



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 19, 2024 – 03:41 AM EDT

PDB ID : 4EL1
Title : Crystal structure of oxidized hPDI (abb'xa')
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Deposited on : 2012-04-10
Resolution : 2.88 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
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)	:	2.37.1

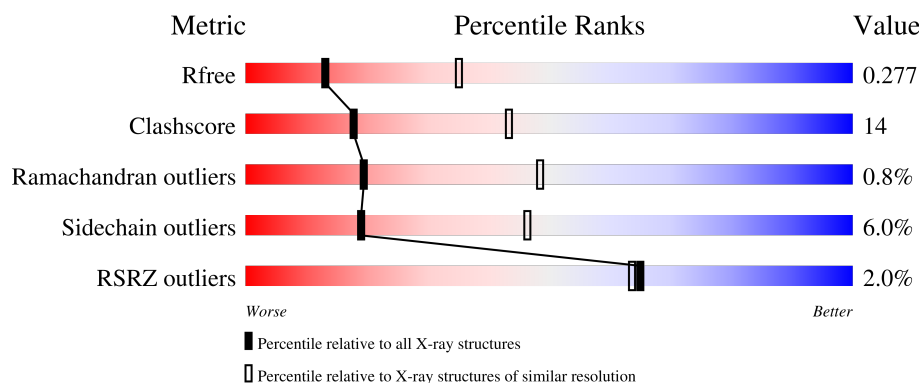
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

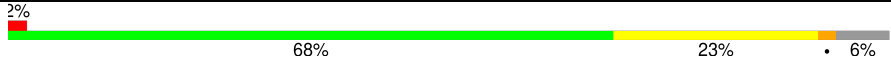

The reported resolution of this entry is 2.88 Å.

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}	130704	2691 (2.90-2.86)
Clashscore	141614	2947 (2.90-2.86)
Ramachandran outliers	138981	2868 (2.90-2.86)
Sidechain outliers	138945	2871 (2.90-2.86)
RSRZ outliers	127900	2629 (2.90-2.86)

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 $\leq 5\%$. 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	482	
1	B	482	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 7222 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 Protein disulfide-isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	452	Total	C	N	O	S	19	2	0
			3601	2310	589	691	11			
1	B	452	Total	C	N	O	S	20	2	0
			3601	2310	589	691	11			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP P07237
A	-18	HIS	-	expression tag	UNP P07237
A	-17	HIS	-	expression tag	UNP P07237
A	-16	HIS	-	expression tag	UNP P07237
A	-15	HIS	-	expression tag	UNP P07237
A	-14	HIS	-	expression tag	UNP P07237
A	-13	HIS	-	expression tag	UNP P07237
A	-12	SER	-	expression tag	UNP P07237
A	-11	SER	-	expression tag	UNP P07237
A	-10	GLY	-	expression tag	UNP P07237
A	-9	LEU	-	expression tag	UNP P07237
A	-8	GLU	-	expression tag	UNP P07237
A	-7	VAL	-	expression tag	UNP P07237
A	-6	LEU	-	expression tag	UNP P07237
A	-5	PHE	-	expression tag	UNP P07237
A	-4	GLN	-	expression tag	UNP P07237
A	-3	GLY	-	expression tag	UNP P07237
A	-2	PRO	-	expression tag	UNP P07237
A	-1	GLY	-	expression tag	UNP P07237
A	0	SER	-	expression tag	UNP P07237
B	-19	MET	-	expression tag	UNP P07237
B	-18	HIS	-	expression tag	UNP P07237
B	-17	HIS	-	expression tag	UNP P07237
B	-16	HIS	-	expression tag	UNP P07237
B	-15	HIS	-	expression tag	UNP P07237

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	HIS	-	expression tag	UNP P07237
B	-13	HIS	-	expression tag	UNP P07237
B	-12	SER	-	expression tag	UNP P07237
B	-11	SER	-	expression tag	UNP P07237
B	-10	GLY	-	expression tag	UNP P07237
B	-9	LEU	-	expression tag	UNP P07237
B	-8	GLU	-	expression tag	UNP P07237
B	-7	VAL	-	expression tag	UNP P07237
B	-6	LEU	-	expression tag	UNP P07237
B	-5	PHE	-	expression tag	UNP P07237
B	-4	GLN	-	expression tag	UNP P07237
B	-3	GLY	-	expression tag	UNP P07237
B	-2	PRO	-	expression tag	UNP P07237
B	-1	GLY	-	expression tag	UNP P07237
B	0	SER	-	expression tag	UNP P07237

