



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 29, 2017 – 12:24 PM EDT

PDB ID : 5CX1
Title : Nitrogenase molybdenum-iron protein beta-K400E mutant
Authors : Owens, C.P.; Luca, M.A.; Tezcan, F.A.
Deposited on : unknown
Resolution : 1.75 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029824
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20029824

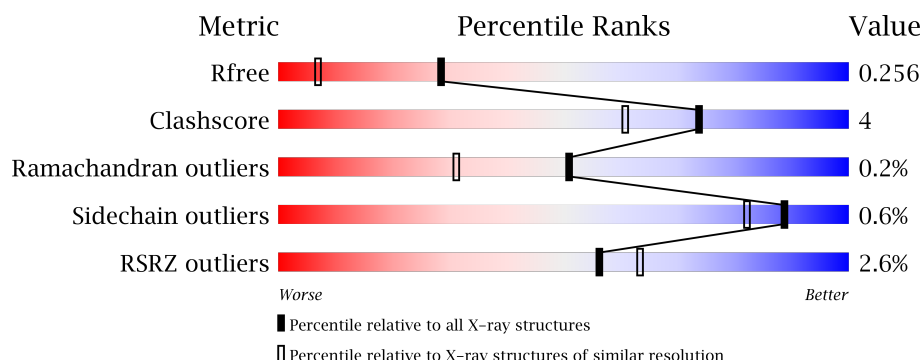
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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}	100719	2694 (1.76-1.72)
Clashscore	112137	2854 (1.76-1.72)
Ramachandran outliers	110173	2824 (1.76-1.72)
Sidechain outliers	110143	2824 (1.76-1.72)
RSRZ outliers	101464	2705 (1.76-1.72)

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	480	
1	C	480	
1	E	480	
1	G	480	
1	I	480	

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Mol	Chain	Length	Quality of chain
1	K	480	<div> <div>4%</div> <div>89%</div> <div>10%</div> <div>.</div> </div>
1	M	480	<div> <div>.%</div> <div>88%</div> <div>11%</div> <div>..</div> </div>
1	O	480	<div> <div>4%</div> <div>89%</div> <div>10%</div> <div>.</div> </div>
2	B	523	<div> <div>3%</div> <div>91%</div> <div>8%</div> </div>
2	D	523	<div> <div>.%</div> <div>91%</div> <div>8%</div> </div>
2	F	523	<div> <div>.%</div> <div>94%</div> <div>6%</div> </div>
2	H	523	<div> <div>.%</div> <div>89%</div> <div>10%</div> <div>.</div> </div>
2	J	523	<div> <div>2%</div> <div>93%</div> <div>6%</div> </div>
2	L	523	<div> <div>3%</div> <div>92%</div> <div>8%</div> </div>
2	N	523	<div> <div>.%</div> <div>95%</div> <div>5%</div> </div>
2	P	523	<div> <div>.%</div> <div>94%</div> <div>6%</div> </div>

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 74588 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 Nitrogenase molybdenum-iron protein alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	477	Total	C	N	O	S	0	0	0
			3774	2399	642	708	25			
1	C	477	Total	C	N	O	S	0	0	0
			3782	2405	644	708	25			
1	E	477	Total	C	N	O	S	0	0	0
			3776	2402	644	705	25			
1	G	477	Total	C	N	O	S	0	0	0
			3786	2407	645	709	25			
1	I	477	Total	C	N	O	S	0	0	0
			3786	2407	645	709	25			
1	K	477	Total	C	N	O	S	0	0	0
			3782	2406	645	706	25			
1	M	477	Total	C	N	O	S	0	0	0
			3790	2410	646	709	25			
1	O	477	Total	C	N	O	S	0	0	0
			3778	2401	643	709	25			

- Molecule 2 is a protein called Nitrogenase molybdenum-iron protein beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	522	Total	C	N	O	S	0	0	0
			4170	2662	703	777	28			
2	D	522	Total	C	N	O	S	0	0	0
			4174	2665	704	777	28			
2	F	522	Total	C	N	O	S	0	0	0
			4174	2665	704	777	28			
2	H	522	Total	C	N	O	S	0	0	0
			4174	2665	704	777	28			
2	J	522	Total	C	N	O	S	0	0	0
			4172	2664	704	776	28			
2	L	522	Total	C	N	O	S	0	0	0
			4170	2662	703	777	28			

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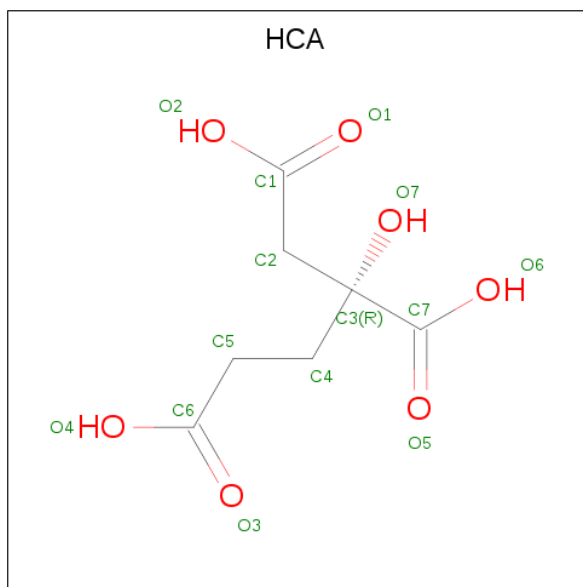
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	N	522	Total	C	N	O	S	0	0	0
			4174	2665	704	777	28			
2	P	522	Total	C	N	O	S	0	0	0
			4174	2665	704	777	28			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	400	GLU	LYS	engineered mutation	UNP P07329
D	400	GLU	LYS	engineered mutation	UNP P07329
F	400	GLU	LYS	engineered mutation	UNP P07329
H	400	GLU	LYS	engineered mutation	UNP P07329
J	400	GLU	LYS	engineered mutation	UNP P07329
L	400	GLU	LYS	engineered mutation	UNP P07329
N	400	GLU	LYS	engineered mutation	UNP P07329
P	400	GLU	LYS	engineered mutation	UNP P07329

- Molecule 3 is 3-HYDROXY-3-CARBOXY-ADIPIC ACID (three-letter code: HCA) (formula: $C_7H_{10}O_7$).



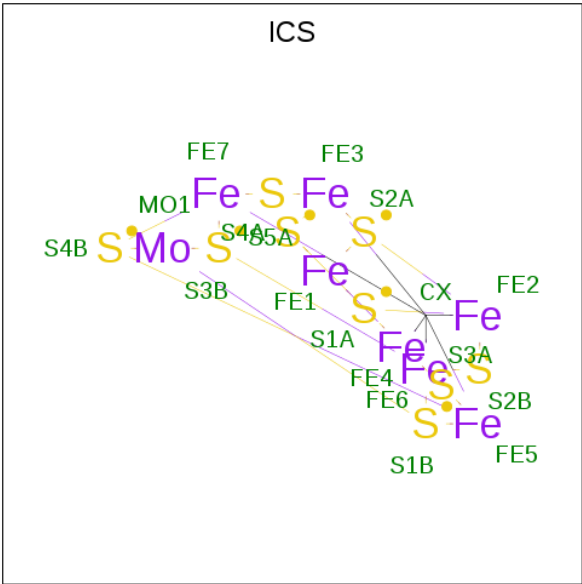
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			14	7	7		
3	C	1	Total	C	O	0	0
			14	7	7		
3	E	1	Total	C	O	0	0
			14	7	7		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	G	1	Total	C	O	0	0
			14	7	7		
3	I	1	Total	C	O	0	0
			14	7	7		
3	K	1	Total	C	O	0	0
			14	7	7		
3	M	1	Total	C	O	0	0
			14	7	7		
3	O	1	Total	C	O	0	0
			14	7	7		

- Molecule 4 is iron-sulfur-molybdenum cluster with interstitial carbon (three-letter code: ICS) (formula: CFe₇MoS₉).



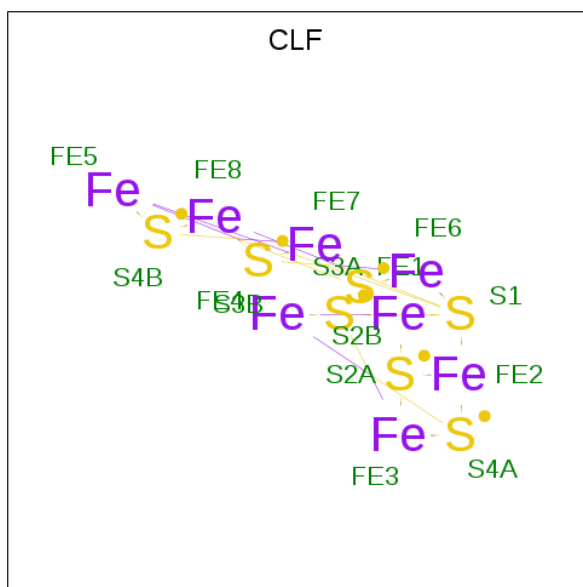
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 18	C 1	Fe 7	Mo 1	S 9	0	0
4	C	1	Total 18	C 1	Fe 7	Mo 1	S 9	0	0
4	E	1	Total 18	C 1	Fe 7	Mo 1	S 9	0	0
4	G	1	Total 18	C 1	Fe 7	Mo 1	S 9	0	0
4	I	1	Total 18	C 1	Fe 7	Mo 1	S 9	0	0
4	K	1	Total 18	C 1	Fe 7	Mo 1	S 9	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	M	1	Total	C	Fe	Mo	S	
			18	1	7	1	9	
4	O	1	Total	C	Fe	Mo	S	
			18	1	7	1	9	

- Molecule 5 is FE(8)-S(7) CLUSTER (three-letter code: CLF) (formula: Fe₈S₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	Fe	S		
			15	8	7		
5	C	1	Total	Fe	S		
			15	8	7		
5	E	1	Total	Fe	S		
			15	8	7		
5	G	1	Total	Fe	S		
			15	8	7		
5	I	1	Total	Fe	S		
			15	8	7		
5	K	1	Total	Fe	S		
			15	8	7		
5	M	1	Total	Fe	S		
			15	8	7		
5	O	1	Total	Fe	S		
			15	8	7		

- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	P	1	Total Ca 1 1	0	0
6	J	1	Total Ca 1 1	0	0
6	D	1	Total Ca 1 1	0	0
6	H	1	Total Ca 1 1	0	0
6	B	1	Total Ca 1 1	0	0
6	N	1	Total Ca 1 1	0	0
6	L	1	Total Ca 1 1	0	0
6	F	1	Total Ca 1 1	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	542	Total O 542 542	0	0
7	B	753	Total O 753 753	0	0
7	C	582	Total O 582 582	0	0
7	D	752	Total O 752 752	0	0
7	E	507	Total O 507 507	0	0
7	F	750	Total O 750 750	0	0
7	G	615	Total O 615 615	0	0
7	H	749	Total O 749 749	0	0
7	I	557	Total O 557 557	0	0
7	J	761	Total O 761 761	0	0
7	K	587	Total O 587 587	0	0
7	L	709	Total O 709 709	0	0

