Full wwPDB X-ray Structure Validation Report (i)

Feb 22, 2024 – 07:59 PM EST

PDB ID	:	4XIM
Title	:	PROTEIN ENGINEERING OF XYLOSE (GLUCOSE) ISOMERASE FROM ACTINOPLANES MISSOURIENSIS. 1. CRYSTALLOGRAPHY AND SITE-DIRECTED MUTAGENESIS OF METAL BINDING SITES
Authors	:	Janin, J.
Deposited on	:	1992-03-11
Resolution	:	2.30 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 (i)) were used in the production of this report:

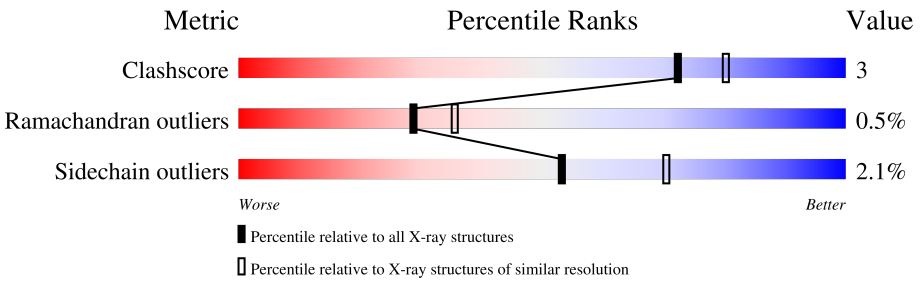
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	393	81% 17% • ••
1	B	393	81% 17% • •
1	C	393	81% 17% • •
1	D	393	83% 15% • •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 12995 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 D-XYLOSE ISOMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	391	3041	1934	529	574	4	0	0	0
1	B	391	3037	1932	527	574	4	0	0	0
1	C	391	3035	1931	525	575	4	0	0	0
1	D	391	3037	1931	527	575	4	0	0	0

- Molecule 2 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Co		
2	A	2	2	2	0	0
2	B	2	2	2	0	0
2	C	2	2	2	0	0
2	D	2	2	2	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	209	209	209	0	0
3	B	207	207	207	0	0
3	C	217	217	217	0	0
3	D	204	204	204	0	0

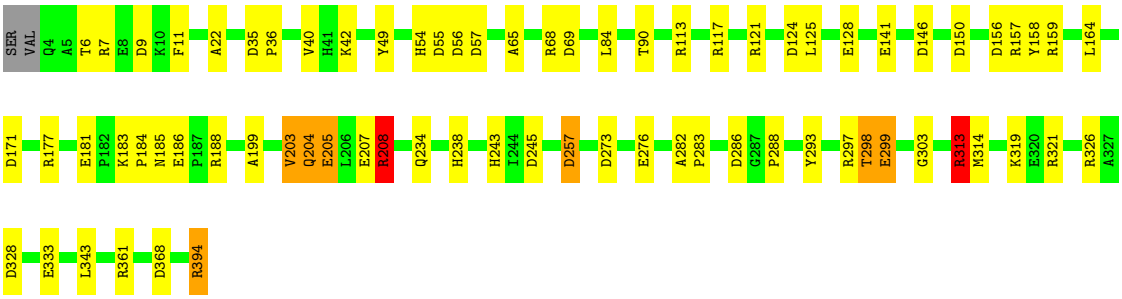
3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

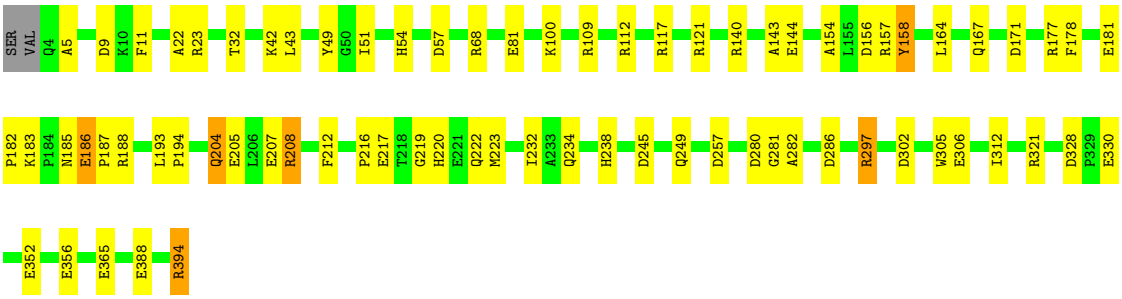
• Molecule 1: D-XYLOSE ISOMERASE

Chain A:



