



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:14 PM GMT

PDB ID : 1WN0
Title : Crystal Structure of Histidine-containing Phosphotransfer Protein, ZmHP2, from maize
Authors : Sugawara, H.; Kawano, Y.; Hatakeyama, T.; Yamaya, T.; Kamiya, N.; Sakakibara, H.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2004-07-24
Resolution : 2.20 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

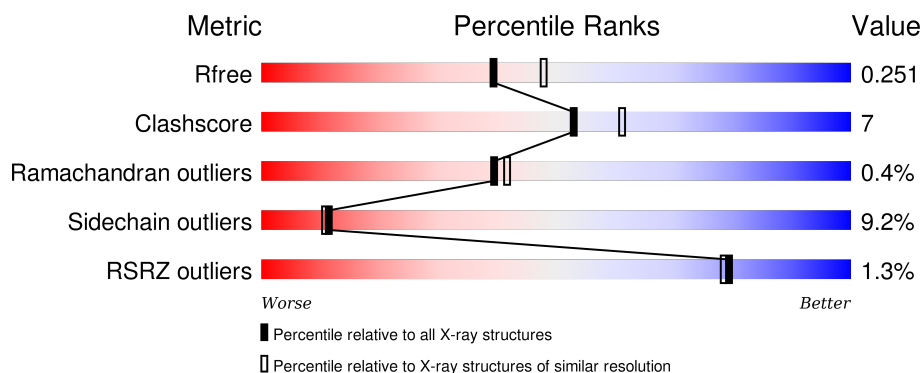
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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	145	<div> <div>2%</div> <div>64% 19% 6% 10%</div> </div>
1	B	145	<div> <div>%</div> <div>58% 21% 6% 14%</div> </div>
1	C	145	<div> <div>%</div> <div>72% 19% 5%</div> </div>
1	D	145	<div> <div>%</div> <div>66% 23% 6% 5%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4278 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 histidine-containing phosphotransfer protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	131	Total	C	N	O	S	0	0	0
			1027	646	173	199	9			
1	B	124	Total	C	N	O	S	0	0	0
			976	617	164	186	9			
1	C	138	Total	C	N	O	S	0	0	0
			1086	682	185	210	9			
1	D	138	Total	C	N	O	S	0	0	0
			1086	682	185	210	9			

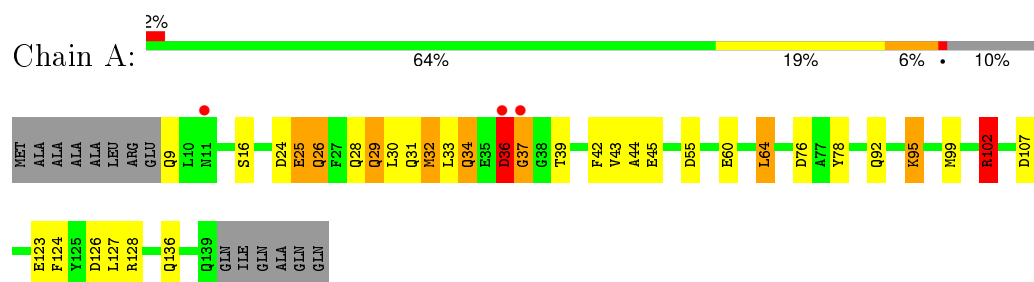
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	27	Total	O	0	0
			27	27		
2	B	12	Total	O	0	0
			12	12		
2	C	37	Total	O	0	0
			37	37		
2	D	27	Total	O	0	0
			27	27		

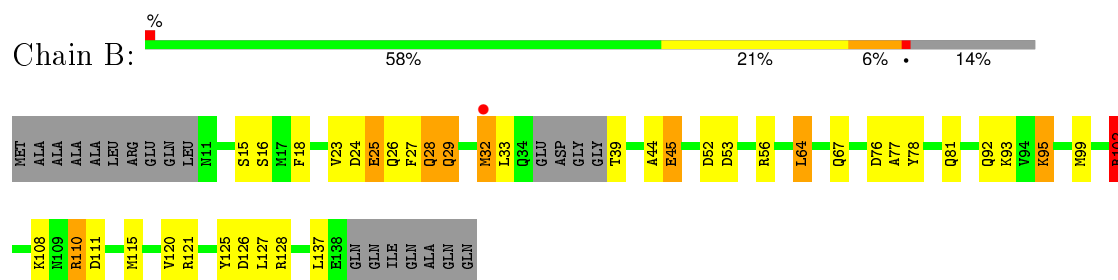
3 Residue-property plots [i](#)

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.