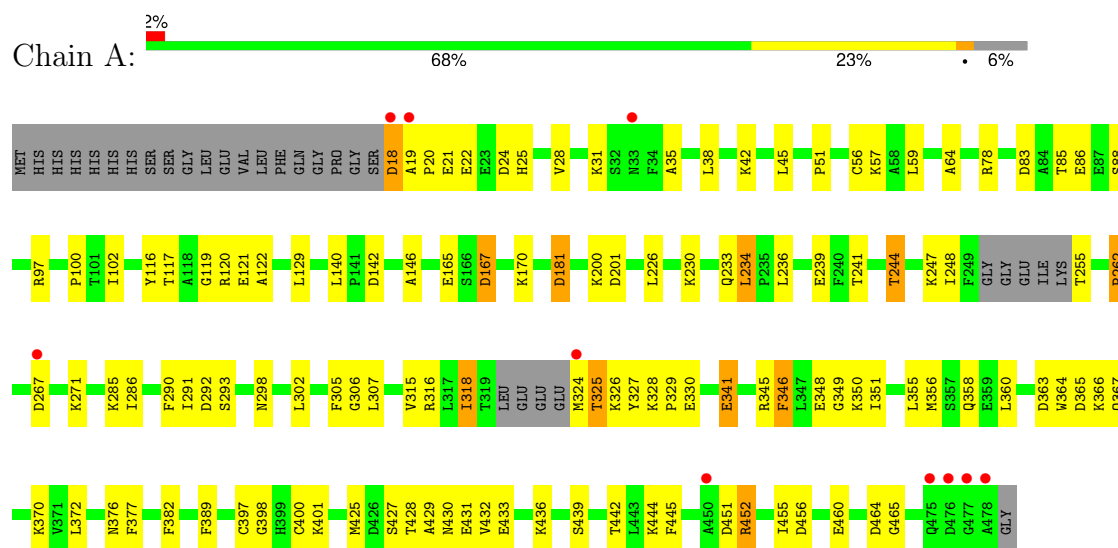
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	10	Total O 10 10	0	0
2	B	10	Total O 10 10	0	0

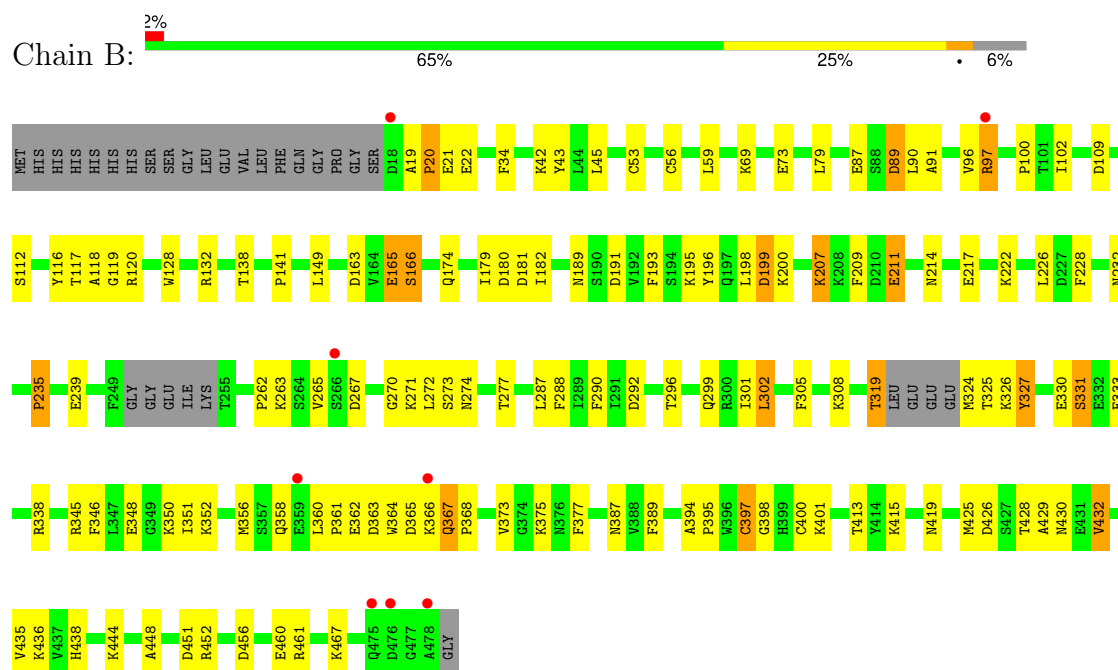
3 Residue-property plots

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.