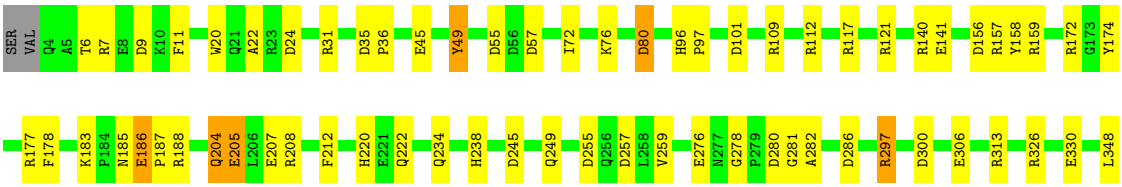
• Molecule 1: D-XYLOSE ISOMERASE

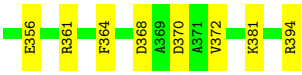
Chain B:



• Molecule 1: D-XYLOSE ISOMERASE

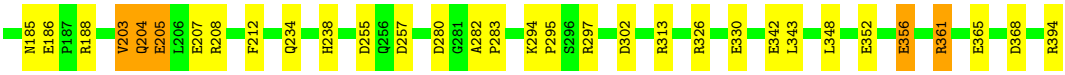
Chain C:





• Molecule 1: D-XYLOSE ISOMERASE

Chain D:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	143.45Å 143.45Å 231.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) – 2.30	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.30)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.158 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	12995	wwPDB-VP
Average B, all atoms ($Å^2$)	20.0	wwPDB-VP

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: CO

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	0.80	0/3113	1.66	58/4216 (1.4%)
1	B	0.82	0/3109	1.64	47/4211 (1.1%)
1	C	0.81	0/3107	1.59	51/4208 (1.2%)
1	D	0.81	0/3109	1.61	44/4211 (1.0%)
All	All	0.81	0/12438	1.62	200/16846 (1.2%)

There are no bond length outliers.