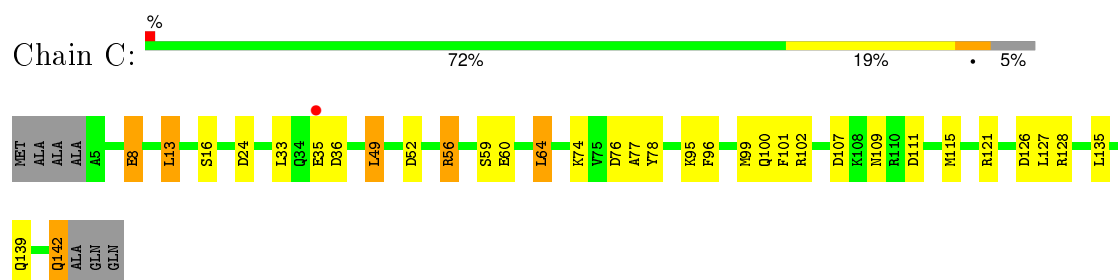
- Molecule 1: histidine-containing phosphotransfer protein



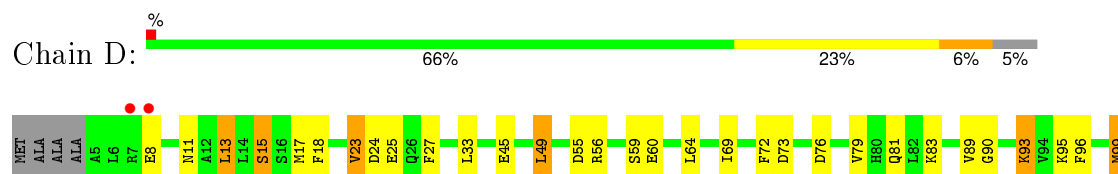
- Molecule 1: histidine-containing phosphotransfer protein



- Molecule 1: histidine-containing phosphotransfer protein



- Molecule 1: histidine-containing phosphotransfer protein



R100	F101	R102	N109	M116	A118	R121	Y125	D126	L127	R128	N129	K130	F131	Q142	ALA	GLN	GLN
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4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	148.80Å 81.41Å 89.50Å 90.00° 123.42° 90.00°	Depositor
Resolution (Å)	19.84 – 2.20 19.82 – 2.20	Depositor EDS
% Data completeness (in resolution range)	94.2 (19.84-2.20) 94.2 (19.82-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.25 (at 2.19Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.209 , 0.248 0.212 , 0.251	Depositor DCC
R_{free} test set	2141 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	39.7	Xtriage
Anisotropy	0.149	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 37.6	EDS
Estimated twinning fraction	0.010 for 1/2*h-3/2*k,-1/2*h-1/2*k,-1/2*h +1/2*k-l 0.008 for 1/2*h+3/2*k,1/2*h-1/2*k,-1/2*h- 1/2*k-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 42707 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4278	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.07% of the height of the origin peak. No significant pseudotranslation is detected.*

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

5.1 Standard geometry

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	1.70	13/1040 (1.2%)	1.44	13/1400 (0.9%)
1	B	1.65	18/988 (1.8%)	1.37	11/1329 (0.8%)
1	C	1.90	15/1099 (1.4%)	1.52	19/1479 (1.3%)
1	D	1.95	27/1099 (2.5%)	1.50	15/1479 (1.0%)
All	All	1.81	73/4226 (1.7%)	1.46	58/5687 (1.0%)