• Molecule 1: Protein disulfide-isomerase



• Molecule 1: Protein disulfide-isomerase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	160.75Å 34.01Å 156.96Å 90.00° 104.89° 90.00°	Depositor
Resolution (Å)	29.84 – 2.88 29.84 – 2.88	Depositor EDS
% Data completeness (in resolution range)	98.9 (29.84-2.88) 94.6 (29.84-2.88)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.70 (at 2.90Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.261 , 0.281 0.258 , 0.277	Depositor DCC
R_{free} test set	981 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å ²)	44.2	Xtriage
Anisotropy	0.216	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 40.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7222	wwPDB-VP
Average B, all atoms (Å ²)	51.0	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 90.49 % 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 2.2531e-08. 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.72	2/3690 (0.1%)	0.54	0/4982
1	B	0.66	1/3690 (0.0%)	0.51	0/4982
All	All	0.69	3/7380 (0.0%)	0.53	0/9964

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	235	PRO	N-CD	5.98	1.56	1.47
1	A	262	PRO	N-CD	5.92	1.56	1.47
1	A	318	ILE	CA-CB	-5.02	1.43	1.54

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	3601	0	3522	94	2
1	B	3601	0	3520	96	2
2	A	10	0	0	0	0
2	B	10	0	0	0	0
All	All	7222	0	7042	190	2

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 14.