All (200) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	394	ARG	NE-CZ-NH2	-18.07	111.27	120.30
1	B	117	ARG	NE-CZ-NH1	17.76	129.18	120.30
1	C	117	ARG	NE-CZ-NH1	16.90	128.75	120.30
1	D	117	ARG	NE-CZ-NH1	15.27	127.94	120.30
1	B	321	ARG	NE-CZ-NH2	-14.33	113.14	120.30
1	B	157	ARG	NE-CZ-NH1	13.61	127.11	120.30
1	B	257	ASP	CB-CG-OD1	12.54	129.59	118.30
1	D	208	ARG	NE-CZ-NH1	12.06	126.33	120.30
1	D	109	ARG	NE-CZ-NH1	11.81	126.20	120.30
1	A	177	ARG	NE-CZ-NH1	11.71	126.15	120.30
1	C	361	ARG	NE-CZ-NH2	11.55	126.08	120.30
1	A	321	ARG	NE-CZ-NH1	11.51	126.05	120.30
1	C	31	ARG	NE-CZ-NH1	11.44	126.02	120.30
1	B	177	ARG	NE-CZ-NH2	-11.40	114.60	120.30
1	A	326	ARG	NE-CZ-NH1	11.22	125.91	120.30
1	A	394	ARG	NE-CZ-NH1	-11.20	114.70	120.30
1	A	117	ARG	NE-CZ-NH1	10.92	125.76	120.30
1	D	150	ASP	CB-CG-OD1	10.51	127.76	118.30
1	D	188	ARG	NE-CZ-NH2	10.49	125.55	120.30
1	D	255	ASP	CB-CG-OD1	10.39	127.65	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	361	ARG	NE-CZ-NH1	10.34	125.47	120.30
1	C	255	ASP	CB-CG-OD1	10.27	127.54	118.30
1	B	117	ARG	NE-CZ-NH2	-10.26	115.17	120.30
1	C	117	ARG	NE-CZ-NH2	-10.13	115.24	120.30
1	B	330	GLU	OE1-CD-OE2	9.88	135.15	123.30
1	A	117	ARG	NE-CZ-NH2	-9.82	115.39	120.30
1	B	121	ARG	NE-CZ-NH1	9.74	125.17	120.30
1	D	113	ARG	NE-CZ-NH1	9.54	125.07	120.30
1	D	150	ASP	CB-CG-OD2	-9.53	109.72	118.30
1	D	35	ASP	CB-CG-OD1	9.38	126.74	118.30
1	C	157	ARG	NE-CZ-NH1	9.30	124.95	120.30
1	D	109	ARG	NE-CZ-NH2	-9.28	115.66	120.30
1	A	257	ASP	CB-CG-OD1	9.19	126.57	118.30
1	A	394	ARG	NH1-CZ-NH2	9.17	129.48	119.40
1	A	326	ARG	NE-CZ-NH2	-9.10	115.75	120.30
1	A	394	ARG	NE-CZ-NH2	-8.97	115.81	120.30
1	B	394	ARG	N-CA-CB	8.92	126.66	110.60
1	C	121	ARG	NE-CZ-NH1	8.89	124.75	120.30
1	D	394	ARG	NE-CZ-NH2	-8.89	115.85	120.30
1	D	112	ARG	NE-CZ-NH1	8.80	124.70	120.30
1	A	146	ASP	CB-CG-OD1	8.79	126.21	118.30
1	A	188	ARG	NE-CZ-NH1	8.59	124.60	120.30
1	D	257	ASP	CB-CG-OD1	8.59	126.03	118.30
1	D	117	ARG	NE-CZ-NH2	-8.59	116.01	120.30
1	A	205	GLU	OE1-CD-OE2	-8.56	113.03	123.30
1	B	188	ARG	NE-CZ-NH1	8.44	124.52	120.30
1	A	273	ASP	CB-CG-OD1	8.35	125.81	118.30
1	A	113	ARG	NE-CZ-NH1	7.92	124.26	120.30
1	A	207	GLU	CG-CD-OE1	7.74	133.78	118.30
1	B	328	ASP	CB-CG-OD2	7.72	125.25	118.30
1	D	313	ARG	CG-CD-NE	7.66	127.89	111.80