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	A	0	1

All (73) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	95	LYS	CE-NZ	10.01	1.74	1.49
1	A	110	ARG	CD-NE	-9.93	1.29	1.46
1	B	95	LYS	CE-NZ	9.25	1.72	1.49
1	C	78	TYR	CG-CD2	-8.56	1.28	1.39
1	C	102	ARG	NE-CZ	8.00	1.43	1.33
1	B	32	MET	SD-CE	7.82	2.21	1.77
1	A	110	ARG	NE-CZ	-7.79	1.23	1.33
1	D	83	LYS	CD-CE	7.38	1.69	1.51
1	D	79	VAL	CB-CG2	-7.14	1.37	1.52
1	C	59	SER	CB-OG	-6.97	1.33	1.42
1	D	60	GLU	CD-OE2	6.90	1.33	1.25
1	D	59	SER	CB-OG	-6.87	1.33	1.42
1	B	93	LYS	CD-CE	6.85	1.68	1.51
1	D	15	SER	CA-CB	6.83	1.63	1.52
1	B	110	ARG	CD-NE	-6.74	1.35	1.46
1	D	102	ARG	NE-CZ	6.72	1.41	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	27	PHE	CE2-CZ	6.70	1.50	1.37
1	B	77	ALA	CA-CB	6.58	1.66	1.52
1	C	60	GLU	CG-CD	6.50	1.61	1.51
1	D	15	SER	CB-OG	6.41	1.50	1.42
1	D	69	ILE	CB-CG2	6.36	1.72	1.52
1	A	44	ALA	CA-CB	6.31	1.65	1.52
1	A	25	GLU	CD-OE1	6.08	1.32	1.25
1	A	25	GLU	CD-OE2	5.99	1.32	1.25
1	B	102	ARG	CB-CG	5.92	1.68	1.52
1	D	130	LYS	CB-CG	5.89	1.68	1.52
1	A	102	ARG	CG-CD	5.87	1.66	1.51
1	D	102	ARG	CB-CG	5.82	1.68	1.52
1	A	110	ARG	CZ-NH1	-5.79	1.25	1.33
1	B	110	ARG	CZ-NH1	-5.78	1.25	1.33
1	C	95	LYS	CD-CE	5.64	1.65	1.51
1	A	123	GLU	CD-OE2	-5.62	1.19	1.25
1	B	45	GLU	CD-OE2	5.62	1.31	1.25
1	D	23	VAL	CB-CG2	5.61	1.64	1.52
1	A	99	MET	CB-CG	5.56	1.69	1.51
1	B	78	TYR	CE1-CZ	-5.53	1.31	1.38
1	D	128	ARG	CZ-NH1	5.51	1.40	1.33
1	C	102	ARG	CB-CG	5.49	1.67	1.52
1	D	81	GLN	CG-CD	5.49	1.63	1.51
1	C	74	LYS	CD-CE	5.45	1.64	1.51
1	D	125	TYR	CE1-CZ	-5.44	1.31	1.38
1	B	108	LYS	C-O	-5.43	1.13	1.23
1	C	74	LYS	CE-NZ	5.43	1.62	1.49
1	B	110	ARG	NE-CZ	-5.39	1.26	1.33
1	C	16	SER	CB-OG	-5.39	1.35	1.42
1	C	8	GLU	CG-CD	5.39	1.60	1.51
1	A	32	MET	CG-SD	5.33	1.95	1.81
1	D	60	GLU	CD-OE1	5.31	1.31	1.25
1	B	125	TYR	CD1-CE1	-5.30	1.31	1.39
1	C	99	MET	CG-SD	5.29	1.95	1.81
1	D	99	MET	SD-CE	5.29	2.07	1.77
1	D	72	PHE	CE2-CZ	5.26	1.47	1.37
1	D	130	LYS	CD-CE	5.26	1.64	1.51
1	B	24	ASP	CB-CG	5.26	1.62	1.51
1	D	89	VAL	CB-CG1	-5.25	1.41	1.52
1	C	121	ARG	CG-CD	5.25	1.65	1.51
1	D	11	ASN	CB-CG	5.24	1.63	1.51
1	D	93	LYS	CE-NZ	5.23	1.62	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	35	GLU	CD-OE1	5.21	1.31	1.25
1	B	81	GLN	CG-CD	5.17	1.62	1.51
1	D	115	MET	CG-SD	5.16	1.94	1.81
1	B	28	GLN	CG-CD	5.16	1.62	1.51
1	B	44	ALA	CA-CB	5.15	1.63	1.52
1	D	45	GLU	CD-OE2	5.14	1.31	1.25
1	A	34	GLN	CG-CD	5.14	1.62	1.51
1	B	99	MET	CB-CG	5.11	1.67	1.51
1	C	77	ALA	CA-CB	5.07	1.63	1.52
1	C	13	LEU	CG-CD2	-5.04	1.33	1.51
1	D	18	PHE	CE1-CZ	5.04	1.47	1.37
1	D	25	GLU	CD-OE1	5.02	1.31	1.25
1	A	124	PHE	CB-CG	-5.02	1.42	1.51
1	B	28	GLN	CB-CG	5.02	1.66	1.52
1	D	121	ARG	CZ-NH1	5.01	1.39	1.33