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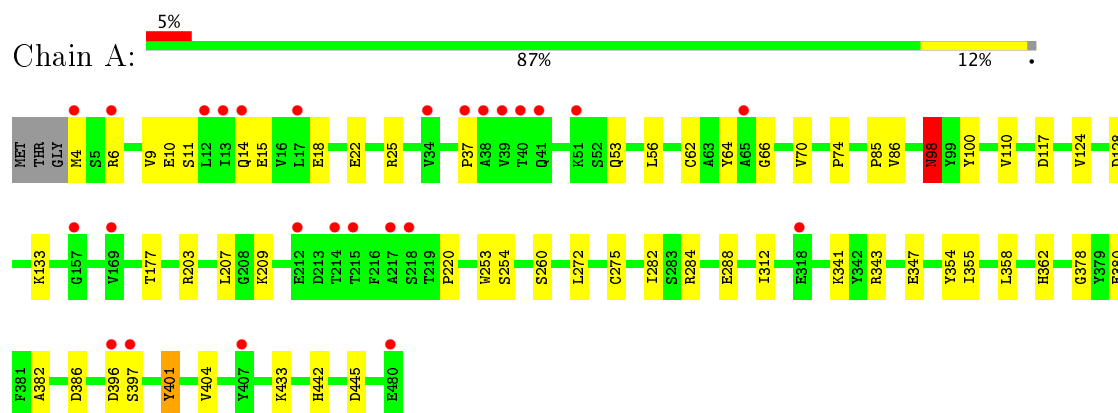
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	M	602	Total 602	O 602	0	0
7	N	797	Total 797	O 797	0	0
7	O	548	Total 548	O 548	0	0
7	P	757	Total 757	O 757	0	0

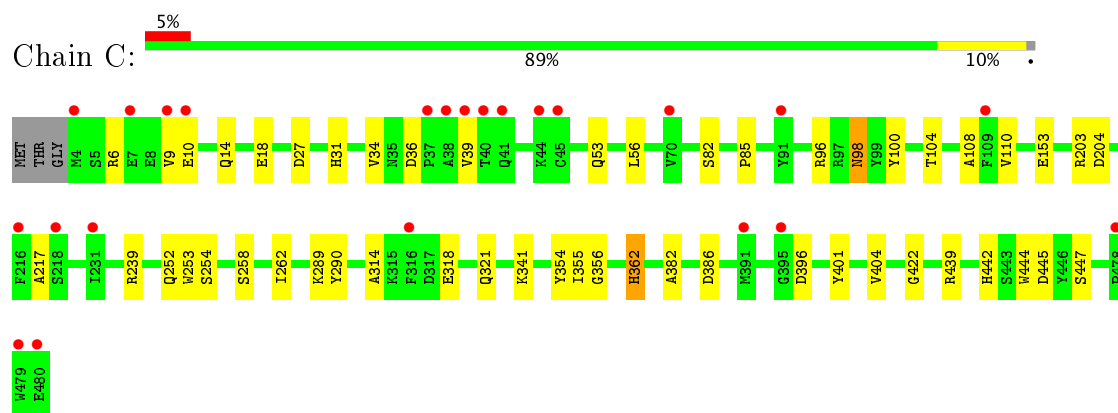
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

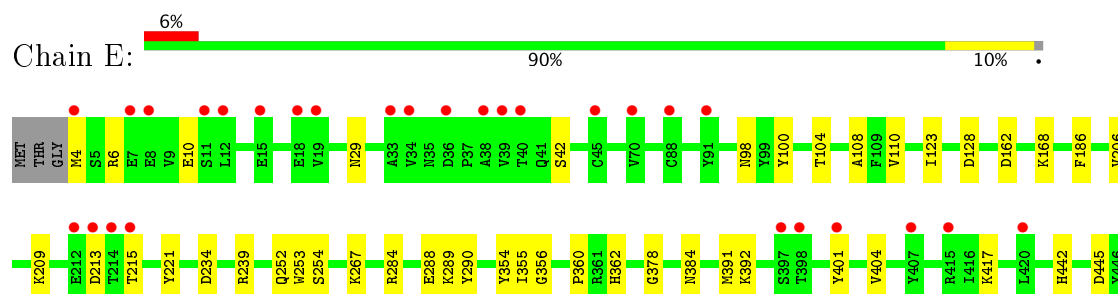
- Molecule 1: Nitrogenase molybdenum-iron protein alpha chain

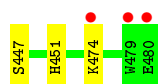


- Molecule 1: Nitrogenase molybdenum-iron protein alpha chain

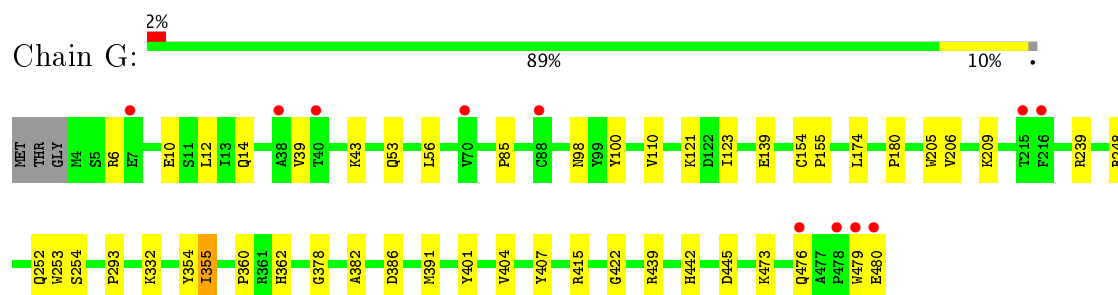


- Molecule 1: Nitrogenase molybdenum-iron protein alpha chain

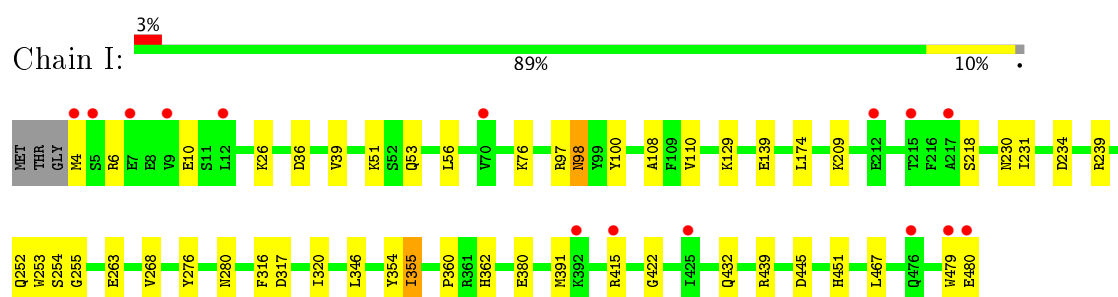




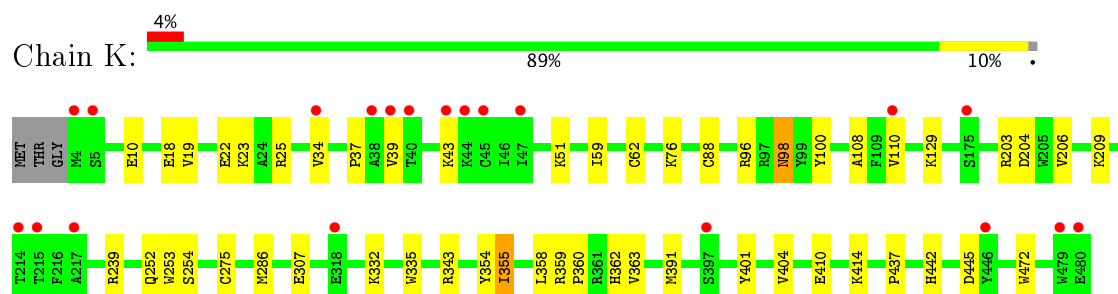
- Molecule 1: Nitrogenase molybdenum-iron protein alpha chain



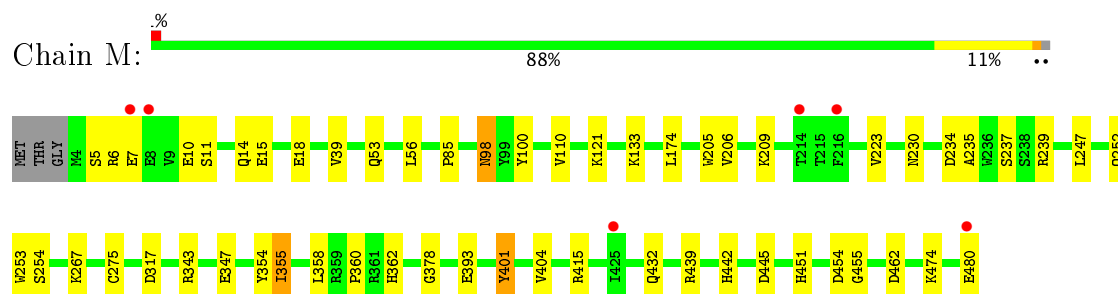
- Molecule 1: Nitrogenase molybdenum-iron protein alpha chain



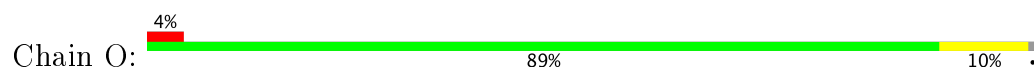
- Molecule 1: Nitrogenase molybdenum-iron protein alpha chain

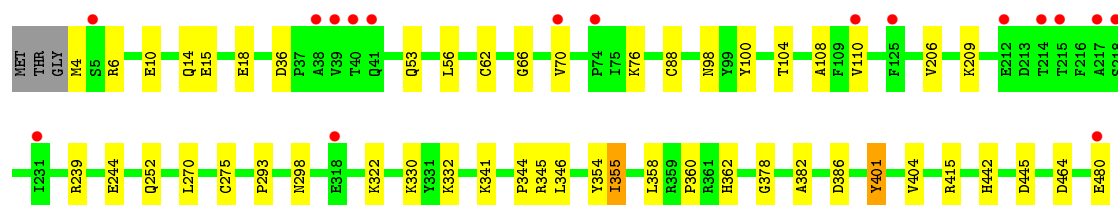


- Molecule 1: Nitrogenase molybdenum-iron protein alpha chain

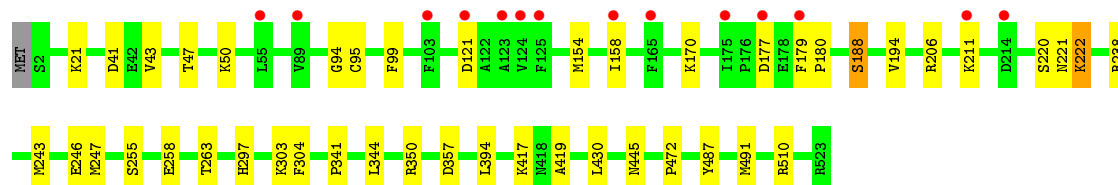


- Molecule 1: Nitrogenase molybdenum-iron protein alpha chain

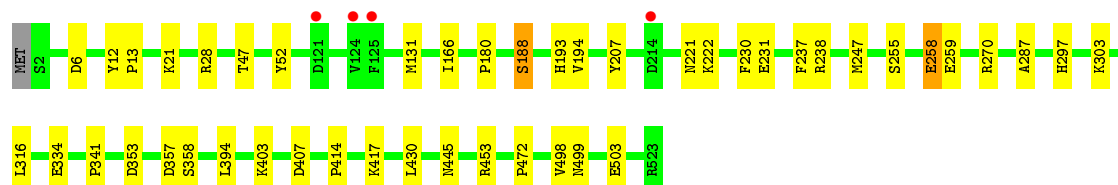
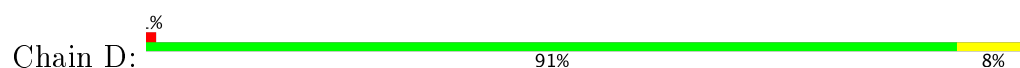




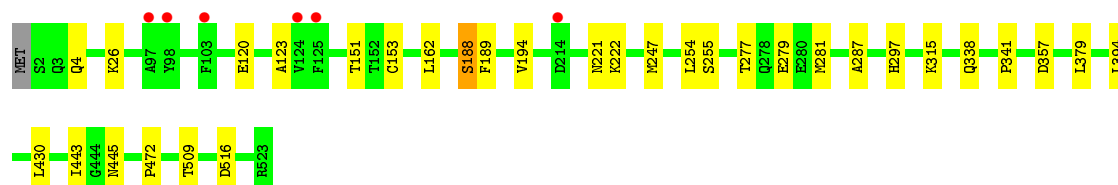
- Molecule 2: Nitrogenase molybdenum-iron protein beta chain