1	D	68	ARG	NE-CZ-NH2	7.64	124.12	120.30
1	B	112	ARG	NE-CZ-NH2	7.60	124.10	120.30
1	B	68	ARG	NE-CZ-NH1	-7.59	116.51	120.30
1	C	205	GLU	OE1-CD-OE2	-7.59	114.20	123.30
1	A	121	ARG	NE-CZ-NH2	-7.46	116.57	120.30
1	B	302	ASP	CB-CG-OD2	-7.42	111.62	118.30
1	D	297	ARG	NE-CZ-NH2	-7.39	116.60	120.30
1	B	23	ARG	CD-NE-CZ	7.34	133.87	123.60
1	C	370	ASP	CB-CG-OD2	7.30	124.87	118.30
1	A	157	ARG	NE-CZ-NH1	7.29	123.94	120.30
1	A	150	ASP	CB-CG-OD1	7.25	124.83	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	56	ASP	CB-CG-OD2	7.18	124.76	118.30
1	A	55	ASP	CB-CG-OD1	7.17	124.75	118.30
1	A	156	ASP	CB-CG-OD2	-7.07	111.94	118.30
1	C	140	ARG	NE-CZ-NH1	7.06	123.83	120.30
1	C	205	GLU	CG-CD-OE2	7.04	132.38	118.30
1	C	245	ASP	CB-CG-OD2	-7.04	111.97	118.30
1	B	140	ARG	NE-CZ-NH2	-7.01	116.80	120.30
1	D	31	ARG	NE-CZ-NH1	6.97	123.79	120.30
1	A	245	ASP	CB-CG-OD2	-6.89	112.10	118.30
1	D	361	ARG	NE-CZ-NH2	6.89	123.74	120.30
1	B	245	ASP	CB-CG-OD2	-6.87	112.12	118.30
1	B	121	ARG	NE-CZ-NH2	-6.86	116.87	120.30
1	D	313	ARG	CA-CB-CG	6.81	128.38	113.40
1	C	177	ARG	CG-CD-NE	6.80	126.07	111.80
1	C	159	ARG	NE-CZ-NH1	-6.79	116.91	120.30
1	A	394	ARG	CA-CB-CG	6.76	128.27	113.40
1	A	207	GLU	CG-CD-OE2	-6.76	104.78	118.30
1	A	181	GLU	OE1-CD-OE2	-6.74	115.21	123.30
1	A	321	ARG	NE-CZ-NH2	-6.73	116.94	120.30
1	A	313	ARG	NE-CZ-NH1	-6.70	116.95	120.30
1	B	394	ARG	CD-NE-CZ	-6.65	114.29	123.60
1	A	188	ARG	CD-NE-CZ	6.63	132.88	123.60
1	C	80	ASP	CB-CG-OD1	-6.62	112.34	118.30
1	C	276	GLU	CG-CD-OE2	6.61	131.52	118.30
1	A	141	GLU	OE1-CD-OE2	-6.57	115.41	123.30
1	C	55	ASP	CB-CG-OD1	6.56	124.20	118.30
1	C	326	ARG	NE-CZ-NH1	-6.52	117.04	120.30
1	B	394	ARG	NH1-CZ-NH2	6.50	126.55	119.40
1	C	326	ARG	NE-CZ-NH2	6.49	123.55	120.30
1	C	276	GLU	OE1-CD-OE2	-6.47	115.53	123.30
1	B	109	ARG	NE-CZ-NH2	-6.46	117.07	120.30
1	C	306	GLU	CG-CD-OE1	6.46	131.21	118.30
1	C	330	GLU	OE1-CD-OE2	6.42	131.01	123.30
1	A	56	ASP	CB-CG-OD2	6.40	124.06	118.30
1	C	207	GLU	CG-CD-OE2	-6.40	105.50	118.30
1	B	207	GLU	CG-CD-OE1	6.39	131.07	118.30
1	B	112	ARG	NE-CZ-NH1	-6.38	117.11	120.30
1	D	368	ASP	CB-CG-OD1	6.32	123.98	118.30
1	B	257	ASP	OD1-CG-OD2	-6.30	111.34	123.30
1	A	57	ASP	CB-CG-OD1	-6.29	112.64	118.30
1	B	302	ASP	CB-CG-OD1	6.29	123.96	118.30