All (58) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	110	ARG	NE-CZ-NH2	-13.25	113.67	120.30
1	D	24	ASP	CB-CG-OD2	11.77	128.90	118.30
1	D	121	ARG	NE-CZ-NH2	-11.13	114.74	120.30
1	D	49	LEU	CA-CB-CG	-10.68	90.73	115.30
1	B	110	ARG	NE-CZ-NH2	-10.59	115.00	120.30
1	C	49	LEU	CA-CB-CG	-10.46	91.24	115.30
1	C	56	ARG	NE-CZ-NH2	-9.73	115.43	120.30
1	C	24	ASP	CB-CG-OD2	9.19	126.57	118.30
1	A	128	ARG	NE-CZ-NH2	-9.00	115.80	120.30
1	C	102	ARG	NE-CZ-NH1	8.94	124.77	120.30
1	B	64	LEU	CB-CG-CD1	8.75	125.87	111.00
1	D	102	ARG	NE-CZ-NH1	8.68	124.64	120.30
1	D	99	MET	CG-SD-CE	8.46	113.73	100.20
1	C	52	ASP	CB-CG-OD2	8.38	125.84	118.30
1	B	24	ASP	CB-CG-OD2	8.03	125.52	118.30
1	C	99	MET	CG-SD-CE	7.94	112.90	100.20
1	C	49	LEU	CB-CG-CD2	7.89	124.42	111.00
1	D	128	ARG	NE-CZ-NH2	-7.88	116.36	120.30
1	C	111	ASP	CB-CG-OD1	7.83	125.34	118.30
1	A	111	ASP	CB-CG-OD2	7.76	125.28	118.30
1	D	121	ARG	NE-CZ-NH1	7.56	124.08	120.30
1	D	76	ASP	CB-CG-OD2	7.53	125.08	118.30
1	C	60	GLU	OE1-CD-OE2	-7.35	114.48	123.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	126	ASP	CB-CG-OD2	7.33	124.90	118.30
1	A	107	ASP	CB-CG-OD2	7.31	124.88	118.30
1	D	56	ARG	NE-CZ-NH2	-7.30	116.65	120.30
1	D	55	ASP	CB-CG-OD2	7.24	124.82	118.30
1	A	24	ASP	CB-CG-OD2	7.11	124.70	118.30
1	C	76	ASP	CB-CG-OD2	7.08	124.68	118.30
1	A	76	ASP	CB-CG-OD2	7.06	124.65	118.30
1	D	76	ASP	CB-CG-OD1	-7.03	111.97	118.30
1	D	73	ASP	CB-CG-OD2	7.02	124.62	118.30
1	B	128	ARG	NE-CZ-NH2	-6.57	117.02	120.30
1	A	110	ARG	CG-CD-NE	-6.29	98.58	111.80
1	B	53	ASP	CB-CG-OD2	6.28	123.95	118.30
1	C	121	ARG	NE-CZ-NH2	-6.26	117.17	120.30
1	C	107	ASP	CB-CG-OD2	6.05	123.74	118.30
1	A	36	ASP	CB-CG-OD1	5.98	123.68	118.30
1	A	64	LEU	CB-CG-CD1	5.90	121.03	111.00
1	C	64	LEU	CB-CG-CD1	5.86	120.97	111.00
1	C	121	ARG	NE-CZ-NH1	5.85	123.22	120.30
1	A	126	ASP	CB-CG-OD1	5.81	123.53	118.30
1	D	128	ARG	NE-CZ-NH1	5.69	123.14	120.30
1	C	36	ASP	CB-CG-OD2	5.68	123.42	118.30
1	B	56	ARG	NE-CZ-NH2	-5.67	117.47	120.30
1	A	55	ASP	CB-CG-OD1	5.56	123.31	118.30
1	B	121	ARG	NE-CZ-NH1	5.56	123.08	120.30
1	D	49	LEU	CB-CG-CD1	5.48	120.31	111.00
1	B	52	ASP	CB-CG-OD2	5.47	123.23	118.30
1	B	128	ARG	NE-CZ-NH1	5.40	123.00	120.30
1	A	110	ARG	CB-CG-CD	-5.39	97.58	111.60
1	C	52	ASP	CB-CG-OD1	-5.36	113.47	118.30
1	A	34	GLN	CA-CB-CG	5.28	125.02	113.40
1	C	60	GLU	CB-CG-CD	5.17	128.15	114.20
1	C	8	GLU	CB-CA-C	5.15	120.70	110.40
1	D	25	GLU	CA-CB-CG	5.09	124.60	113.40
1	B	24	ASP	OD1-CG-OD2	-5.07	113.66	123.30
1	C	126	ASP	CB-CG-OD2	5.07	122.86	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	37	GLY	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	1027	0	1013	20	0
1	B	976	0	969	21	0
1	C	1086	0	1075	18	0
1	D	1086	0	1075	19	0
2	A	27	0	0	0	0
2	B	12	0	0	0	0
2	C	37	0	0	2	0
2	D	27	0	0	0	0