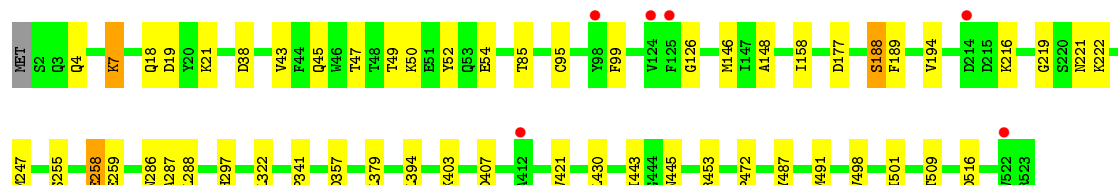
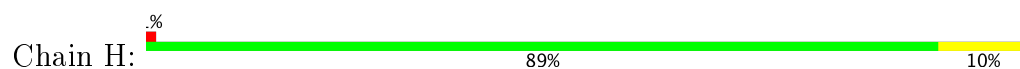
- Molecule 2: Nitrogenase molybdenum-iron protein beta chain



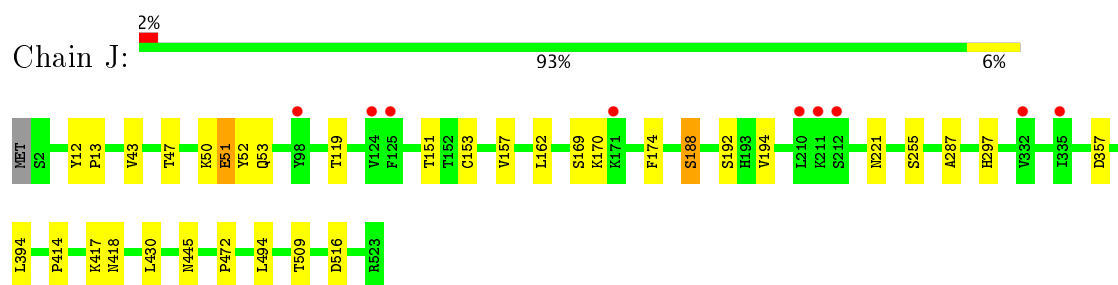
- Molecule 2: Nitrogenase molybdenum-iron protein beta chain



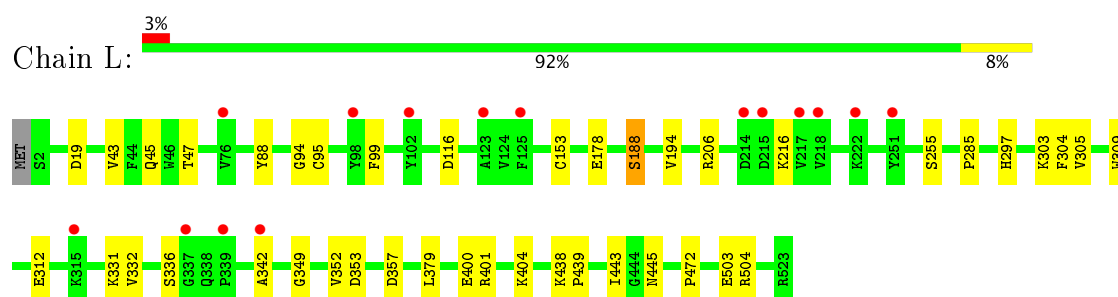
- Molecule 2: Nitrogenase molybdenum-iron protein beta chain



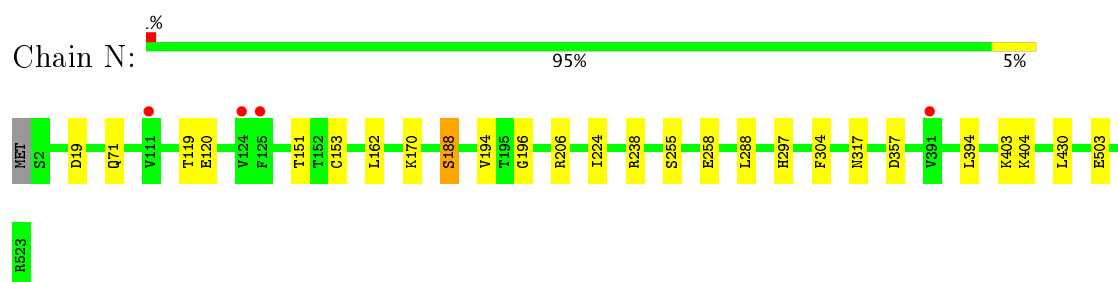
- Molecule 2: Nitrogenase molybdenum-iron protein beta chain



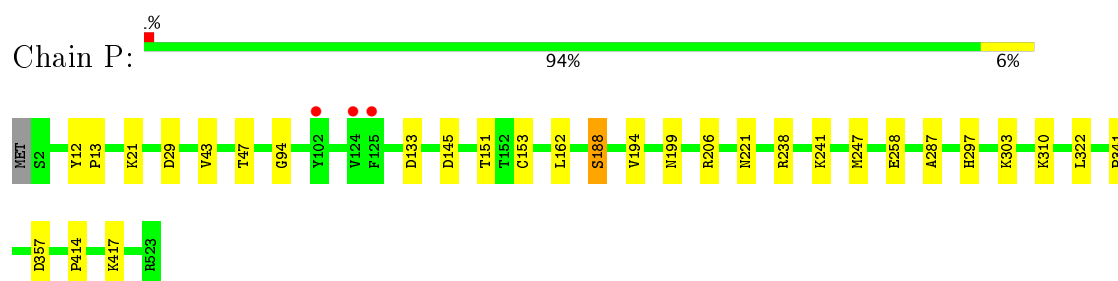
- Molecule 2: Nitrogenase molybdenum-iron protein beta chain



- Molecule 2: Nitrogenase molybdenum-iron protein beta chain



- Molecule 2: Nitrogenase molybdenum-iron protein beta chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	175.50Å 144.59Å 177.75Å 90.00° 114.27° 90.00°	Depositor
Resolution (Å)	38.68 – 1.75 39.01 – 1.75	Depositor EDS
% Data completeness (in resolution range)	95.6 (38.68-1.75) 96.4 (39.01-1.75)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.98 (at 1.75Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.198 , 0.245 0.213 , 0.256	Depositor DCC
R_{free} test set	78317 reflections (11.09%)	DCC
Wilson B-factor (Å ²)	13.2	Xtriage
Anisotropy	0.536	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.039 for l,-k,h	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	74588	wwPDB-VP
Average B, all atoms (Å ²)	17.0	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 34.33 % 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 6.9357e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ICS, CLF, HCA, CA

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	0.55	0/3862	0.67	0/5212
1	C	0.55	0/3870	0.66	0/5220
1	E	0.50	0/3864	0.65	0/5212
1	G	0.54	0/3874	0.65	0/5225
1	I	0.52	0/3874	0.65	0/5225
1	K	0.54	0/3870	0.67	0/5219
1	M	0.57	0/3878	0.68	0/5229
1	O	0.53	0/3866	0.66	0/5217
2	B	0.56	1/4276 (0.0%)	0.69	3/5783 (0.1%)
2	D	0.59	1/4280 (0.0%)	0.69	3/5787 (0.1%)
2	F	0.56	2/4280 (0.0%)	0.66	3/5787 (0.1%)
2	H	0.57	2/4280 (0.0%)	0.68	4/5787 (0.1%)
2	J	0.56	2/4278 (0.0%)	0.68	3/5784 (0.1%)
2	L	0.55	2/4276 (0.0%)	0.70	5/5783 (0.1%)
2	N	0.58	1/4280 (0.0%)	0.69	3/5787 (0.1%)
2	P	0.58	2/4280 (0.0%)	0.69	3/5787 (0.1%)
All	All	0.55	13/65188 (0.0%)	0.67	27/88044 (0.0%)

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
1	I	0	1
1	M	0	1
All	All	0	3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	188	SER	CA-CB	8.72	1.66	1.52
2	J	188	SER	CB-OG	8.14	1.52	1.42
2	P	188	SER	CB-OG	8.08	1.52	1.42
2	F	188	SER	CB-OG	7.64	1.52	1.42
2	F	188	SER	CA-CB	7.61	1.64	1.52
2	P	188	SER	CA-CB	7.43	1.64	1.52
2	L	188	SER	CB-OG	7.37	1.51	1.42
2	L	188	SER	CA-CB	7.37	1.64	1.52
2	D	188	SER	CA-CB	7.08	1.63	1.52
2	N	188	SER	CA-CB	6.74	1.63	1.52
2	H	188	SER	CB-OG	6.01	1.50	1.42
2	B	188	SER	CA-CB	5.84	1.61	1.52
2	H	188	SER	CA-CB	5.42	1.61	1.52

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	357	ASP	CB-CG-OD1	12.86	129.88	118.30
2	B	357	ASP	CB-CG-OD1	11.96	129.06	118.30
2	H	357	ASP	CB-CG-OD1	11.67	128.80	118.30
2	P	357	ASP	CB-CG-OD1	11.62	128.76	118.30
2	F	357	ASP	CB-CG-OD1	10.97	128.17	118.30
2	D	357	ASP	CB-CG-OD1	9.86	127.18	118.30
2	L	357	ASP	CB-CG-OD1	9.80	127.12	118.30
2	N	357	ASP	CB-CG-OD1	8.90	126.31	118.30
2	J	188	SER	CA-CB-OG	8.70	134.68	111.20
2	P	188	SER	CA-CB-OG	8.67	134.62	111.20
2	L	188	SER	CA-CB-OG	8.24	133.44	111.20
2	L	353	ASP	CB-CG-OD1	7.78	125.30	118.30
2	F	188	SER	CA-CB-OG	7.60	131.73	111.20
2	D	353	ASP	CB-CG-OD1	6.47	124.12	118.30
2	J	357	ASP	CB-CG-OD2	-6.06	112.85	118.30
2	P	357	ASP	CB-CG-OD2	-5.90	112.99	118.30
2	D	188	SER	CA-CB-OG	5.81	126.90	111.20
2	B	222	LYS	CD-CE-NZ	-5.81	98.34	111.70
2	N	19	ASP	CB-CG-OD1	5.61	123.35	118.30
2	H	19	ASP	CB-CG-OD1	5.58	123.32	118.30
2	H	188	SER	CA-CB-OG	5.53	126.14	111.20
2	B	357	ASP	CB-CG-OD2	-5.46	113.39	118.30
2	L	19	ASP	CB-CG-OD1	5.28	123.05	118.30
2	F	357	ASP	CB-CG-OD2	-5.25	113.58	118.30
2	N	188	SER	CA-CB-OG	5.12	125.02	111.20
2	L	357	ASP	CB-CG-OD2	-5.05	113.76	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	357	ASP	CB-CG-OD2	-5.00	113.80	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	98	ASN	Sidechain
1	I	98	ASN	Sidechain
1	M	98	ASN	Sidechain

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	3774	0	3690	47	0
1	C	3782	0	3712	33	0
1	E	3776	0	3703	33	0
1	G	3786	0	3718	30	0
1	I	3786	0	3718	33	0
1	K	3782	0	3719	31	0
1	M	3790	0	3729	39	0
1	O	3778	0	3696	31	0
2	B	4170	0	4069	30	0
2	D	4174	0	4080	34	0
2	F	4174	0	4080	21	0
2	H	4174	0	4080	41	0
2	J	4172	0	4076	22	0
2	L	4170	0	4069	25	0
2	N	4174	0	4080	20	0
2	P	4174	0	4080	23	0
3	A	14	0	7	2	0
3	C	14	0	7	3	0
3	E	14	0	6	2	0
3	G	14	0	7	2	0
3	I	14	0	6	1	0
3	K	14	0	6	2	0
3	M	14	0	7	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	O	14	0	7	4	0
4	A	18	0	0	0	0
4	C	18	0	0	1	0
4	E	18	0	0	2	0
4	G	18	0	0	0	0
4	I	18	0	0	0	0
4	K	18	0	0	0	0
4	M	18	0	0	0	0
4	O	18	0	0	0	0
5	A	15	0	0	0	0
5	C	15	0	0	0	0
5	E	15	0	0	0	0
5	G	15	0	0	0	0
5	I	15	0	0	0	0
5	K	15	0	0	0	0
5	M	15	0	0	0	0
5	O	15	0	0	0	0
6	B	1	0	0	0	0
6	D	1	0	0	0	0
6	F	1	0	0	0	0
6	H	1	0	0	0	0
6	J	1	0	0	0	0
6	L	1	0	0	0	0
6	N	1	0	0	0	0
6	P	1	0	0	0	0
7	A	542	0	0	15	3
7	B	753	0	0	8	1
7	C	582	0	0	6	3
7	D	752	0	0	16	0
7	E	507	0	0	13	2
7	F	750	0	0	9	1
7	G	615	0	0	8	0
7	H	749	0	0	16	0
7	I	557	0	0	15	2
7	J	761	0	0	7	1
7	K	587	0	0	9	2
7	L	709	0	0	11	2
7	M	602	0	0	16	2
7	N	797	0	0	11	2
7	O	548	0	0	8	1
7	P	757	0	0	10	0
All	All	74588	0	62352	485	11

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 4.