1	D	203	VAL	CA-CB-CG1	6.27	120.30	110.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	57	ASP	CB-CG-OD2	6.23	123.91	118.30
1	C	361	ARG	NE-CZ-NH1	-6.21	117.19	120.30
1	C	109	ARG	NE-CZ-NH2	6.20	123.40	120.30
1	A	156	ASP	CB-CG-OD1	6.18	123.86	118.30
1	A	313	ARG	CG-CD-NE	6.18	124.77	111.80
1	C	208	ARG	CD-NE-CZ	-6.14	115.00	123.60
1	A	177	ARG	CD-NE-CZ	6.13	132.18	123.60
1	B	286	ASP	CB-CG-OD1	6.11	123.80	118.30
1	A	208	ARG	NE-CZ-NH1	6.06	123.33	120.30
1	B	23	ARG	NE-CZ-NH2	-6.06	117.27	120.30
1	A	159	ARG	NE-CZ-NH1	6.05	123.32	120.30
1	B	330	GLU	CG-CD-OE2	-6.05	106.20	118.30
1	A	299	GLU	OE1-CD-OE2	5.98	130.47	123.30
1	A	181	GLU	CG-CD-OE1	5.96	130.22	118.30
1	D	24	ASP	CB-CG-OD2	-5.93	112.96	118.30
1	B	208	ARG	NE-CZ-NH1	5.93	123.26	120.30
1	D	342	GLU	CG-CD-OE2	5.92	130.15	118.30
1	D	356	GLU	CG-CD-OE2	5.92	130.15	118.30
1	C	297	ARG	NE-CZ-NH2	5.92	123.26	120.30
1	D	207	GLU	CA-CB-CG	5.87	126.32	113.40
1	A	57	ASP	CB-CG-OD2	5.83	123.55	118.30
1	B	57	ASP	CB-CG-OD2	5.82	123.53	118.30
1	A	368	ASP	CB-CG-OD1	5.80	123.53	118.30
1	C	281	GLY	N-CA-C	-5.80	98.61	113.10
1	D	205	GLU	OE1-CD-OE2	-5.78	116.36	123.30
1	C	300	ASP	CB-CG-OD2	5.74	123.46	118.30
1	D	159	ARG	NE-CZ-NH2	-5.73	117.43	120.30
1	A	124	ASP	CB-CG-OD1	5.73	123.45	118.30
1	C	306	GLU	CG-CD-OE2	-5.69	106.92	118.30
1	C	188	ARG	NE-CZ-NH1	5.66	123.13	120.30
1	B	204	GLN	OE1-CD-NE2	-5.66	108.89	121.90
1	D	356	GLU	OE1-CD-OE2	-5.65	116.52	123.30
1	A	7	ARG	NE-CZ-NH2	-5.58	117.51	120.30
1	D	80	ASP	CB-CG-OD2	-5.56	113.30	118.30
1	C	112	ARG	CG-CD-NE	5.55	123.45	111.80
1	D	330	GLU	OE1-CD-OE2	5.53	129.94	123.30
1	C	141	GLU	OE1-CD-OE2	-5.53	116.66	123.30
1	C	356	GLU	OE1-CD-OE2	-5.52	116.67	123.30
1	D	204	GLN	OE1-CD-NE2	-5.48	109.31	121.90
1	C	31	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	C	45	GLU	CA-CB-CG	5.46	125.40	113.40
1	A	177	ARG	NE-CZ-NH2	-5.45	117.58	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	144	GLU	OE1-CD-OE2	-5.45	116.76	123.30
1	B	140	ARG	NE-CZ-NH1	5.44	123.02	120.30
1	B	54	HIS	N-CA-CB	5.44	120.38	110.60
1	B	171	ASP	CB-CG-OD1	5.43	123.19	118.30
1	C	6	THR	N-CA-CB	5.42	120.59	110.30
1	A	205	GLU	CG-CD-OE2	5.40	129.10	118.30
1	C	187	PRO	N-CA-C	5.39	126.12	112.10
1	A	171	ASP	CB-CG-OD1	5.39	123.15	118.30
1	C	313	ARG	CA-CB-CG	5.39	125.25	113.40