All	All	4278	0	4132	55	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 (55) 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:95:LYS:NZ	1:B:95:LYS:CE	1.72	1.51
1:A:95:LYS:NZ	1:A:95:LYS:CE	1.74	1.49
1:D:99:MET:CE	1:D:99:MET:SD	2.07	1.43
1:B:32:MET:SD	1:B:32:MET:CE	2.21	1.28
1:A:26:GLN:HE21	1:D:99:MET:CE	1.71	1.01
1:A:26:GLN:HE21	1:D:99:MET:HE2	1.31	0.93
1:A:26:GLN:NE2	1:D:99:MET:HE2	1.84	0.92
1:A:45:GLU:OE1	1:D:109:ASN:ND2	2.08	0.86
1:A:26:GLN:NE2	1:D:99:MET:CE	2.41	0.79
1:B:26:GLN:HG2	1:C:96:PHE:CD1	2.30	0.67
1:D:33:LEU:C	1:D:33:LEU:HD23	2.16	0.65
1:C:142:GLN:HE21	1:C:142:GLN:HA	1.61	0.65
1:B:67:GLN:O	1:B:110:ARG:NH2	2.26	0.64
1:B:26:GLN:OE1	1:C:100:GLN:NE2	2.30	0.64
1:B:45:GLU:OE1	1:C:109:ASN:ND2	2.34	0.60
1:B:76:ASP:OD1	1:B:102:ARG:HD2	2.01	0.60
1:A:34:GLN:HB2	1:A:43:VAL:HG21	1.84	0.59
1:B:26:GLN:NE2	1:C:96:PHE:HB3	2.17	0.58
1:B:29:GLN:NE2	1:C:96:PHE:HD1	2.02	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:GLN:HG2	1:C:96:PHE:CG	2.40	0.56
1:A:102:ARG:HD3	1:A:102:ARG:N	2.19	0.56
1:A:29:GLN:HE21	1:D:96:PHE:HD1	1.53	0.55
1:B:111:ASP:O	1:B:115:MET:HG3	2.07	0.55
1:B:29:GLN:NE2	1:C:96:PHE:CD1	2.75	0.55
1:C:142:GLN:CA	1:C:142:GLN:HE21	2.19	0.55
1:A:29:GLN:NE2	1:D:96:PHE:HD1	2.06	0.52
1:C:128:ARG:NH2	2:C:173:HOH:O	2.35	0.51
1:A:29:GLN:NE2	1:D:93:LYS:HA	2.25	0.51
1:B:25:GLU:O	1:B:26:GLN:C	2.49	0.51
1:A:26:GLN:NE2	1:D:96:PHE:HB3	2.25	0.51
1:D:115:MET:HE3	1:D:118:ALA:HB3	1.93	0.50
1:C:128:ARG:NE	2:C:173:HOH:O	2.31	0.49
1:C:33:LEU:HD23	1:C:33:LEU:C	2.33	0.49
1:D:23:VAL:HA	1:D:90:GLY:O	2.14	0.47
1:A:39:THR:HG22	1:A:42:PHE:HB2	1.97	0.46
1:C:142:GLN:NE2	1:C:142:GLN:HA	2.29	0.46
1:A:36:ASP:O	1:A:37:GLY:C	2.54	0.46
1:A:60:GLU:OE1	1:A:78:TYR:CE1	2.69	0.46
1:A:39:THR:HG23	1:D:115:MET:SD	2.56	0.45
1:B:18:PHE:CE2	1:B:28:GLN:HG2	2.52	0.44
1:B:26:GLN:HE21	1:C:96:PHE:HB3	1.83	0.44
1:C:135:LEU:O	1:C:139:GLN:HG3	2.17	0.44
1:B:26:GLN:CD	1:C:100:GLN:HE22	2.21	0.43
1:B:76:ASP:OD1	1:B:102:ARG:CD	2.66	0.43
1:A:39:THR:HG22	1:A:42:PHE:CB	2.49	0.43
1:A:30:LEU:HD22	1:A:43:VAL:HG22	2.01	0.42
1:D:13:LEU:O	1:D:17:MET:HG3	2.19	0.42
1:A:29:GLN:NE2	1:D:96:PHE:CD1	2.86	0.42
1:B:26:GLN:NE2	1:C:100:GLN:HE22	2.18	0.42
1:B:23:VAL:HG21	1:B:27:PHE:CD1	2.54	0.41
1:D:33:LEU:O	1:D:33:LEU:HD23	2.20	0.41
1:D:127:LEU:HD13	1:D:131:PHE:CE2	2.55	0.41
1:B:39:THR:HG22	1:C:115:MET:CE	2.50	0.41
1:A:26:GLN:CD	1:D:96:PHE:HB3	2.41	0.41
1:B:102:ARG:HA	1:B:102:ARG:HD3	1.84	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	129/145 (89%)	126 (98%)	3 (2%)	0	100	100
1	B	120/145 (83%)	116 (97%)	2 (2%)	2 (2%)	11	7
1	C	136/145 (94%)	135 (99%)	1 (1%)	0	100	100
1	D	136/145 (94%)	135 (99%)	1 (1%)	0	100	100
All	All	521/580 (90%)	512 (98%)	7 (1%)	2 (0%)	39	42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	137	LEU
1	B	15	SER

