11:THR:CG2	1:B:45:PHE:HE1	2.30	0.44
1:A:234:ARG:NH1	5:A:653:HOH:O	2.49	0.44
1:A:323:VAL:CG2	3:A:402:C8E:H21	2.48	0.44
1:B:207:ARG:HG3	1:B:236:ASP:HB2	2.00	0.44
1:A:344:ARG:HD2	3:A:412:C8E:H32	2.00	0.44
1:A:207:ARG:HD3	1:A:234:ARG:HH12	1.83	0.43
1:A:64:PHE:HB2	3:A:407:C8E:H42	2.00	0.43
1:A:325:TYR:HB2	3:A:402:C8E:H12	2.00	0.43
1:A:234:ARG:HD2	5:A:716:HOH:O	2.18	0.43
1:B:11:THR:HG23	1:B:45:PHE:CD1	2.53	0.43
1:B:25:ARG:O	1:B:26:ASP:C	2.57	0.43
1:A:344:ARG:HH11	3:A:412:C8E:H62	1.84	0.42
1:A:229:GLY:HA3	1:A:250:TYR:CE2	2.54	0.42
1:B:163:MET:CB	3:B:413:C8E:H202	2.43	0.42
1:A:290:MET:CE	1:A:324:ARG:HG3	2.50	0.41
1:A:308:ASP:OD2	5:A:702:HOH:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:24:PHE:O	1:B:25:ARG:CB	2.68	0.41
1:A:374:ASN:O	5:A:463:HOH:O	2.22	0.41

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	370/398 (93%)	361 (98%)	9 (2%)	0	100	100
1	B	369/398 (93%)	359 (97%)	9 (2%)	1 (0%)	46	24
All	All	739/796 (93%)	720 (97%)	18 (2%)	1 (0%)	56	33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	25	ARG

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	301/315 (96%)	300 (100%)	1 (0%)	94	90
1	B	300/315 (95%)	298 (99%)	2 (1%)	88	78
All	All	601/630 (95%)	598 (100%)	3 (0%)	92	86

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	TYR
1	B	18	TYR
1	B	70	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	76	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

37 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	EDO	A	399	-	3,3,3	0.45	0	2,2,2	0.43	0
3	C8E	A	400	-	8,8,20	0.22	0	7,7,19	0.57	0
3	C8E	A	401	-	6,6,20	0.27	0	5,5,19	0.43	0
3	C8E	A	402	-	5,5,20	0.27	0	4,4,19	0.38	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	C8E	A	403	-	8,8,20	0.39	0	7,7,19	0.19	0
3	C8E	A	404	-	13,13,20	0.37	0	12,12,19	0.43	0
3	C8E	A	405	-	14,14,20	0.37	0	12,12,19	0.35	0
3	C8E	A	406	-	4,4,20	0.34	0	3,3,19	0.34	0
3	C8E	A	407	-	8,8,20	0.26	0	7,7,19	0.42	0
3	C8E	A	408	-	6,6,20	0.38	0	5,5,19	0.33	0
3	C8E	A	409	-	8,8,20	0.46	0	7,7,19	0.24	0
3	C8E	A	410	-	5,5,20	0.44	0	4,4,19	0.35	0
3	C8E	A	411	-	8,8,20	0.46	0	7,7,19	0.27	0
3	C8E	A	412	-	8,8,20	0.25	0	7,7,19	0.53	0
3	C8E	A	413	-	14,14,20	0.48	0	13,13,19	0.19	0
4	VNL	A	414	-	9,12,12	0.61	0	12,16,16	1.53	1 (8%)
4	VNL	A	415	-	9,12,12	0.65	0	12,16,16	1.55	2 (16%)
2	EDO	B	399	-	3,3,3	0.54	0	2,2,2	0.34	0
2	EDO	B	400	-	3,3,3	0.48	0	2,2,2	0.43	0
2	EDO	B	401	-	3,3,3	0.47	0	2,2,2	0.42	0
3	C8E	B	402	-	6,6,20	0.26	0	5,5,19	0.44	0
3	C8E	B	403	-	4,4,20	0.25	0	3,3,19	0.41	0
3	C8E	B	404	-	10,10,20	0.30	0	9,9,19	0.60	0
3	C8E	B	405	-	5,5,20	0.25	0	4,4,19	0.36	0
3	C8E	B	406	-	11,11,20	0.47	0	10,10,19	0.29	0
3	C8E	B	407	-	7,7,20	0.37	0	6,6,19	0.19	0
3	C8E	B	408	-	6,6,20	0.28	0	5,5,19	0.38	0
3	C8E	B	409	-	9,9,20	0.41	0	8,8,19	0.26	0
3	C8E	B	410	-	10,10,20	0.33	0	9,9,19	0.49	0
3	C8E	B	411	-	5,5,20	0.28	0	4,4,19	0.38	0
3	C8E	B	412	-	13,13,20	0.39	0	12,12,19	0.32	0
3	C8E	B	413	-	4,4,20	0.33	0	3,3,19	0.23	0
3	C8E	B	414	-	3,3,20	0.47	0	2,2,19	0.67	0
3	C8E	B	415	-	6,6,20	0.27	0	5,5,19	0.44	0
3	C8E	B	416	-	4,4,20	0.29	0	3,3,19	0.37	0
4	VNL	B	417	-	9,12,12	0.60	0	12,16,16	1.69	3 (25%)
4	VNL	B	418	-	9,12,12	0.54	0	12,16,16	1.42	1 (8%)