1	A	298	THR	CA-CB-CG2	5.38	119.93	112.40
1	B	158	TYR	CB-CG-CD2	5.38	124.23	121.00
1	D	207	GLU	CG-CD-OE1	5.37	129.05	118.30
1	D	172	ARG	NE-CZ-NH1	5.37	122.98	120.30
1	A	204	GLN	OE1-CD-NE2	-5.37	109.56	121.90
1	C	121	ARG	NE-CZ-NH2	-5.35	117.62	120.30
1	D	342	GLU	OE1-CD-OE2	-5.35	116.88	123.30
1	A	199	ALA	CB-CA-C	5.33	118.10	110.10
1	A	203	VAL	N-CA-CB	-5.32	99.79	111.50
1	B	217	GLU	OE1-CD-OE2	5.32	129.69	123.30
1	A	394	ARG	CG-CD-NE	-5.32	100.63	111.80
1	B	297	ARG	CD-NE-CZ	5.31	131.03	123.60
1	A	314	MET	CG-SD-CE	5.29	108.66	100.20
1	B	388	GLU	CG-CD-OE1	-5.29	107.73	118.30
1	B	32	THR	CA-CB-CG2	-5.28	105.01	112.40
1	D	124	ASP	CB-CG-OD2	-5.26	113.57	118.30
1	A	68	ARG	NE-CZ-NH2	5.25	122.93	120.30
1	D	297	ARG	NH1-CZ-NH2	5.25	125.18	119.40
1	B	143	ALA	N-CA-CB	-5.24	102.77	110.10
1	C	174	TYR	CB-CG-CD2	-5.23	117.86	121.00
1	D	302	ASP	CB-CG-OD1	-5.22	113.60	118.30
1	C	286	ASP	CB-CG-OD1	5.21	122.99	118.30
1	C	172	ARG	CG-CD-NE	5.21	122.75	111.80
1	A	313	ARG	NE-CZ-NH2	-5.21	117.70	120.30
1	B	54	HIS	CB-CA-C	-5.21	99.98	110.40
1	A	128	GLU	CG-CD-OE1	-5.19	107.92	118.30
1	D	326	ARG	NE-CZ-NH2	5.18	122.89	120.30
1	C	207	GLU	CG-CD-OE1	5.18	128.66	118.30
1	C	101	ASP	CB-CG-OD1	-5.17	113.64	118.30
1	A	328	ASP	CB-CG-OD2	5.16	122.95	118.30
1	D	205	GLU	CG-CD-OE2	5.15	128.61	118.30
1	B	23	ARG	NE-CZ-NH1	5.15	122.87	120.30
1	B	365	GLU	OE1-CD-OE2	-5.13	117.14	123.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	172	ARG	NE-CZ-NH2	-5.11	117.74	120.30
1	A	203	VAL	CA-CB-CG1	5.11	118.57	110.90
1	C	257	ASP	CB-CG-OD1	5.11	122.90	118.30
1	B	156	ASP	CB-CG-OD2	-5.10	113.71	118.30
1	C	156	ASP	CB-CG-OD1	5.10	122.89	118.30
1	D	113	ARG	NE-CZ-NH2	-5.10	117.75	120.30
1	B	305	TRP	CA-CB-CG	-5.08	104.05	113.70
1	A	113	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	C	186	GLU	OE1-CD-OE2	-5.04	117.26	123.30
1	C	259	VAL	CA-CB-CG1	5.03	118.45	110.90
1	C	204	GLN	OE1-CD-NE2	-5.03	110.33	121.90
1	D	124	ASP	CB-CG-OD1	5.01	122.81	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3041	0	2942	26	0
1	B	3037	0	2935	26	0
1	C	3035	0	2930	22	0
1	D	3037	0	2933	20	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	209	0	0	1	0
3	B	207	0	0	0	0
3	C	217	0	0	0	0
3	D	204	0	0	0	0
All	All	12995	0	11740	82	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 3.