All (485) 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:K:286:MET:SD	7:K:728:HOH:O	2.17	1.02
4:E:502:ICS:S1A	7:E:926:HOH:O	2.20	0.98
2:H:85:THR:HG23	7:H:726:HOH:O	1.77	0.84
1:E:206:VAL:HA	1:E:209:LYS:HE2	1.60	0.82
1:O:345:ARG:HG3	7:O:601:HOH:O	1.80	0.81
1:M:455:GLY:N	7:M:602:HOH:O	2.15	0.79
2:F:279:GLU:OE1	7:F:701:HOH:O	2.00	0.78
1:O:332:LYS:NZ	7:O:602:HOH:O	2.13	0.78
2:H:4:GLN:HG3	2:H:7:LYS:HE3	1.66	0.78
2:B:220:SER:O	2:B:222:LYS:NZ	2.16	0.76
2:H:45:GLN:NE2	7:H:704:HOH:O	2.19	0.76
2:H:403:LYS:O	7:H:701:HOH:O	2.02	0.75
2:L:178:GLU:OE2	7:L:701:HOH:O	2.04	0.75
1:M:18:GLU:OE2	7:M:601:HOH:O	2.04	0.75
2:L:332:VAL:HG13	7:L:744:HOH:O	1.87	0.75
2:H:50:LYS:NZ	2:H:54:GLU:OE2	2.21	0.74
2:J:414:PRO:O	2:J:417:LYS:HG3	1.88	0.73
2:N:120:GLU:OE1	7:N:701:HOH:O	2.06	0.72
1:E:29:ASN:ND2	7:E:604:HOH:O	2.22	0.72
2:D:6:ASP:HB3	7:D:1281:HOH:O	1.89	0.71
1:A:209:LYS:NZ	7:A:602:HOH:O	2.16	0.71
2:J:50:LYS:NZ	7:J:703:HOH:O	2.23	0.71
2:F:338:GLN:NE2	7:F:706:HOH:O	2.26	0.69
1:A:74:PRO:HG3	1:A:98:ASN:OD1	1.93	0.69
2:B:350:ARG:NH2	7:B:705:HOH:O	2.25	0.69
2:P:258:GLU:OE2	7:P:701:HOH:O	2.10	0.69
1:C:447:SER:HB3	7:C:601:HOH:O	1.91	0.69
1:O:341:LYS:O	7:O:601:HOH:O	2.11	0.68
1:I:4:MET:N	7:I:608:HOH:O	2.26	0.68
1:C:6:ARG:O	1:C:10:GLU:HG3	1.94	0.68
1:M:205:TRP:O	1:M:209:LYS:NZ	2.26	0.68
1:I:51:LYS:NZ	7:I:602:HOH:O	2.13	0.67
2:N:258:GLU:OE2	7:N:702:HOH:O	2.11	0.67
1:A:53:GLN:OE1	7:A:601:HOH:O	2.11	0.67
2:J:153:CYS:HB3	2:J:188:SER:OG	1.93	0.67
1:K:51:LYS:NZ	7:K:602:HOH:O	2.22	0.67
2:L:401:ARG:HA	2:L:404:LYS:HE3	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:177:ASP:OD2	7:H:702:HOH:O	2.12	0.67
1:E:128:ASP:OD2	7:E:601:HOH:O	2.13	0.66
1:G:248:ARG:NH1	7:G:607:HOH:O	2.28	0.66
2:H:38:ASP:OD1	7:H:703:HOH:O	2.13	0.66
2:J:169:SER:O	7:J:701:HOH:O	2.13	0.66
1:I:209:LYS:NZ	1:I:263:GLU:OE2	2.27	0.66
1:I:6:ARG:NH2	7:I:616:HOH:O	2.29	0.66
2:P:310:LYS:NZ	7:P:710:HOH:O	2.29	0.65
2:L:503:GLU:OE2	7:L:702:HOH:O	2.13	0.65
2:J:174:PHE:N	7:J:701:HOH:O	2.29	0.65
1:I:320:ILE:HG12	7:I:603:HOH:O	1.97	0.64
1:E:221:TYR:N	7:E:607:HOH:O	2.25	0.64
2:P:199:ASN:OD1	7:P:702:HOH:O	2.15	0.64
2:L:349:GLY:O	7:L:704:HOH:O	2.15	0.64
1:A:124:VAL:HG12	1:G:121:LYS:HE3	1.80	0.63
1:K:22:GLU:OE1	1:K:25:ARG:NH1	2.30	0.63
1:C:444:TRP:O	7:C:601:HOH:O	2.15	0.63
2:H:52:TYR:N	7:H:708:HOH:O	2.30	0.63
2:B:222:LYS:N	2:B:222:LYS:HD2	2.14	0.63
1:I:4:MET:SD	1:I:415:ARG:NH2	2.72	0.62
2:P:206:ARG:HD3	7:P:968:HOH:O	2.00	0.62
2:F:4:GLN:NE2	7:F:710:HOH:O	2.32	0.62
2:F:281:MET:SD	7:F:1212:HOH:O	2.56	0.62
2:J:51:GLU:OE1	7:J:702:HOH:O	2.16	0.62
3:M:501:HCA:O7	3:M:501:HCA:O1	2.16	0.61
2:L:216:LYS:HG2	2:L:285:PRO:HB2	1.82	0.61
2:L:504:ARG:NH2	7:L:708:HOH:O	2.33	0.61
1:M:206:VAL:HA	1:M:209:LYS:HE2	1.82	0.61
1:A:98:ASN:H	1:A:98:ASN:HD22	1.49	0.61
2:H:221:ASN:O	2:H:222:LYS:HG2	2.01	0.61
1:G:473:LYS:HE3	7:G:1053:HOH:O	2.00	0.60
1:M:480:GLU:O	7:M:603:HOH:O	2.16	0.60
1:A:4:MET:HE3	1:A:9:VAL:HG22	1.84	0.60
2:P:151:THR:HG23	2:P:162:LEU:HD11	1.83	0.60
1:E:186:PHE:HA	7:E:656:HOH:O	2.01	0.60
2:N:170:LYS:NZ	7:N:715:HOH:O	2.35	0.59
1:I:6:ARG:O	1:I:10:GLU:HG3	2.03	0.59
1:M:415:ARG:NH1	7:M:610:HOH:O	2.36	0.59
1:A:18:GLU:OE1	7:A:603:HOH:O	2.17	0.59
3:G:501:HCA:O1	3:G:501:HCA:O7	2.21	0.59
1:I:139:GLU:HG3	1:I:174:LEU:HD13	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:162:ASP:OD2	7:E:602:HOH:O	2.17	0.58
1:E:100:TYR:CE1	1:E:110:VAL:HB	2.38	0.58
2:J:394:LEU:HD13	2:J:430:LEU:HB2	1.85	0.58
1:K:203:ARG:HD2	1:K:204:ASP:OD1	2.03	0.58
2:B:394:LEU:HD13	2:B:430:LEU:HB2	1.85	0.58
1:G:43:LYS:HG3	7:G:739:HOH:O	2.04	0.58
2:N:404:LYS:NZ	7:N:717:HOH:O	2.37	0.58
1:C:96:ARG:HH11	1:C:98:ASN:HD22	1.52	0.58
3:C:501:HCA:O7	3:C:501:HCA:O1	2.21	0.58
1:O:6:ARG:O	1:O:10:GLU:HG3	2.03	0.58
1:I:100:TYR:CE1	1:I:110:VAL:HB	2.39	0.57
1:C:341:LYS:NZ	7:C:606:HOH:O	2.28	0.57
2:L:352:VAL:HB	7:L:704:HOH:O	2.04	0.57
1:M:39:VAL:HG11	7:M:1045:HOH:O	2.02	0.57
2:N:288:LEU:HB2	7:N:704:HOH:O	2.05	0.57
1:G:14:GLN:OE1	7:G:602:HOH:O	2.18	0.57
1:E:267:LYS:HE2	7:E:698:HOH:O	2.05	0.57
1:E:447:SER:HA	7:E:635:HOH:O	2.05	0.56
1:I:346:LEU:HD23	7:I:612:HOH:O	2.05	0.56
2:B:417:LYS:O	7:B:701:HOH:O	2.18	0.56
2:N:288:LEU:HD12	7:N:704:HOH:O	2.03	0.56
1:I:239:ARG:HD2	1:I:252:GLN:OE1	2.04	0.56
1:M:100:TYR:CE1	1:M:110:VAL:HB	2.40	0.56
2:L:153:CYS:HB3	2:L:188:SER:OG	2.06	0.56
1:I:317:ASP:OD1	7:I:603:HOH:O	2.18	0.56
1:K:206:VAL:O	1:K:209:LYS:HG3	2.06	0.56
1:M:237:SER:HB2	7:M:602:HOH:O	2.05	0.56
1:C:444:TRP:HB3	7:C:601:HOH:O	2.05	0.56
2:F:153:CYS:HB3	2:F:188:SER:OG	2.06	0.56
1:O:415:ARG:NH1	7:O:614:HOH:O	2.36	0.56
1:C:10:GLU:HG2	1:C:34:VAL:HG21	1.87	0.55
1:I:479:TRP:O	1:I:480:GLU:HB2	2.06	0.55
1:A:177:THR:OG1	1:A:209:LYS:NZ	2.31	0.55
1:K:239:ARG:HD2	1:K:252:GLN:OE1	2.07	0.55
2:P:247:MET:HG2	2:P:341:PRO:HD3	1.87	0.55
1:A:98:ASN:H	1:A:98:ASN:ND2	2.04	0.55
3:O:501:HCA:O2	3:O:501:HCA:O7	2.23	0.55
1:K:410:GLU:HG2	1:K:414:LYS:HE2	1.88	0.55
1:A:347:GLU:O	7:A:604:HOH:O	2.18	0.55
1:O:100:TYR:CE1	1:O:110:VAL:HB	2.41	0.55
2:B:41:ASP:OD2	7:B:702:HOH:O	2.18	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:LEU:HB2	7:A:726:HOH:O	2.06	0.54
2:P:414:PRO:HA	2:P:417:LYS:HE2	1.89	0.54
2:P:238:ARG:HE	2:P:258:GLU:HG3	1.73	0.54
2:D:28:ARG:NH1	7:D:722:HOH:O	2.41	0.54
1:E:474:LYS:HE2	2:H:322:LEU:CD2	2.37	0.54
1:I:53:GLN:HB2	1:I:56:LEU:HD12	1.89	0.54
2:P:29:ASP:OD2	7:P:704:HOH:O	2.19	0.54
2:D:258:GLU:HG3	2:D:259:GLU:N	2.22	0.54
1:O:275:CYS:HA	1:O:358:LEU:HD22	1.90	0.54
1:A:22:GLU:OE2	1:A:25:ARG:NE	2.32	0.54
1:G:6:ARG:O	1:G:10:GLU:HG3	2.08	0.54
1:O:322:LYS:NZ	7:O:615:HOH:O	2.37	0.54
1:E:213:ASP:OD2	1:E:215:THR:HG22	2.08	0.54
1:A:124:VAL:CG1	1:G:121:LYS:HE3	2.37	0.54
2:H:221:ASN:C	2:H:222:LYS:HG2	2.29	0.54
2:P:145:ASP:OD1	7:P:703:HOH:O	2.18	0.54
1:M:11:SER:O	1:M:15:GLU:HG3	2.09	0.53
2:D:194:VAL:HA	7:D:784:HOH:O	2.08	0.53
2:J:221:ASN:OD1	2:J:287:ALA:HA	2.08	0.53
2:H:194:VAL:HB	2:H:297:HIS:CG	2.44	0.53
2:B:243:MET:HA	2:B:246:GLU:HG2	1.91	0.53
1:A:396:ASP:O	1:A:397:SER:HB3	2.08	0.53
1:E:6:ARG:O	1:E:10:GLU:HG3	2.09	0.53
1:A:14:GLN:NE2	7:A:610:HOH:O	2.25	0.53
1:A:22:GLU:OE1	1:A:22:GLU:HA	2.09	0.53
2:B:419:ALA:HB2	7:B:909:HOH:O	2.09	0.52
2:B:510:ARG:NH2	7:B:725:HOH:O	2.41	0.52
2:D:194:VAL:HB	2:D:297:HIS:CG	2.45	0.52
1:A:37:PRO:HD3	1:A:396:ASP:HA	1.92	0.52
1:G:476:GLN:HG2	7:G:605:HOH:O	2.08	0.52
2:D:193:HIS:CD2	7:D:784:HOH:O	2.62	0.52
1:C:442:HIS:HB3	3:C:501:HCA:O5	2.10	0.52
2:D:453:ARG:NH2	7:D:723:HOH:O	2.41	0.52
1:M:275:CYS:HA	1:M:358:LEU:HD22	1.90	0.52
2:N:317:ASN:ND2	7:N:723:HOH:O	2.41	0.52
1:A:220:PRO:HG2	7:A:968:HOH:O	2.10	0.52
2:B:303:LYS:HD3	7:B:1105:HOH:O	2.10	0.52
1:I:432:GLN:NE2	7:I:610:HOH:O	2.26	0.52
1:C:318:GLU:H	1:C:318:GLU:CD	2.13	0.52
3:A:501:HCA:O7	3:A:501:HCA:O2	2.27	0.52
2:F:281:MET:HA	7:F:1212:HOH:O	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:4:GLN:CG	2:H:7:LYS:HE3	2.38	0.52
1:M:442:HIS:HB3	3:M:501:HCA:O5	2.09	0.52
1:E:354:TYR:CZ	1:E:404:VAL:HG12	2.45	0.51
1:E:4:MET:HA	7:E:950:HOH:O	2.10	0.51
1:M:393:GLU:OE1	7:M:604:HOH:O	2.19	0.51
2:P:21:LYS:HG2	7:P:957:HOH:O	2.09	0.51
1:C:6:ARG:NH2	1:C:396:ASP:OD1	2.43	0.51
1:E:289:LYS:HD3	1:E:290:TYR:CZ	2.46	0.51
1:E:378:GLY:HA3	1:E:401:TYR:CD1	2.45	0.51
2:H:407:ASP:N	7:H:701:HOH:O	2.43	0.51
1:A:275:CYS:HA	1:A:358:LEU:HD22	1.91	0.51
2:B:206:ARG:HG2	2:B:304:PHE:CE1	2.45	0.51
2:H:148:ALA:N	7:H:726:HOH:O	2.43	0.51
1:I:316:PHE:HB3	7:I:603:HOH:O	2.10	0.51
1:A:85:PRO:HB2	2:B:188:SER:HB3	1.93	0.51
2:P:241:LYS:HD3	7:P:1216:HOH:O	2.11	0.51
1:E:284:ARG:O	1:E:288:GLU:HG3	2.11	0.51
3:I:501:HCA:O7	3:I:501:HCA:O1	2.29	0.50
1:C:100:TYR:CE1	1:C:110:VAL:HB	2.45	0.50
2:F:222:LYS:NZ	7:F:727:HOH:O	2.43	0.50
2:P:303:LYS:HE3	7:P:1232:HOH:O	2.11	0.50
1:A:133:LYS:NZ	7:A:622:HOH:O	2.42	0.50
2:H:54:GLU:OE2	7:H:705:HOH:O	2.19	0.50
1:I:129:LYS:NZ	7:I:601:HOH:O	2.06	0.50
1:A:433:LYS:NZ	2:B:263:THR:O	2.45	0.50
1:G:139:GLU:HG3	1:G:174:LEU:HD13	1.93	0.50
1:G:100:TYR:CE1	1:G:110:VAL:HB	2.47	0.50
1:G:53:GLN:HB2	1:G:56:LEU:HD12	1.94	0.50
1:C:362:HIS:HD2	7:C:981:HOH:O	1.95	0.50
2:D:193:HIS:HD2	7:D:784:HOH:O	1.93	0.50
2:D:403:LYS:NZ	2:D:407:ASP:OD2	2.42	0.50
2:L:336:SER:HB3	7:L:744:HOH:O	2.12	0.50
2:P:194:VAL:HB	2:P:297:HIS:CG	2.46	0.50
1:K:25:ARG:NE	7:K:611:HOH:O	2.34	0.49
2:H:286:ASN:ND2	7:H:728:HOH:O	2.45	0.49
2:J:53:GLN:NE2	7:J:722:HOH:O	2.45	0.49
1:M:317:ASP:OD2	7:M:605:HOH:O	2.20	0.49
1:M:347:GLU:OE2	7:M:606:HOH:O	2.20	0.49
1:M:355:ILE:HB	1:M:360:PRO:HD3	1.94	0.49
1:K:437:PRO:HA	1:K:472:TRP:CZ2	2.46	0.49
1:C:85:PRO:HB2	2:D:188:SER:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:194:VAL:HB	2:L:297:HIS:CG	2.48	0.49
1:C:239:ARG:HD2	1:C:252:GLN:OE1	2.12	0.49
2:F:151:THR:HG23	2:F:162:LEU:HD11	1.94	0.49
2:H:146:MET:HG2	7:H:726:HOH:O	2.12	0.49
2:H:221:ASN:OD1	2:H:287:ALA:HA	2.12	0.49
1:A:100:TYR:CE1	1:A:110:VAL:HB	2.48	0.49
1:K:10:GLU:HG2	1:K:34:VAL:HG21	1.95	0.49
1:A:397:SER:O	1:A:397:SER:OG	2.29	0.49
1:C:203:ARG:HD2	1:C:204:ASP:OD1	2.12	0.49
1:K:355:ILE:HB	1:K:360:PRO:HD3	1.95	0.49
2:B:154:MET:O	2:B:158:ILE:HG13	2.13	0.48
1:I:209:LYS:NZ	7:I:604:HOH:O	2.19	0.48
2:N:151:THR:HG23	2:N:162:LEU:HD11	1.93	0.48
2:B:95:CYS:HB3	2:B:99:PHE:CZ	2.48	0.48
1:I:36:ASP:HB3	1:I:39:VAL:HG23	1.96	0.48
1:O:442:HIS:ND1	3:O:501:HCA:H52	2.28	0.48
1:O:53:GLN:HB2	1:O:56:LEU:HD12	1.95	0.48
2:D:445:ASN:HB2	2:D:472:PRO:O	2.13	0.48
2:H:258:GLU:HG3	2:H:259:GLU:N	2.28	0.48
1:I:467:LEU:HD22	7:I:612:HOH:O	2.13	0.48
1:A:98:ASN:N	1:A:98:ASN:HD22	2.09	0.48
2:D:230:PHE:CD2	7:D:784:HOH:O	2.55	0.48
2:D:394:LEU:HD13	2:D:430:LEU:HB2	1.95	0.48
2:N:206:ARG:NH1	7:N:731:HOH:O	2.45	0.48
2:J:194:VAL:HB	2:J:297:HIS:CG	2.48	0.48
2:J:43:VAL:O	2:J:47:THR:HG23	2.14	0.48
2:L:303:LYS:HB3	2:L:303:LYS:HE3	1.62	0.48
2:D:180:PRO:HA	2:D:207:TYR:OH	2.14	0.47
1:E:29:ASN:ND2	7:E:624:HOH:O	2.47	0.47
2:B:194:VAL:HB	2:B:297:HIS:CG	2.48	0.47
1:E:234:ASP:HB3	1:E:451:HIS:ND1	2.28	0.47
1:O:4:MET:N	7:O:623:HOH:O	2.47	0.47
2:H:216:LYS:HD2	7:H:728:HOH:O	2.14	0.47
2:L:342:ALA:HA	7:L:856:HOH:O	2.13	0.47
2:L:45:GLN:HG2	7:L:1021:HOH:O	2.13	0.47
1:O:239:ARG:HD2	1:O:252:GLN:OE1	2.14	0.47
1:E:206:VAL:O	1:E:209:LYS:HG3	2.15	0.47
1:K:343:ARG:NH1	7:K:610:HOH:O	2.33	0.47
1:M:6:ARG:O	1:M:10:GLU:HG3	2.15	0.47
1:O:354:TYR:CZ	1:O:404:VAL:HG12	2.49	0.47
1:A:341:LYS:NZ	7:A:630:HOH:O	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:221:ASN:C	2:B:222:LYS:HD2	2.35	0.47