All (190) 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:244:THR:HG22	1:A:247:LYS:HE3	1.27	1.14
1:B:397:CYS:SG	1:B:400:CYS:CB	2.36	1.14
1:B:397:CYS:SG	1:B:400:CYS:N	2.30	1.04
1:A:244:THR:HG22	1:A:247:LYS:CE	1.87	1.04
1:B:163:ASP:OD1	1:B:165:GLU:HG2	1.61	1.00
1:B:19:ALA:HB1	1:B:20:PRO:HD2	1.48	0.93
1:B:397:CYS:SG	1:B:400:CYS:HB2	2.06	0.92
1:A:117:THR:HG22	1:A:117:THR:O	1.74	0.86
1:B:413:THR:HG21	1:B:467:LYS:CE	2.07	0.85
1:B:356:MET:HE3	1:B:428:THR:O	1.77	0.84
1:B:179:ILE:HD11	1:B:226:LEU:CD2	2.09	0.82
1:B:163:ASP:OD1	1:B:165:GLU:CG	2.26	0.82
1:A:360:LEU:HD13	1:A:376:ASN:ND2	1.95	0.81
1:B:179:ILE:HD11	1:B:226:LEU:HD22	1.61	0.80
1:A:306:GLY:HA3	1:A:356:MET:CE	2.12	0.80
1:A:19:ALA:N	1:A:20:PRO:CD	2.47	0.77
1:B:42:LYS:HE2	1:B:43:TYR:OH	1.86	0.76
1:B:53[A]:CYS:CB	1:B:56[A]:CYS:SG	2.73	0.76
1:A:200:LYS:HG2	1:A:201:ASP:H	1.51	0.75
1:B:102:ILE:HB	1:B:116:TYR:HB3	1.69	0.75
1:A:181:ASP:OD1	1:A:181:ASP:N	2.14	0.74
1:A:326:LYS:O	1:A:327:TYR:HD1	1.69	0.74
1:B:413:THR:HG21	1:B:467:LYS:HE2	1.71	0.73
1:B:141:PRO:O	1:B:189:ASN:ND2	2.21	0.73
1:A:19:ALA:N	1:A:20:PRO:HD3	2.05	0.72
1:A:377:PHE:CD2	1:A:432:VAL:HG21	2.24	0.72
1:A:200:LYS:HG2	1:A:201:ASP:N	2.05	0.71
1:B:179:ILE:CD1	1:B:226:LEU:CD2	2.68	0.70
1:A:306:GLY:HA3	1:A:356:MET:HE1	1.74	0.70
1:A:325:THR:HG22	1:A:327:TYR:HE1	1.57	0.69
1:A:360:LEU:CD1	1:A:376:ASN:HD22	2.05	0.69
1:B:270:GLY:O	1:B:274:ASN:ND2	2.26	0.69
1:A:358:GLN:OE1	1:A:430:ASN:ND2	2.26	0.69
1:B:363:ASP:O	1:B:365:ASP:N	2.26	0.68
1:B:209:PHE:CD1	1:B:235:PRO:HG3	2.28	0.68
1:A:428:THR:OG1	1:A:429:ALA:N	2.24	0.68
1:B:397:CYS:SG	1:B:400:CYS:CA	2.82	0.68
1:A:397:CYS:CB	1:A:400:CYS:SG	2.80	0.68
1:B:53[A]:CYS:HB3	1:B:56[A]:CYS:SG	2.34	0.68
1:A:56[B]:CYS:SG	1:A:100:PRO:HG3	2.34	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:THR:CG2	1:A:247:LYS:HE3	2.17	0.67
1:A:315:VAL:O	1:A:316:ARG:NH1	2.26	0.67
1:A:398:GLY:HA2	1:A:401:LYS:HE2	1.75	0.67
1:B:362:GLU:O	1:B:366:LYS:NZ	2.28	0.66
1:A:363:ASP:HA	1:A:366:LYS:HD3	1.77	0.66
1:A:142:ASP:N	1:A:142:ASP:OD1	2.27	0.66
1:B:91:ALA:HB1	1:B:96:VAL:HG21	1.77	0.66
1:A:360:LEU:CD1	1:A:376:ASN:ND2	2.58	0.66
1:B:19:ALA:HB1	1:B:20:PRO:CD	2.23	0.66
1:A:365:ASP:HB2	1:A:370:LYS:HE2	1.77	0.66
1:B:228:PHE:O	1:B:232:ASN:ND2	2.30	0.65
1:A:397:CYS:HB3	1:A:400:CYS:SG	2.36	0.65
1:A:21:GLU:HG3	1:A:28:VAL:HB	1.78	0.65
1:A:349:GLY:O	1:A:351:ILE:N	2.30	0.64
1:B:181:ASP:O	1:B:182:ILE:HD13	1.97	0.64
1:B:367:GLN:HG3	1:B:368:PRO:HD2	1.79	0.64
1:B:363:ASP:HA	1:B:366:LYS:NZ	2.13	0.63
1:A:117:THR:O	1:A:117:THR:CG2	2.47	0.63
1:B:267:ASP:HB3	1:B:271:LYS:HZ3	1.63	0.63
1:A:306:GLY:HA3	1:A:356:MET:HE3	1.79	0.62
1:A:360:LEU:HD13	1:A:376:ASN:HD22	1.58	0.62
1:A:83:ASP:OD2	1:A:86:GLU:HG2	1.99	0.62
1:A:377:PHE:CE2	1:A:432:VAL:HG21	2.35	0.62