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	EDO	A	399	-	-	0/1/1/1	0/0/0/0
3	C8E	A	400	-	-	0/6/6/18	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	C8E	A	401	-	-	0/4/4/18	0/0/0/0
3	C8E	A	402	-	-	0/3/3/18	0/0/0/0
3	C8E	A	403	-	-	0/6/6/18	0/0/0/0
3	C8E	A	404	-	-	0/11/11/18	0/0/0/0
3	C8E	A	405	-	-	0/10/10/18	0/0/0/0
3	C8E	A	406	-	-	0/2/2/18	0/0/0/0
3	C8E	A	407	-	-	0/6/6/18	0/0/0/0
3	C8E	A	408	-	-	0/4/4/18	0/0/0/0
3	C8E	A	409	-	-	0/6/6/18	0/0/0/0
3	C8E	A	410	-	-	0/3/3/18	0/0/0/0
3	C8E	A	411	-	-	0/6/6/18	0/0/0/0
3	C8E	A	412	-	-	0/6/6/18	0/0/0/0
3	C8E	A	413	-	-	0/12/12/18	0/0/0/0
4	VNL	A	414	-	-	0/2/6/6	0/1/1/1
4	VNL	A	415	-	-	0/2/6/6	0/1/1/1
2	EDO	B	399	-	-	0/1/1/1	0/0/0/0
2	EDO	B	400	-	-	0/1/1/1	0/0/0/0
2	EDO	B	401	-	-	0/1/1/1	0/0/0/0
3	C8E	B	402	-	-	0/4/4/18	0/0/0/0
3	C8E	B	403	-	-	0/2/2/18	0/0/0/0
3	C8E	B	404	-	-	0/8/8/18	0/0/0/0
3	C8E	B	405	-	-	0/3/3/18	0/0/0/0
3	C8E	B	406	-	-	0/9/9/18	0/0/0/0
3	C8E	B	407	-	-	0/5/5/18	0/0/0/0
3	C8E	B	408	-	-	0/4/4/18	0/0/0/0
3	C8E	B	409	-	-	0/7/7/18	0/0/0/0
3	C8E	B	410	-	-	0/8/8/18	0/0/0/0
3	C8E	B	411	-	-	0/3/3/18	0/0/0/0
3	C8E	B	412	-	-	0/11/11/18	0/0/0/0
3	C8E	B	413	-	-	0/2/2/18	0/0/0/0
3	C8E	B	414	-	-	0/1/1/18	0/0/0/0
3	C8E	B	415	-	-	0/4/4/18	0/0/0/0
3	C8E	B	416	-	-	0/2/2/18	0/0/0/0
4	VNL	B	417	-	-	0/2/6/6	0/1/1/1
4	VNL	B	418	-	-	0/2/6/6	0/1/1/1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	417	VNL	OM-CM2-CO2	-2.31	120.26	124.21
4	A	415	VNL	OM-CM2-CO2	-2.16	120.52	124.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	417	VNL	CV-OM-CM2	2.99	122.08	117.54
4	B	418	VNL	OM-CM2-CZ	3.35	118.98	114.57
4	A	414	VNL	OM-CM2-CZ	3.81	119.59	114.57
4	B	417	VNL	OM-CM2-CZ	3.94	119.75	114.57
4	A	415	VNL	OM-CM2-CZ	4.01	119.85	114.57

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

11 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	400	C8E	1	0
3	A	402	C8E	4	0
3	A	407	C8E	1	0
3	A	412	C8E	7	0
3	A	413	C8E	7	0
2	B	399	EDO	1	0
3	B	404	C8E	1	0
3	B	407	C8E	1	0
3	B	410	C8E	2	0
3	B	413	C8E	6	0
3	B	415	C8E	1	0

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, 95th 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 ²)	Q<0.9
1	A	374/398 (93%)	0.10	24 (6%)	23 20	12, 22, 46, 95	4 (1%)
1	B	374/398 (93%)	-0.03	20 (5%)	30 27	13, 21, 43, 109	6 (1%)
All	All	748/796 (93%)	0.04	44 (5%)	26 23	12, 21, 45, 109	10 (1%)