2:D:247:MET:HG2	2:D:341:PRO:CD	2.45	0.47
1:M:234:ASP:HB3	1:M:451:HIS:ND1	2.30	0.47
1:A:53:GLN:HB2	1:A:56:LEU:HD12	1.97	0.47
2:N:224:ILE:HG12	7:N:704:HOH:O	2.15	0.47
1:O:62:CYS:HB3	2:P:94:GLY:HA3	1.97	0.47
2:H:177:ASP:HB2	7:H:1201:HOH:O	2.15	0.47
2:H:453:ARG:NH1	7:H:719:HOH:O	2.40	0.47
2:N:194:VAL:HB	2:N:297:HIS:CG	2.50	0.47
2:P:221:ASN:OD1	2:P:287:ALA:HA	2.15	0.47
1:G:39:VAL:O	1:G:391:MET:HE3	2.15	0.47
1:K:39:VAL:HG13	7:K:890:HOH:O	2.15	0.47
2:D:247:MET:HG2	2:D:341:PRO:HD3	1.96	0.47
2:H:487:TYR:O	2:H:491:MET:HG3	2.15	0.47
1:K:354:TYR:CZ	1:K:404:VAL:HG12	2.50	0.47
2:N:71:GLN:O	2:N:196:GLY:HA3	2.15	0.47
2:B:247:MET:HG2	2:B:341:PRO:HD3	1.97	0.46
2:D:166:ILE:HG13	7:D:753:HOH:O	2.14	0.46
1:K:100:TYR:CE1	1:K:110:VAL:HB	2.51	0.46
1:K:253:TRP:HA	1:K:254:SER:HA	1.70	0.46
1:O:344:PRO:HD2	7:O:601:HOH:O	2.15	0.46
1:A:6:ARG:O	1:A:10:GLU:HG3	2.15	0.46
2:B:170:LYS:HB3	2:B:177:ASP:OD1	2.14	0.46
1:I:268:VAL:HG22	7:I:656:HOH:O	2.14	0.46
1:C:27:ASP:O	1:C:31:HIS:HD2	1.98	0.46
1:C:354:TYR:CZ	1:C:404:VAL:HG12	2.50	0.46
1:K:59:ILE:HD11	7:K:955:HOH:O	2.15	0.46
1:E:384:ASN:HB2	7:E:973:HOH:O	2.15	0.46
2:P:153:CYS:HB3	2:P:188:SER:OG	2.15	0.46
1:M:354:TYR:CZ	1:M:404:VAL:HG12	2.51	0.46
2:F:445:ASN:HB2	2:F:472:PRO:O	2.14	0.46
2:H:379:LEU:HD21	2:H:443:ILE:HG21	1.96	0.46
1:K:129:LYS:NZ	7:K:636:HOH:O	2.49	0.46
1:O:244:GLU:OE2	1:O:330:LYS:NZ	2.46	0.46
1:A:209:LYS:HD2	7:A:980:HOH:O	2.15	0.46
1:K:442:HIS:HB3	3:K:501:HCA:O6	2.15	0.46
1:M:133:LYS:NZ	7:M:629:HOH:O	2.48	0.46
2:P:133:ASP:OD1	7:P:705:HOH:O	2.21	0.46
1:C:314:ALA:HA	1:C:321:GLN:HE21	1.81	0.46
1:I:253:TRP:HA	1:I:254:SER:HA	1.74	0.46
1:M:53:GLN:HB2	1:M:56:LEU:HD12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:SER:HB3	7:A:731:HOH:O	2.15	0.45
1:C:53:GLN:HB2	1:C:56:LEU:HD12	1.97	0.45
2:H:49:THR:HG22	7:H:704:HOH:O	2.15	0.45
1:E:392:LYS:N	7:E:630:HOH:O	2.49	0.45
1:E:253:TRP:HA	1:E:254:SER:HA	1.69	0.45
1:A:22:GLU:CD	1:A:25:ARG:HE	2.18	0.45
2:L:331:LYS:HD2	7:L:1094:HOH:O	2.16	0.45
1:M:439:ARG:CZ	1:M:462:ASP:HB3	2.46	0.45
2:L:206:ARG:HG2	2:L:304:PHE:CE1	2.52	0.45
1:E:474:LYS:HE2	2:H:322:LEU:HD23	1.98	0.45
1:M:85:PRO:HB2	2:N:188:SER:HB3	1.99	0.45
2:J:445:ASN:HB2	2:J:472:PRO:O	2.17	0.45
2:J:47:THR:HA	2:J:52:TYR:CG	2.52	0.45
2:J:509:THR:O	2:J:516:ASP:HA	2.17	0.45
2:L:400:GLU:O	2:L:404:LYS:HG3	2.17	0.45
1:E:355:ILE:HB	1:E:360:PRO:HD3	1.99	0.45
2:F:26:LYS:HD2	7:F:886:HOH:O	2.17	0.45
2:H:43:VAL:O	2:H:47:THR:HG23	2.16	0.45
2:D:221:ASN:OD1	2:D:287:ALA:HA	2.17	0.45
2:H:445:ASN:HB2	2:H:472:PRO:O	2.17	0.45
2:J:418:ASN:ND2	7:J:706:HOH:O	2.28	0.45
1:K:209:LYS:HE2	1:K:209:LYS:HB3	1.71	0.45
1:C:36:ASP:HB3	1:C:39:VAL:HG23	1.99	0.44
2:D:414:PRO:O	2:D:417:LYS:HG3	2.17	0.44
1:G:382:ALA:HB1	1:G:386:ASP:HB2	1.98	0.44
2:H:95:CYS:HB3	2:H:99:PHE:CZ	2.51	0.44
1:I:234:ASP:HB3	1:I:451:HIS:ND1	2.32	0.44
2:H:394:LEU:HD13	2:H:430:LEU:HB2	1.98	0.44
1:M:5:SER:OG	1:M:7:GLU:HG2	2.17	0.44
1:A:62:CYS:HB3	2:B:94:GLY:HA3	1.98	0.44
2:B:238:ARG:HE	2:B:258:GLU:HG3	1.82	0.44
1:G:239:ARG:HD2	1:G:252:GLN:OE1	2.17	0.44
1:I:97:ARG:O	1:I:231:ILE:HA	2.18	0.44
2:J:12:TYR:HA	2:J:13:PRO:HA	1.84	0.44
1:M:454:ASP:HB2	7:M:602:HOH:O	2.17	0.44
2:H:126:GLY:HA2	2:H:158:ILE:HD12	1.99	0.44
1:G:85:PRO:HB2	2:H:188:SER:HB3	2.00	0.44
1:I:276:TYR:O	1:I:280:ASN:HB3	2.17	0.44
2:L:305:VAL:O	2:L:309:TRP:HB2	2.16	0.44
2:D:222:LYS:N	2:D:222:LYS:HD2	2.32	0.44
1:E:168:LYS:HE2	7:E:960:HOH:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:18:GLN:OE1	2:H:21:LYS:HD3	2.17	0.44
1:O:206:VAL:O	1:O:209:LYS:HG3	2.17	0.44
2:D:334:GLU:O	7:D:701:HOH:O	2.20	0.44
7:I:602:HOH:O	2:J:119:THR:OG1	2.14	0.44
1:A:442:HIS:ND1	3:A:501:HCA:H52	2.33	0.44
1:G:378:GLY:HA3	1:G:401:TYR:CD1	2.52	0.44
1:G:355:ILE:HB	1:G:360:PRO:HD3	1.99	0.44
1:E:239:ARG:HD2	1:E:252:GLN:OE1	2.18	0.44
2:F:379:LEU:HD21	2:F:443:ILE:HG21	2.00	0.44
2:J:170:LYS:HA	7:J:701:HOH:O	2.18	0.44
1:M:442:HIS:CG	3:M:501:HCA:H52	2.53	0.44
1:O:355:ILE:HB	1:O:360:PRO:HD3	1.99	0.44
1:O:442:HIS:HB3	3:O:501:HCA:O6	2.18	0.44
1:O:66:GLY:O	1:O:70:VAL:HB	2.18	0.44
1:A:282:ILE:HD11	7:A:726:HOH:O	2.17	0.43
1:A:272:LEU:HD22	1:A:312:ILE:HG12	2.01	0.43
2:H:247:MET:HG2	2:H:341:PRO:HD3	2.00	0.43
1:K:76:LYS:O	1:K:108:ALA:HA	2.18	0.43
1:A:66:GLY:O	1:A:70:VAL:HB	2.17	0.43
2:D:131:MET:HE3	7:D:753:HOH:O	2.18	0.43
1:E:104:THR:HA	1:E:108:ALA:O	2.19	0.43
2:L:88:TYR:OH	2:L:116:ASP:HB3	2.18	0.43
2:N:153:CYS:HB3	2:N:188:SER:HB2	2.00	0.43
2:B:222:LYS:NZ	7:B:739:HOH:O	2.49	0.43
1:C:382:ALA:HB1	1:C:386:ASP:HB2	2.01	0.43
2:H:421:VAL:HG21	7:H:701:HOH:O	2.19	0.43
1:K:62:CYS:HB3	2:L:94:GLY:HA3	2.01	0.43
1:M:378:GLY:HA3	1:M:401:TYR:CD1	2.53	0.43
2:N:503:GLU:OE2	7:N:703:HOH:O	2.21	0.43
1:C:422:GLY:HA2	1:C:439:ARG:O	2.19	0.43
2:F:254:LEU:HD13	7:F:1212:HOH:O	2.19	0.43
2:F:394:LEU:HD13	2:F:430:LEU:HB2	2.00	0.43
1:M:267:LYS:HG2	7:M:781:HOH:O	2.19	0.43
1:O:104:THR:HA	1:O:108:ALA:O	2.18	0.43
1:O:442:HIS:CG	3:O:501:HCA:H52	2.53	0.43
1:C:85:PRO:CB	2:D:188:SER:HB3	2.48	0.43
1:K:23:LYS:HE2	7:L:1087:HOH:O	2.18	0.43
1:M:206:VAL:HA	1:M:209:LYS:CE	2.46	0.43
1:A:253:TRP:HA	1:A:254:SER:HA	1.75	0.43
1:C:356:GLY:HA3	4:C:502:ICS:S1B	2.58	0.43
1:E:42:SER:HA	1:E:391:MET:HE1	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:120:GLU:O	2:F:123:ALA:HB3	2.19	0.43
2:L:43:VAL:O	2:L:47:THR:HG23	2.19	0.43
1:A:382:ALA:HB1	1:A:386:ASP:HB2	2.01	0.43
1:G:354:TYR:CZ	1:G:404:VAL:HG12	2.54	0.43
1:K:307:GLU:OE1	7:K:601:HOH:O	2.21	0.43
1:O:298:ASN:ND2	7:O:632:HOH:O	2.52	0.43
1:E:123:ILE:HG13	2:F:189:PHE:CG	2.54	0.43
1:G:293:PRO:HB3	7:G:826:HOH:O	2.18	0.43
1:M:230:ASN:HA	1:M:235:ALA:H	1.84	0.43
2:B:21:LYS:HE2	2:B:21:LYS:HB3	1.73	0.42
2:B:445:ASN:HB2	2:B:472:PRO:O	2.18	0.42
1:C:253:TRP:HA	1:C:254:SER:HA	1.76	0.42
1:K:51:LYS:HE3	1:K:51:LYS:HB2	1.61	0.42
1:M:432:GLN:NE2	7:M:613:HOH:O	2.38	0.42
1:I:355:ILE:HB	1:I:360:PRO:HD3	2.02	0.42
2:B:43:VAL:O	2:B:47:THR:HG23	2.20	0.42
1:G:442:HIS:HB3	3:G:501:HCA:O5	2.19	0.42
2:J:153:CYS:O	2:J:157:VAL:HG23	2.19	0.42
2:J:494:LEU:C	2:J:494:LEU:HD23	2.40	0.42
1:M:253:TRP:HA	1:M:254:SER:HA	1.74	0.42
1:I:317:ASP:N	7:I:603:HOH:O	2.38	0.42
1:K:332:LYS:HA	1:K:335:TRP:NE1	2.34	0.42
1:A:128:ASP:OD2	7:A:606:HOH:O	2.21	0.42
1:A:343:ARG:NH1	7:A:613:HOH:O	2.35	0.42
2:D:47:THR:HA	2:D:52:TYR:CG	2.54	0.42
1:G:253:TRP:HA	1:G:254:SER:HA	1.82	0.42
2:H:219:GLY:HA2	2:H:288:LEU:HA	2.02	0.42
1:O:14:GLN:O	1:O:18:GLU:HG3	2.20	0.42
2:B:50:LYS:NZ	1:O:36:ASP:OD2	2.42	0.42
1:C:289:LYS:HD3	1:C:290:TYR:CZ	2.55	0.42
2:F:247:MET:HG2	2:F:341:PRO:HD3	2.02	0.42
1:I:354:TYR:OH	1:I:380:GLU:HA	2.19	0.42
1:K:359:ARG:O	1:K:363:VAL:HG22	2.19	0.42
1:M:14:GLN:O	1:M:18:GLU:HG2	2.20	0.42
1:A:354:TYR:CZ	1:A:404:VAL:HG12	2.54	0.42
2:B:487:TYR:O	2:B:491:MET:HG3	2.20	0.42
1:G:180:PRO:HD2	1:G:205:TRP:CE2	2.55	0.42
2:N:206:ARG:HG2	2:N:304:PHE:CE1	2.55	0.41
2:D:21:LYS:HE2	2:D:21:LYS:HB2	1.93	0.41
1:G:479:TRP:O	1:G:480:GLU:HG2	2.20	0.41
2:J:151:THR:HG23	2:J:162:LEU:HD11	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:394:LEU:HD13	2:N:430:LEU:HB2	2.02	0.41
2:P:238:ARG:NE	2:P:258:GLU:HG3	2.34	0.41
2:B:121:ASP:HA	7:B:707:HOH:O	2.20	0.41
1:C:14:GLN:O	1:C:18:GLU:HG3	2.19	0.41
1:C:217:ALA:HB3	7:C:741:HOH:O	2.20	0.41
1:C:9:VAL:HG12	1:C:34:VAL:HG22	2.02	0.41
3:E:501:HCA:O7	3:E:501:HCA:O2	2.38	0.41
2:H:498:VAL:HA	2:H:501:ILE:HD12	2.02	0.41
2:J:192:SER:OG	2:J:194:VAL:HG22	2.21	0.41
1:M:223:VAL:HG11	1:M:247:LEU:HD13	2.02	0.41
7:M:790:HOH:O	2:N:119:THR:HB	2.20	0.41
1:O:382:ALA:HB1	1:O:386:ASP:HB2	2.02	0.41
1:C:442:HIS:CG	3:C:501:HCA:H52	2.56	0.41
1:E:417:LYS:HE3	1:E:417:LYS:HB3	1.79	0.41
2:F:277:THR:HB	7:F:701:HOH:O	2.21	0.41
2:F:247:MET:HG2	2:F:341:PRO:CD	2.51	0.41
1:G:422:GLY:HA2	1:G:439:ARG:O	2.20	0.41
1:I:76:LYS:O	1:I:108:ALA:HA	2.20	0.41
1:M:474:LYS:HB3	2:P:322:LEU:HD21	2.02	0.41
1:A:378:GLY:HA3	1:A:401:TYR:CD1	2.56	0.41
2:D:303:LYS:NZ	7:D:759:HOH:O	2.53	0.41
1:I:422:GLY:HA2	1:I:439:ARG:O	2.20	0.41
2:L:379:LEU:HD21	2:L:443:ILE:HG21	2.02	0.41
2:L:95:CYS:HB3	2:L:99:PHE:CZ	2.55	0.41
1:O:76:LYS:O	1:O:108:ALA:HA	2.20	0.41
1:O:346:LEU:HD21	1:O:464:ASP:HA	2.01	0.41
1:A:354:TYR:OH	1:A:380:GLU:HA	2.20	0.41
2:D:12:TYR:HA	2:D:13:PRO:HA	1.87	0.41
1:E:356:GLY:HA3	4:E:502:ICS:S1B	2.60	0.41
2:L:438:LYS:HG2	2:L:439:PRO:O	2.21	0.41
1:M:121:LYS:HE2	7:M:1007:HOH:O	2.19	0.41
1:O:270:LEU:HD12	1:O:293:PRO:O	2.21	0.41
1:C:104:THR:HA	1:C:108:ALA:O	2.21	0.41
2:F:221:ASN:OD1	2:F:287:ALA:HA	2.20	0.41
2:F:509:THR:O	2:F:516:ASP:HA	2.21	0.41
1:K:37:PRO:HA	1:K:391:MET:O	2.19	0.41
2:L:445:ASN:HB2	2:L:472:PRO:O	2.21	0.41
1:O:378:GLY:HA3	1:O:401:TYR:CD1	2.56	0.41
1:A:11:SER:O	1:A:15:GLU:HG3	2.20	0.41
1:A:203:ARG:NH2	7:A:624:HOH:O	2.43	0.41
1:A:284:ARG:O	1:A:288:GLU:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:258:SER:O	1:C:262:ILE:HG12	2.21	0.41
2:D:231:GLU:HB3	2:D:237:PHE:CZ	2.56	0.41
2:D:238:ARG:NH1	7:D:764:HOH:O	2.54	0.41
1:I:218:SER:OG	7:I:605:HOH:O	2.20	0.41
1:O:15:GLU:OE1	1:O:415:ARG:NH2	2.39	0.41
1:A:86:VAL:HB	1:A:117:ASP:OD1	2.20	0.41
1:G:154:CYS:HB2	1:G:155:PRO:HD3	2.02	0.41
2:H:509:THR:O	2:H:516:ASP:HA	2.21	0.41
1:M:206:VAL:HA	1:M:209:LYS:HZ1	1.85	0.41
2:D:316:LEU:HA	7:D:736:HOH:O	2.21	0.41
2:D:499:ASN:O	2:D:503:GLU:HG3	2.20	0.41
1:K:43:LYS:NZ	7:K:605:HOH:O	2.25	0.41
1:M:239:ARG:HD2	1:M:252:GLN:OE1	2.20	0.41
2:N:238:ARG:HE	2:N:258:GLU:CD	2.24	0.41
2:P:12:TYR:HA	2:P:13:PRO:HA	1.88	0.41
2:F:194:VAL:HB	2:F:297:HIS:CG	2.56	0.40
1:G:407:TYR:OH	7:G:601:HOH:O	2.17	0.40
3:K:501:HCA:O7	3:K:501:HCA:O2	2.39	0.40
2:D:270:ARG:NH2	7:D:752:HOH:O	2.51	0.40
2:D:358:SER:CB	7:D:747:HOH:O	2.69	0.40
1:E:442:HIS:HB3	3:E:501:HCA:O6	2.21	0.40
1:G:206:VAL:O	1:G:209:LYS:HG3	2.21	0.40
1:G:123:ILE:HG13	2:H:189:PHE:CG	2.57	0.40
2:P:43:VAL:O	2:P:47:THR:HG23	2.22	0.40
2:B:179:PHE:HA	2:B:180:PRO:HD3	1.85	0.40
1:C:82:SER:HB3	1:C:153:GLU:OE2	2.21	0.40
2:H:18:GLN:HA	2:H:18:GLN:OE1	2.22	0.40
1:I:230:ASN:HB2	1:I:255:GLY:HA3	2.03	0.40
1:M:343:ARG:NH1	7:M:607:HOH:O	2.30	0.40
2:P:238:ARG:HE	2:P:258:GLU:CG	2.33	0.40
1:G:332:LYS:HE3	7:G:743:HOH:O	2.22	0.40
1:K:275:CYS:HA	1:K:358:LEU:HD22	2.04	0.40
2:B:243:MET:HG2	2:B:344:LEU:HD21	2.03	0.40
2:D:498:VAL:HG11	7:D:747:HOH:O	2.21	0.40
1:G:12:LEU:HD13	1:G:415:ARG:HG2	2.03	0.40
1:I:39:VAL:O	1:I:391:MET:HE3	2.21	0.40
1:K:96:ARG:HH11	1:K:98:ASN:HD22	1.68	0.40
2:N:403:LYS:NZ	7:N:759:HOH:O	2.55	0.40