1:A:327:TYR:CE2	1:A:346:PHE:HD1	2.17	0.62
1:B:69:LYS:O	1:B:73:GLU:HG3	2.00	0.61
1:B:207:LYS:HE3	1:B:211:GLU:HG3	1.81	0.61
1:A:326:LYS:C	1:A:327:TYR:HD1	2.04	0.61
1:A:244:THR:HG22	1:A:247:LYS:HE2	1.76	0.60
1:B:207:LYS:HD2	1:B:209:PHE:O	2.00	0.60
1:B:56[B]:CYS:SG	1:B:100:PRO:HB3	2.42	0.60
1:B:263:LYS:HG3	1:B:292:ASP:OD1	2.02	0.60
1:B:87:GLU:O	1:B:89:ASP:N	2.31	0.59
1:A:21:GLU:CG	1:A:28:VAL:HB	2.34	0.58
1:B:363:ASP:HA	1:B:366:LYS:HZ3	1.68	0.58
1:B:174:GLN:HB3	1:B:222:LYS:HD2	1.85	0.58
1:A:239:GLU:HG2	1:A:290:PHE:CZ	2.39	0.57
1:B:345:ARG:HB2	1:B:351:ILE:HD11	1.85	0.57
1:A:444:LYS:NZ	1:A:456:ASP:OD1	2.33	0.57
1:A:398:GLY:HA2	1:A:401:LYS:HG2	1.87	0.56
1:A:59:LEU:HD13	1:A:120:ARG:HB3	1.88	0.56
1:B:325:THR:HG1	1:B:327:TYR:HE2	1.54	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:426:ASP:O	1:B:430:ASN:HB2	2.05	0.56
1:A:327:TYR:HE2	1:A:346:PHE:HD1	1.53	0.55
1:B:42:LYS:HE2	1:B:43:TYR:CZ	2.40	0.55
1:B:45:LEU:HB3	1:B:79:LEU:HD22	1.88	0.55
1:A:200:LYS:CG	1:A:201:ASP:H	2.19	0.54
1:B:209:PHE:CE1	1:B:235:PRO:HG3	2.42	0.54
1:A:292:ASP:O	1:A:298:ASN:ND2	2.31	0.54
1:A:341:GLU:HG3	1:A:345:ARG:HD2	1.88	0.54
1:B:207:LYS:HE2	1:B:214:ASN:ND2	2.23	0.54
1:B:53[B]:CYS:HB3	1:B:56[B]:CYS:HB2	1.90	0.53
1:A:22:GLU:OE1	1:A:78:ARG:NH2	2.40	0.53
1:B:97:ARG:HH11	1:B:97:ARG:HG2	1.73	0.53
1:B:305:PHE:HA	1:B:326:LYS:NZ	2.23	0.53
1:A:363:ASP:O	1:A:365:ASP:N	2.42	0.52
1:B:199:ASP:OD1	1:B:199:ASP:N	2.24	0.52
1:A:326:LYS:C	1:A:327:TYR:CD1	2.83	0.52
1:A:355:LEU:HD12	1:A:431:GLU:HG3	1.92	0.52
1:B:330:GLU:N	1:B:330:GLU:OE1	2.41	0.52
1:B:387:ASN:OD1	1:B:448:ALA:N	2.41	0.52
1:A:445:PHE:HB3	1:A:455:ILE:HG23	1.91	0.51
1:A:24:ASP:HB3	1:A:64:ALA:HB1	1.93	0.51
1:B:398:GLY:HA2	1:B:401:LYS:HE2	1.92	0.51
1:B:426:ASP:OD2	1:B:428:THR:OG1	2.26	0.51
1:A:200:LYS:CG	1:A:201:ASP:N	2.73	0.51
1:B:333:GLU:HB2	1:B:338:ARG:HD3	1.92	0.51
1:A:102:ILE:HB	1:A:116:TYR:HB3	1.93	0.51
1:B:181:ASP:OD1	1:B:181:ASP:N	2.38	0.51
1:A:233:GLN:O	1:A:234:LEU:HB2	2.11	0.50
1:A:349:GLY:C	1:A:351:ILE:H	2.14	0.50
1:A:226:LEU:O	1:A:230:LYS:HG2	2.11	0.50
1:B:179:ILE:HG23	1:B:181:ASP:OD1	2.11	0.50
1:B:319:THR:OG1	1:B:325:THR:HG23	2.12	0.50
1:A:18:ASP:C	1:A:20:PRO:HD2	2.32	0.50
1:B:432:VAL:O	1:B:436:LYS:HE3	2.12	0.50
1:A:18:ASP:C	1:A:20:PRO:CD	2.80	0.49
1:A:376:ASN:OD1	1:A:377:PHE:N	2.45	0.49
1:B:59:LEU:HD13	1:B:120:ARG:HB3	1.93	0.49
1:B:387:ASN:N	1:B:419:ASN:O	2.32	0.49
1:A:285:LYS:HB3	1:A:286:ILE:HD12	1.94	0.49
1:A:439:SER:O	1:A:442:THR:OG1	2.31	0.48
1:A:262:PRO:HD3	1:A:293:SER:OG	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:382:PHE:CD1	1:A:452:ARG:HG2	2.48	0.48
1:B:128:TRP:O	1:B:132:ARG:NH1	2.45	0.48
1:A:165:GLU:HA	1:A:170:LYS:HE2	1.95	0.48
1:B:345:ARG:C	1:B:351:ILE:HD12	2.34	0.48
1:B:345:ARG:HB2	1:B:351:ILE:CD1	2.44	0.47