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	33	LEU	8.4
1	B	84	ASP	6.4
1	A	390	TRP	6.2
1	A	84	ASP	5.8
1	B	45	PHE	5.7
1	A	70	SER	5.4
1	A	87	ARG	5.3
1	B	86	GLY	5.0
1	A	85	ASP	4.9
1	B	85	ASP	4.9
1	A	219	VAL	4.6
1	B	390	TRP	4.5
1	A	76	ASN	4.5
1	B	87	ARG	4.4
1	A	86	GLY	4.1
1	B	335	ALA	4.0
1	A	34	VAL	3.8
1	A	6	LEU	3.7
1	B	6	LEU	3.6
1	A	355	GLY	3.5
1	A	10	LYS	3.3
1	A	82	LEU	3.3
1	B	356	PRO	3.1
1	A	218	ARG	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	25	ARG	3.1
1	A	354	SER	3.0
1	B	8	ASP	2.9
1	A	8	ASP	2.9
1	B	70	SER	2.9
1	B	334	LYS	2.9
1	B	9	ALA	2.9
1	B	10	LYS	2.9
1	B	26	ASP	2.8
1	A	388	LEU	2.8
1	B	83	HIS	2.6
1	B	33	LEU	2.5
1	B	82	LEU	2.3
1	A	9	ALA	2.3
1	A	83	HIS	2.2
1	A	224	LEU	2.1
1	A	7	GLU	2.1
1	A	220	GLY	2.1
1	A	356	PRO	2.1
1	B	219	VAL	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, 95th 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 ²)	Q<0.9
2	EDO	B	400	4/4	0.79	0.30	21.13	54,58,61,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	C8E	B	404	11/21	0.84	0.17	14.11	40,46,63,69	0
3	C8E	B	412	14/21	0.70	0.25	10.43	44,58,72,72	0
3	C8E	A	401	7/21	0.78	0.13	9.83	34,38,43,45	0
3	C8E	B	414	4/21	0.93	0.18	9.52	35,36,39,44	0
3	C8E	B	405	6/21	0.95	0.16	8.38	33,41,50,55	0
3	C8E	A	406	5/21	0.88	0.15	8.24	35,36,57,61	0
3	C8E	A	407	9/21	0.79	0.13	7.08	44,48,56,59	0
3	C8E	A	400	9/21	0.87	0.19	6.04	44,48,56,57	0
3	C8E	B	410	11/21	0.77	0.22	5.77	29,40,55,57	0
3	C8E	A	413	15/21	0.68	0.27	5.65	28,49,61,62	0
3	C8E	B	409	10/21	0.75	0.20	5.27	35,51,58,58	0
4	VNL	A	415	12/12	0.87	0.18	5.24	29,34,44,51	0
3	C8E	B	415	7/21	0.76	0.31	5.14	47,51,53,54	0
3	C8E	A	404	14/21	0.83	0.16	4.36	29,58,62,62	0
3	C8E	B	403	5/21	0.91	0.20	3.51	24,31,36,37	0
3	C8E	A	405	16/21	0.82	0.13	3.51	29,55,62,63	0
3	C8E	B	408	7/21	0.74	0.19	3.22	36,43,52,54	0
2	EDO	B	399	4/4	0.68	0.15	2.60	41,46,47,48	0
3	C8E	B	411	6/21	0.83	0.15	2.44	29,39,42,43	0
3	C8E	A	409	9/21	0.81	0.14	2.07	45,51,60,62	0
3	C8E	B	402	7/21	0.88	0.13	2.04	38,47,51,51	0
3	C8E	A	411	9/21	0.76	0.17	1.90	47,53,60,61	0
3	C8E	A	402	6/21	0.81	0.14	1.67	52,53,57,58	0
4	VNL	B	418	12/12	0.92	0.09	1.29	21,23,32,33	0
3	C8E	A	412	9/21	0.77	0.15	1.25	45,47,53,53	0
4	VNL	A	414	12/12	0.94	0.10	1.11	24,26,31,31	0
3	C8E	A	410	6/21	0.88	0.12	1.04	56,58,58,58	0
3	C8E	A	403	9/21	0.86	0.14	1.00	37,44,52,56	0
4	VNL	B	417	12/12	0.97	0.10	0.06	20,24,27,29	0
2	EDO	B	401	4/4	0.89	0.09	-	53,54,55,58	0
3	C8E	B	413	5/21	0.79	0.40	-	38,43,51,56	0
2	EDO	A	399	4/4	0.87	0.24	-	47,48,50,53	0
3	C8E	B	406	12/21	0.77	0.18	-	54,58,62,62	0
3	C8E	A	408	7/21	0.75	0.22	-	69,70,71,73	0
3	C8E	B	416	5/21	0.66	0.18	-	46,46,52,53	0
3	C8E	B	407	8/21	0.87	0.13	-	26,42,55,56	0

6.5 Other polymers ⓘ

There are no such residues in this entry.