All (11) 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)
7:I:605:HOH:O	7:L:811:HOH:O[2_748]	2.04	0.16
7:B:1319:HOH:O	7:K:828:HOH:O[2_748]	2.13	0.07
7:C:976:HOH:O	7:J:1140:HOH:O[1_554]	2.14	0.06
7:F:1442:HOH:O	7:O:1126:HOH:O[2_848]	2.14	0.06
7:A:1127:HOH:O	7:M:1160:HOH:O[1_455]	2.16	0.04
7:E:935:HOH:O	7:N:1307:HOH:O[2_848]	2.16	0.04
7:A:1036:HOH:O	7:C:1031:HOH:O[2_757]	2.17	0.03
7:E:626:HOH:O	7:N:1060:HOH:O[2_848]	2.17	0.03
7:I:787:HOH:O	7:L:1044:HOH:O[2_748]	2.17	0.03
7:A:931:HOH:O	7:M:1094:HOH:O[1_455]	2.18	0.02
7:C:1036:HOH:O	7:K:996:HOH:O[1_554]	2.19	0.01

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	475/480 (99%)	456 (96%)	18 (4%)	1 (0%)	51	31
1	C	475/480 (99%)	457 (96%)	17 (4%)	1 (0%)	51	31
1	E	475/480 (99%)	457 (96%)	18 (4%)	0	100	100
1	G	475/480 (99%)	458 (96%)	16 (3%)	1 (0%)	51	31
1	I	475/480 (99%)	455 (96%)	19 (4%)	1 (0%)	51	31
1	K	475/480 (99%)	458 (96%)	16 (3%)	1 (0%)	51	31
1	M	475/480 (99%)	456 (96%)	18 (4%)	1 (0%)	51	31
1	O	475/480 (99%)	455 (96%)	19 (4%)	1 (0%)	51	31
2	B	520/523 (99%)	511 (98%)	8 (2%)	1 (0%)	51	31
2	D	520/523 (99%)	510 (98%)	9 (2%)	1 (0%)	51	31
2	F	520/523 (99%)	509 (98%)	10 (2%)	1 (0%)	51	31
2	H	520/523 (99%)	511 (98%)	8 (2%)	1 (0%)	51	31
2	J	520/523 (99%)	510 (98%)	9 (2%)	1 (0%)	51	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	L	520/523 (99%)	509 (98%)	10 (2%)	1 (0%)	51	31
2	N	520/523 (99%)	513 (99%)	6 (1%)	1 (0%)	51	31
2	P	520/523 (99%)	509 (98%)	11 (2%)	0	100	100
All	All	7960/8024 (99%)	7734 (97%)	212 (3%)	14 (0%)	51	31