All (82) 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:204:GLN:OE1	1:D:204:GLN:OE1	1.57	1.20
1:A:204:GLN:OE1	1:C:204:GLN:OE1	1.61	1.18
1:C:234:GLN:HE21	1:C:238:HIS:HE1	1.17	0.86
1:D:234:GLN:HE21	1:D:238:HIS:HE1	1.23	0.86
1:B:234:GLN:HE21	1:B:238:HIS:HE1	1.25	0.83
1:A:234:GLN:HE21	1:A:238:HIS:HE1	1.25	0.82
1:A:238:HIS:HD2	1:C:205:GLU:OE2	1.76	0.67
1:B:164:LEU:HD12	1:D:348:LEU:HD11	1.78	0.66
1:B:205:GLU:OE2	1:D:238:HIS:HD2	1.79	0.64
1:A:276:GLU:HG3	1:A:319:LYS:HG3	1.82	0.62
1:C:24:ASP:O	1:D:23:ARG:NH2	2.33	0.62
1:B:22:ALA:HB1	1:B:297:ARG:HG3	1.82	0.60
1:A:22:ALA:HB1	1:A:297:ARG:HG3	1.83	0.60
1:A:36:PRO:O	1:A:40:VAL:HG23	2.01	0.60
1:C:22:ALA:HB1	1:C:297:ARG:HG3	1.83	0.59
1:A:205:GLU:OE2	1:C:238:HIS:HD2	1.86	0.58
1:A:204:GLN:HG2	3:A:541:HOH:O	2.03	0.58
1:A:9:ASP:HB3	1:A:11:PHE:CE2	2.41	0.56
1:D:361:ARG:HA	1:D:365:GLU:OE1	2.08	0.53
1:C:72:ILE:O	1:C:76:LYS:HG3	2.11	0.51
1:C:183:LYS:HG3	1:C:220:HIS:CG	2.45	0.50
1:D:72:ILE:O	1:D:76:LYS:HG3	2.11	0.50
1:A:257:ASP:HB3	1:A:293:TYR:HA	1.95	0.49
1:A:313:ARG:HG3	1:A:313:ARG:HH11	1.78	0.49
1:B:216:PRO:HG2	1:B:232:ILE:HD11	1.96	0.47
1:B:238:HIS:HD2	1:D:205:GLU:OE2	1.97	0.47
1:A:299:GLU:HB3	1:A:303:GLY:HA3	1.96	0.47
1:C:20:TRP:CZ2	1:C:22:ALA:HA	2.50	0.47
1:A:298:THR:HA	1:B:100:LYS:HD2	1.97	0.47
1:A:6:THR:O	1:A:9:ASP:HB2	2.16	0.46
1:B:306:GLU:HG2	1:C:381:LYS:HB2	1.96	0.46
1:A:208:ARG:HB3	1:A:208:ARG:NH1	2.30	0.46
1:A:164:LEU:HD12	1:C:348:LEU:HD11	1.96	0.46
1:C:278:GLY:HA3	1:C:282:ALA:O	2.15	0.46
1:D:43:LEU:HD12	1:D:51:ILE:HD12	1.98	0.46
1:B:164:LEU:C	1:B:164:LEU:HD23	2.37	0.45
1:D:352:GLU:HG3	1:D:356:GLU:HB2	1.98	0.45
1:A:313:ARG:HH11	1:A:313:ARG:CG	2.29	0.45
1:C:234:GLN:HE21	1:C:238:HIS:CE1	2.10	0.44
1:D:178:PHE:HB2	1:D:212:PHE:CD2	2.53	0.44
1:A:65:ALA:O	1:A:69:ASP:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:361:ARG:HB3	1:D:365:GLU:HB2	2.00	0.44
1:C:178:PHE:HB2	1:C:212:PHE:CD2	2.52	0.44
1:B:42:LYS:HD3	1:B:42:LYS:HA	1.84	0.43
1:D:294:LYS:HA	1:D:295:PRO:HD3	1.84	0.43
1:A:243:HIS:CD2	1:A:288:PRO:HG2	2.53	0.43
1:B:222:GLN:HE21	1:B:249:GLN:HB3	1.84	0.43
1:B:154:ALA:HB2	1:D:343:LEU:HD21	2.01	0.43
1:C:7:ARG:HD2	1:C:49:TYR:HB2	2.00	0.43
1:C:394:ARG:HH11	1:C:394:ARG:HD3	1.64	0.43
1:A:282:ALA:HA	1:A:283:PRO:HD3	1.89	0.42
1:B:193:LEU:N	1:B:194:PRO:CD	2.81	0.42
1:C:20:TRP:CE2	1:C:22:ALA:HA	2.54	0.42
1:D:282:ALA:HA	1:D:283:PRO:HD3	1.90	0.42
1:D:9:ASP:HB3	1:D:11:PHE:CE2	2.54	0.42
1:C:368:ASP:O	1:C:372:VAL:HG23	2.20	0.42
1:A:183:LYS:HG2	1:A:184:PRO:HD2	2.02	0.42
1:B:186:GLU:HA	1:B:187:PRO:HA	1.87	0.42
1:A:42:LYS:HD3	1:A:42:LYS:HA	1.84	0.42
1:B:9:ASP:HB3	1:B:11:PHE:CE2	2.55	0.41
1:B:219:GLY:O	1:B:223:MET:HG3	2.20	0.41
1:A:35:ASP:HA	1:A:36:PRO:HD3	1.88	0.41
1:C:9:ASP:HB3	1:C:11:PHE:CE2	2.55	0.41
1:D:234:GLN:HE21	1:D:238:HIS:CE1	2.15	0.41
1:B:280:ASP:C	1:B:282:ALA:H	2.22	0.41
1:C:222:GLN:HE21	1:C:249:GLN:HB3	1.84	0.41
1:A:343:LEU:HD12	1:A:343:LEU:HA	1.95	0.41
1:A:54:HIS:CD2	1:A:90:THR:HG23	2.56	0.41
1:B:352:GLU:HG2	1:B:356:GLU:HB2	2.03	0.41
1:D:54:HIS:CD2	1:D:90:THR:HG23	2.56	0.41
1:B:43:LEU:HD12	1:B:51:ILE:HD12	2.03	0.41
1:B:178:PHE:HB2	1:B:212:PHE:CD2	2.56	0.41
1:B:183:LYS:HG3	1:B:220:HIS:CG	2.55	0.41
1:B:234:GLN:HE21	1:B:238:HIS:CE1	2.17	0.41
1:B:167:GLN:OE1	1:B:208:ARG:NH2	2.54	0.41
1:B:181:GLU:HA	1:B:182:PRO:HD3	1.91	0.41
1:A:125:LEU:HD12	1:A:125:LEU:HA	1.76	0.40
1:B:5:ALA:HB2	1:B:312:ILE:HG21	2.02	0.40
1:C:35:ASP:HA	1:C:36:PRO:HD3	1.82	0.40
1:D:181:GLU:HA	1:D:182:PRO:HD3	1.92	0.40
1:C:96:HIS:HA	1:C:97:PRO:HD3	1.93	0.40
1:D:102:GLY:HA2	1:D:140:ARG:HB2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	389/393 (99%)	376 (97%)	12 (3%)	1 (0%)	41	50
1	B	389/393 (99%)	375 (96%)	12 (3%)	2 (0%)	29	35
1	C	389/393 (99%)	375 (96%)	11 (3%)	3 (1%)	19	23
1	D	389/393 (99%)	375 (96%)	12 (3%)	2 (0%)	29	35
All	All	1556/1572 (99%)	1501 (96%)	47 (3%)	8 (0%)	29	35