1:B:163:ASP:O	1:B:166:SER:OG	2.31	0.46
1:A:267:ASP:O	1:A:271:LYS:HG3	2.15	0.46
1:B:262:PRO:HG2	1:B:265:VAL:HB	1.97	0.46
1:A:460:GLU:HG3	1:A:465:GLY:HA3	1.97	0.46
1:A:433:GLU:O	1:A:436:LYS:NZ	2.48	0.46
1:B:109:ASP:OD1	1:B:112:SER:N	2.48	0.46
1:A:85:THR:OG1	1:A:86:GLU:OE2	2.22	0.46
1:B:432:VAL:HG22	1:B:435:VAL:H	1.80	0.46
1:A:45:LEU:HD22	1:A:129:LEU:HD21	1.98	0.46
1:A:328:LYS:HG3	1:A:329:PRO:HD2	1.97	0.46
1:A:116:TYR:OH	1:A:119:GLY:O	2.23	0.46
1:B:116:TYR:OH	1:B:119:GLY:O	2.25	0.46
1:B:348:GLU:HB2	1:B:350:LYS:HD3	1.96	0.46
1:B:327:TYR:CD2	1:B:327:TYR:N	2.84	0.45
1:A:233:GLN:HG3	1:A:234:LEU:HD13	1.97	0.45
1:B:179:ILE:CD1	1:B:226:LEU:HD22	2.36	0.45
1:A:372:LEU:HB2	1:A:425:MET:HB2	1.98	0.45
1:B:356:MET:HG2	1:B:429:ALA:O	2.17	0.45
1:A:244:THR:HB	1:A:248:ILE:HD11	1.98	0.45
1:B:34:PHE:CD1	1:B:90:LEU:HD21	2.51	0.45
1:B:287:LEU:HD12	1:B:288:PHE:N	2.32	0.45
1:A:327:TYR:CE2	1:A:346:PHE:CD1	3.03	0.44
1:A:464:ASP:OD1	1:A:464:ASP:C	2.55	0.44
1:B:195:LYS:HD3	1:B:196:TYR:CE2	2.53	0.44
1:B:299:GLN:HA	1:B:302:LEU:HB2	2.00	0.44
1:B:373:VAL:HG23	1:B:375:LYS:H	1.82	0.44
1:B:352:LYS:HB3	1:B:352:LYS:HE2	1.66	0.44
1:A:51:PRO:HD3	1:A:83:ASP:OD1	2.18	0.44
1:A:255:THR:CG2	1:A:286:ILE:HG13	2.47	0.44
1:A:325:THR:HG22	1:A:327:TYR:CE1	2.45	0.44
1:B:325:THR:HG23	1:B:327:TYR:HE2	1.83	0.43
1:B:189:ASN:O	1:B:193:PHE:HD2	2.01	0.43
1:B:360:LEU:HD13	1:B:373:VAL:HG22	2.00	0.43
1:B:179:ILE:HG22	1:B:180:ASP:N	2.34	0.43
1:A:360:LEU:HD11	1:A:376:ASN:HD22	1.80	0.43
1:B:331:SER:HB3	1:B:338:ARG:HH21	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:LEU:HD13	1:A:146:ALA:HA	2.01	0.43
1:A:24:ASP:O	1:A:25:HIS:HB2	2.19	0.43
1:A:121:GLU:HG2	1:A:122:ALA:N	2.34	0.42
1:B:273:SER:O	1:B:277:THR:HG23	2.20	0.42
1:B:358:GLN:OE1	1:B:430:ASN:ND2	2.51	0.42
1:B:444:LYS:NZ	1:B:456:ASP:OD1	2.52	0.42
1:A:305:PHE:O	1:A:356:MET:HE1	2.20	0.42
1:B:239:GLU:HG2	1:B:290:PHE:CZ	2.55	0.42
1:B:368:PRO:HB3	1:B:415:LYS:HB3	2.01	0.42
1:B:394:ALA:HA	1:B:395:PRO:HD3	1.75	0.42
1:A:167:ASP:OD1	1:A:167:ASP:N	2.52	0.42
1:A:451:ASP:OD1	1:A:451:ASP:N	2.42	0.42
1:B:21:GLU:O	1:B:22:GLU:C	2.57	0.42
1:B:377:PHE:HB2	1:B:425:MET:HE1	2.01	0.42
1:A:31:LYS:HE3	1:A:31:LYS:HB2	1.83	0.42
1:A:236:LEU:HD12	1:A:236:LEU:HA	1.93	0.42
1:B:360:LEU:HA	1:B:361:PRO:HD3	1.85	0.42
1:A:318:ILE:HA	1:A:326:LYS:HA	2.02	0.41
1:B:198:LEU:HD22	1:B:200:LYS:O	2.20	0.41
1:B:308:LYS:HE2	1:B:308:LYS:HB3	1.92	0.41
1:A:35:ALA:HA	1:A:38:LEU:HD12	2.03	0.41
1:B:327:TYR:N	1:B:327:TYR:HD2	2.18	0.41
1:B:20:PRO:HB2	1:B:21:GLU:H	1.63	0.41
1:A:330:GLU:OE2	1:A:345:ARG:NH1	2.54	0.41
1:B:363:ASP:O	1:B:366:LYS:N	2.46	0.40
1:A:302:LEU:HD23	1:A:307:LEU:O	2.21	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:ASP:O	1:B:438:HIS:NE2[1_545]	1.49	0.71
1:A:18:ASP:O	1:B:438:HIS:CE1[1_545]	1.90	0.30