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	255	SER
2	F	255	SER
2	H	255	SER
2	J	255	SER
2	L	255	SER
2	N	255	SER
2	B	255	SER
1	C	355	ILE
1	G	355	ILE
1	O	355	ILE
1	A	355	ILE
1	K	355	ILE
1	M	355	ILE
1	I	355	ILE

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	403/409 (98%)	398 (99%)	5 (1%)	75	60
1	C	405/409 (99%)	401 (99%)	4 (1%)	80	67
1	E	403/409 (98%)	400 (99%)	3 (1%)	87	78
1	G	406/409 (99%)	403 (99%)	3 (1%)	87	78
1	I	406/409 (99%)	402 (99%)	4 (1%)	80	67
1	K	405/409 (99%)	398 (98%)	7 (2%)	66	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	407/409 (100%)	402 (99%)	5 (1%)	75	60
1	O	404/409 (99%)	398 (98%)	6 (2%)	70	52
2	B	453/455 (100%)	452 (100%)	1 (0%)	94	92
2	D	454/455 (100%)	453 (100%)	1 (0%)	94	92
2	F	454/455 (100%)	453 (100%)	1 (0%)	94	92
2	H	454/455 (100%)	452 (100%)	2 (0%)	93	89
2	J	453/455 (100%)	452 (100%)	1 (0%)	94	92
2	L	453/455 (100%)	452 (100%)	1 (0%)	94	92
2	N	454/455 (100%)	454 (100%)	0	100	100
2	P	454/455 (100%)	454 (100%)	0	100	100
All	All	6868/6912 (99%)	6824 (99%)	44 (1%)	89	82

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	64	TYR
1	A	98	ASN
1	A	362	HIS
1	A	401	TYR
1	A	445	ASP
2	B	211	LYS
1	C	98	ASN
1	C	362	HIS
1	C	401	TYR
1	C	445	ASP
2	D	258	GLU
1	E	98	ASN
1	E	362	HIS
1	E	445	ASP
2	F	315	LYS
1	G	98	ASN
1	G	362	HIS
1	G	445	ASP
2	H	7	LYS
2	H	258	GLU
1	I	26	LYS
1	I	98	ASN
1	I	362	HIS

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Mol	Chain	Res	Type
1	I	445	ASP
2	J	51	GLU
1	K	18	GLU
1	K	19	VAL
1	K	88	CYS
1	K	98	ASN
1	K	362	HIS
1	K	401	TYR
1	K	445	ASP
2	L	312	GLU
1	M	98	ASN
1	M	174	LEU
1	M	362	HIS
1	M	401	TYR
1	M	445	ASP
1	O	88	CYS
1	O	98	ASN
1	O	362	HIS
1	O	401	TYR
1	O	445	ASP
1	O	480	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	338	GLN
1	C	98	ASN
1	C	362	HIS
1	G	98	ASN
1	K	98	ASN
2	N	317	ASN

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

Of 32 ligands modelled in this entry, 8 are monoatomic - leaving 24 for Mogul analysis.