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	280	ASP
1	A	186	GLU
1	B	186	GLU
1	C	186	GLU
1	C	364	PHE
1	D	186	GLU
1	D	280	ASP
1	B	281	GLY

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	303/310 (98%)	293 (97%)	10 (3%)	38	53
1	B	302/310 (97%)	297 (98%)	5 (2%)	60	76
1	C	301/310 (97%)	297 (99%)	4 (1%)	69	82
1	D	302/310 (97%)	296 (98%)	6 (2%)	55	72
All	All	1208/1240 (97%)	1183 (98%)	25 (2%)	53	70

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	TYR
1	A	84	LEU
1	A	158	TYR
1	A	185	ASN
1	A	203	VAL
1	A	208	ARG
1	A	286	ASP
1	A	313	ARG
1	A	333	GLU
1	A	394	ARG
1	B	49	TYR
1	B	81	GLU
1	B	158	TYR
1	B	185	ASN
1	B	394	ARG
1	C	49	TYR
1	C	80	ASP
1	C	158	TYR
1	C	185	ASN
1	D	49	TYR
1	D	80	ASP
1	D	158	TYR
1	D	180	ILE
1	D	185	ASN
1	D	203	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	185	ASN
1	A	204	GLN

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Mol	Chain	Res	Type
1	A	238	HIS
1	B	185	ASN
1	B	204	GLN
1	B	222	GLN
1	B	238	HIS
1	C	185	ASN
1	C	222	GLN
1	C	238	HIS
1	D	185	ASN
1	D	238	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)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.