5.3 Torsion angles

5.3.1 Protein backbone

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	448/482 (93%)	420 (94%)	24 (5%)	4 (1%)	17	45
1	B	448/482 (93%)	428 (96%)	17 (4%)	3 (1%)	22	52
All	All	896/964 (93%)	848 (95%)	41 (5%)	7 (1%)	19	48

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	348	GLU
1	A	350	LYS
1	B	364	TRP
1	A	364	TRP
1	B	20	PRO
1	A	234	LEU
1	B	118	ALA

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	386/408 (95%)	369 (96%)	17 (4%)	28	59
1	B	386/408 (95%)	357 (92%)	29 (8%)	13	35
All	All	772/816 (95%)	726 (94%)	46 (6%)	19	46

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	ASP
1	A	42	LYS
1	A	88	SER
1	A	97	ARG
1	A	167	ASP

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Mol	Chain	Res	Type
1	A	181	ASP
1	A	241	THR
1	A	244	THR
1	A	291	ILE
1	A	324	MET
1	A	325	THR
1	A	341	GLU
1	A	346	PHE
1	A	367	GLN
1	A	389	PHE
1	A	427	SER
1	A	452	ARG
1	B	89	ASP
1	B	97	ARG
1	B	117	THR
1	B	138	THR
1	B	149	LEU
1	B	165	GLU
1	B	166	SER
1	B	191	ASP
1	B	199	ASP
1	B	207	LYS
1	B	211	GLU
1	B	217	GLU
1	B	272	LEU
1	B	296	THR
1	B	301	ILE
1	B	302	LEU
1	B	319	THR
1	B	324	MET
1	B	327	TYR
1	B	331	SER
1	B	346	PHE
1	B	367	GLN
1	B	389	PHE
1	B	397	CYS
1	B	432	VAL
1	B	451	ASP
1	B	452	ARG
1	B	460	GLU
1	B	461	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	214	ASN
1	A	232	ASN
1	A	274	ASN
1	B	214	ASN
1	B	231	HIS
1	B	354	HIS

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](#)

There are no ligands in this entry.

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, 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	452/482 (93%)	0.09	10 (2%) 62 60	24, 52, 79, 118	10 (2%)
1	B	452/482 (93%)	0.02	8 (1%) 68 67	24, 50, 73, 105	10 (2%)
All	All	904/964 (93%)	0.06	18 (1%) 65 63	24, 51, 76, 118	20 (2%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	19	ALA	4.4
1	A	477	GLY	4.0
1	B	476	ASP	3.9
1	A	476	ASP	3.7
1	A	18	ASP	3.5
1	A	478	ALA	3.3
1	B	266	SER	3.2
1	B	18	ASP	3.2
1	A	33	ASN	2.7
1	B	478	ALA	2.6
1	B	475	GLN	2.6
1	B	366	LYS	2.6
1	A	324	MET	2.4
1	B	97	ARG	2.3
1	B	359	GLU	2.2
1	A	450	ALA	2.2
1	A	267	ASP	2.1
1	A	475	GLN	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.