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	113/122 (93%)	97 (86%)	16 (14%)	4	3
1	B	108/122 (88%)	99 (92%)	9 (8%)	14	13
1	C	119/122 (98%)	111 (93%)	8 (7%)	20	21
1	D	119/122 (98%)	110 (92%)	9 (8%)	16	16
All	All	459/488 (94%)	417 (91%)	42 (9%)	11	11

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	GLN
1	A	16	SER
1	A	25	GLU
1	A	26	GLN
1	A	28	GLN
1	A	29	GLN
1	A	31	GLN
1	A	32	MET
1	A	33	LEU
1	A	36	ASP
1	A	64	LEU
1	A	92	GLN
1	A	102	ARG
1	A	120	VAL
1	A	127	LEU
1	A	136	GLN
1	B	16	SER
1	B	25	GLU
1	B	29	GLN
1	B	33	LEU
1	B	64	LEU
1	B	92	GLN
1	B	102	ARG
1	B	120	VAL
1	B	127	LEU
1	C	8	GLU
1	C	13	LEU
1	C	49	LEU
1	C	56	ARG
1	C	64	LEU
1	C	101	PHE
1	C	127	LEU
1	C	142	GLN
1	D	8	GLU
1	D	13	LEU
1	D	15	SER
1	D	49	LEU
1	D	64	LEU
1	D	95	LYS
1	D	101	PHE
1	D	127	LEU
1	D	130	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	ASN
1	A	26	GLN
1	A	29	GLN
1	A	31	GLN
1	A	92	GLN
1	A	132	GLN
1	B	26	GLN
1	B	29	GLN
1	B	92	GLN
1	C	11	ASN
1	C	100	GLN
1	C	103	GLN
1	C	106	GLN
1	C	122	ASN
1	C	132	GLN
1	C	142	GLN
1	D	11	ASN
1	D	100	GLN
1	D	122	ASN
1	D	132	GLN
1	D	142	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 ⓘ

There are no ligands in this entry.

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	131/145 (90%)	-0.08	3 (2%) 64 63	30, 41, 70, 80	0
1	B	124/145 (85%)	-0.01	1 (0%) 87 87	32, 42, 73, 78	0
1	C	138/145 (95%)	-0.20	1 (0%) 89 88	29, 37, 56, 77	0
1	D	138/145 (95%)	-0.11	2 (1%) 78 77	31, 40, 70, 83	0
All	All	531/580 (91%)	-0.10	7 (1%) 79 78	29, 40, 71, 83	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	32	MET	4.6
1	A	37	GLY	2.9
1	A	11	ASN	2.3
1	A	36	ASP	2.2
1	D	8	GLU	2.2
1	D	7	ARG	2.1
1	C	35	GLU	2.1

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.