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	$\# Z > 2$
3	HCA	A	501	-	4,13,13	0.93	0	4,18,18	2.02	2 (50%)
4	ICS	A	502	1	6,30,30	1.39	1 (16%)	0,78,78	0.00	-
5	CLF	A	503	1,2,7	0,24,24	0.00	-	0,57,57	0.00	-
3	HCA	C	501	-	4,13,13	0.67	0	4,18,18	2.49	3 (75%)
4	ICS	C	502	1	6,30,30	1.41	1 (16%)	0,78,78	0.00	-
5	CLF	C	503	1,2	0,24,24	0.00	-	0,57,57	0.00	-
3	HCA	E	501	-	4,13,13	0.67	0	4,18,18	2.03	1 (25%)
4	ICS	E	502	1	6,30,30	2.23	2 (33%)	0,78,78	0.00	-
5	CLF	E	503	1,2	0,24,24	0.00	-	0,57,57	0.00	-
3	HCA	G	501	-	4,13,13	1.01	0	4,18,18	2.36	1 (25%)
4	ICS	G	502	1,7	6,30,30	1.49	1 (16%)	0,78,78	0.00	-
5	CLF	G	503	1,2	0,24,24	0.00	-	0,57,57	0.00	-
3	HCA	I	501	-	4,13,13	1.22	0	4,18,18	1.58	1 (25%)
4	ICS	I	502	1	6,30,30	1.49	2 (33%)	0,78,78	0.00	-
5	CLF	I	503	1,2	0,24,24	0.00	-	0,57,57	0.00	-
3	HCA	K	501	-	4,13,13	0.61	0	4,18,18	1.43	1 (25%)
4	ICS	K	502	1	6,30,30	1.76	2 (33%)	0,78,78	0.00	-
5	CLF	K	503	1,2	0,24,24	0.00	-	0,57,57	0.00	-
3	HCA	M	501	-	4,13,13	0.30	0	4,18,18	2.65	3 (75%)
4	ICS	M	502	1	6,30,30	1.82	1 (16%)	0,78,78	0.00	-
5	CLF	M	503	1,2	0,24,24	0.00	-	0,57,57	0.00	-
3	HCA	O	501	-	4,13,13	0.73	0	4,18,18	2.29	2 (50%)
4	ICS	O	502	1	6,30,30	1.78	2 (33%)	0,78,78	0.00	-
5	CLF	O	503	1,2	0,24,24	0.00	-	0,57,57	0.00	-

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
3	HCA	A	501	-	-	0/7/17/17	0/0/0/0
4	ICS	A	502	1	-	0/0/204/204	0/0/13/13
5	CLF	A	503	1,2,7	-	0/0/132/132	0/12/10/10
3	HCA	C	501	-	-	0/7/17/17	0/0/0/0
4	ICS	C	502	1	-	0/0/204/204	0/0/13/13
5	CLF	C	503	1,2	-	0/0/132/132	0/12/10/10
3	HCA	E	501	-	-	0/7/17/17	0/0/0/0
4	ICS	E	502	1	-	0/0/204/204	0/0/13/13
5	CLF	E	503	1,2	-	0/0/132/132	0/12/10/10
3	HCA	G	501	-	-	0/7/17/17	0/0/0/0
4	ICS	G	502	1,7	-	0/0/204/204	0/0/13/13
5	CLF	G	503	1,2	-	0/0/132/132	0/12/10/10
3	HCA	I	501	-	-	0/7/17/17	0/0/0/0
4	ICS	I	502	1	-	0/0/204/204	0/0/13/13
5	CLF	I	503	1,2	-	0/0/132/132	0/12/10/10
3	HCA	K	501	-	-	0/7/17/17	0/0/0/0
4	ICS	K	502	1	-	0/0/204/204	0/0/13/13
5	CLF	K	503	1,2	-	0/0/132/132	0/12/10/10
3	HCA	M	501	-	-	0/7/17/17	0/0/0/0
4	ICS	M	502	1	-	0/0/204/204	0/0/13/13
5	CLF	M	503	1,2	-	0/0/132/132	0/12/10/10
3	HCA	O	501	-	-	0/7/17/17	0/0/0/0
4	ICS	O	502	1	-	0/0/204/204	0/0/13/13
5	CLF	O	503	1,2	-	0/0/132/132	0/12/10/10

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	502	ICS	S5A-FE7	-3.75	2.16	2.24
4	O	502	ICS	S5A-FE7	-3.24	2.17	2.24
4	M	502	ICS	S5A-FE7	-3.04	2.17	2.24
4	E	502	ICS	S2B-FE6	-2.99	2.17	2.24
4	A	502	ICS	S2B-FE6	-2.81	2.18	2.24
4	K	502	ICS	S5A-FE7	-2.78	2.18	2.24
4	G	502	ICS	S5A-FE7	-2.67	2.18	2.24
4	I	502	ICS	S2B-FE6	-2.52	2.19	2.24
4	O	502	ICS	S2B-FE6	-2.32	2.19	2.24
4	I	502	ICS	S3A-FE4	-2.07	2.20	2.24
4	C	502	ICS	S2B-FE6	-2.05	2.20	2.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	K	502	ICS	S3A-FE5	2.04	2.29	2.24

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	501	HCA	C3-C2-C1	-3.61	109.32	114.95
3	M	501	HCA	C4-C3-C7	-3.40	105.33	111.46
3	C	501	HCA	C4-C3-C7	-3.36	105.39	111.46
3	E	501	HCA	C3-C2-C1	-3.19	109.97	114.95
3	O	501	HCA	C4-C3-C7	-3.05	105.95	111.46
3	A	501	HCA	C3-C2-C1	-2.87	110.47	114.95
3	M	501	HCA	C3-C2-C1	-2.74	110.67	114.95
3	I	501	HCA	C3-C2-C1	-2.73	110.68	114.95
3	O	501	HCA	C3-C2-C1	-2.61	110.87	114.95
3	C	501	HCA	C3-C2-C1	-2.48	111.08	114.95
3	M	501	HCA	O7-C3-C4	-2.45	100.71	106.81
3	A	501	HCA	O7-C3-C4	-2.33	101.00	106.81
3	C	501	HCA	O7-C3-C4	-2.31	101.06	106.81
3	K	501	HCA	C4-C3-C7	-2.14	107.59	111.46

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	HCA	2	0
3	C	501	HCA	3	0
4	C	502	ICS	1	0
3	E	501	HCA	2	0
4	E	502	ICS	2	0
3	G	501	HCA	2	0
3	I	501	HCA	1	0
3	K	501	HCA	2	0
3	M	501	HCA	3	0
3	O	501	HCA	4	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	477/480 (99%)	0.51	26 (5%)	26 31	9, 16, 31, 50	0
1	C	477/480 (99%)	0.49	23 (4%)	31 37	10, 15, 30, 44	0
1	E	477/480 (99%)	0.64	31 (6%)	20 25	11, 19, 34, 50	0
1	G	477/480 (99%)	0.29	11 (2%)	61 68	9, 14, 29, 40	0
1	I	477/480 (99%)	0.46	15 (3%)	49 57	10, 16, 27, 52	0
1	K	477/480 (99%)	0.46	20 (4%)	37 43	8, 15, 31, 43	0
1	M	477/480 (99%)	0.23	6 (1%)	77 83	8, 13, 24, 39	0
1	O	477/480 (99%)	0.39	17 (3%)	43 50	9, 15, 29, 40	0
2	B	522/523 (99%)	0.38	14 (2%)	55 62	9, 15, 26, 38	0
2	D	522/523 (99%)	0.19	4 (0%)	86 90	9, 14, 23, 37	0
2	F	522/523 (99%)	0.30	6 (1%)	80 86	8, 15, 25, 34	0
2	H	522/523 (99%)	0.23	6 (1%)	80 86	8, 15, 23, 33	0
2	J	522/523 (99%)	0.37	9 (1%)	70 78	9, 16, 25, 35	0
2	L	522/523 (99%)	0.42	15 (2%)	52 59	9, 16, 28, 42	0
2	N	522/523 (99%)	0.18	4 (0%)	86 90	7, 13, 23, 35	0
2	P	522/523 (99%)	0.17	3 (0%)	89 92	7, 13, 22, 29	0
All	All	7992/8024 (99%)	0.35	210 (2%)	56 63	7, 15, 27, 52	0

All (210) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	38	ALA	8.5
1	C	38	ALA	7.9
1	A	38	ALA	7.8
1	O	38	ALA	7.4
1	A	40	THR	7.1

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Mol	Chain	Res	Type	RSRZ
1	E	4	MET	6.2
1	K	40	THR	5.7
1	E	39	VAL	5.7
1	G	38	ALA	5.2
1	A	37	PRO	5.2
1	C	39	VAL	5.2
2	D	124	VAL	5.0
2	D	125	PHE	4.8
2	N	125	PHE	4.6
1	A	480	GLU	4.6
1	E	40	THR	4.6
2	B	125	PHE	4.6
1	G	480	GLU	4.5
2	H	125	PHE	4.4
2	B	124	VAL	4.4
2	J	125	PHE	4.4
1	G	40	THR	4.3
2	B	158	ILE	4.3
1	E	7	GLU	4.1
1	C	218	SER	4.0
2	B	211	LYS	3.9
2	L	125	PHE	3.9
1	E	480	GLU	3.8
1	I	4	MET	3.8
1	O	125	PHE	3.7
1	C	40	THR	3.6
1	M	214	THR	3.6
1	E	397	SER	3.5
1	A	318	GLU	3.5
2	H	124	VAL	3.5
1	K	38	ALA	3.5
2	P	124	VAL	3.4
1	I	480	GLU	3.4
1	A	215	THR	3.4
2	B	177	ASP	3.3
2	B	175	ILE	3.3
1	E	214	THR	3.3
2	F	125	PHE	3.3
2	L	214	ASP	3.3
2	L	218	VAL	3.3
1	K	214	THR	3.2
1	C	44	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
1	O	480	GLU	3.2
1	I	7	GLU	3.2
1	C	45	CYS	3.2
1	K	397	SER	3.2
2	J	332	VAL	3.1
1	K	39	VAL	3.1
1	C	9	VAL	3.1
1	M	7	GLU	3.0
1	A	39	VAL	3.0
2	P	125	PHE	3.0
1	O	212	GLU	3.0
1	E	34	VAL	3.0
1	E	415	ARG	2.9
1	I	476	GLN	2.9
1	O	5	SER	2.9
2	L	222	LYS	2.9
1	I	12	LEU	2.9
1	K	479	TRP	2.8
2	H	214	ASP	2.8
1	C	480	GLU	2.8
1	O	318	GLU	2.8
2	N	124	VAL	2.8
1	E	398	THR	2.8
1	C	37	PRO	2.8
1	E	45	CYS	2.8
2	L	102	TYR	2.8
1	I	5	SER	2.8
1	G	479	TRP	2.8
1	M	480	GLU	2.7
2	F	98	TYR	2.7
1	A	214	THR	2.7
1	O	39	VAL	2.7
1	G	216	PHE	2.7
1	K	4	MET	2.7
1	G	7	GLU	2.7
1	O	40	THR	2.7
1	E	36	ASP	2.7
2	J	171	LYS	2.7
1	A	13	ILE	2.7
2	L	217	VAL	2.6
1	O	215	THR	2.6
2	J	212	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	K	43	LYS	2.6
1	E	215	THR	2.6
1	C	70	VAL	2.6
2	F	124	VAL	2.6
1	C	316	PHE	2.6
1	M	216	PHE	2.6
1	K	215	THR	2.6
1	E	19	VAL	2.6
2	L	251	TYR	2.6
2	B	214	ASP	2.6
2	B	103	PHE	2.6
1	I	212	GLU	2.6
2	F	214	ASP	2.6
2	H	412	ALA	2.6
1	E	8	GLU	2.5
1	I	425	ILE	2.5
1	A	218	SER	2.5
1	E	401	TYR	2.5
1	G	88	CYS	2.5
1	O	70	VAL	2.5
1	E	15	GLU	2.5
1	A	217	ALA	2.5
1	I	415	ARG	2.5
1	K	110	VAL	2.5
1	A	4	MET	2.4
1	O	218	SER	2.4
1	C	395	GLY	2.4
1	K	318	GLU	2.4
1	O	217	ALA	2.4
1	A	14	GLN	2.4
2	D	214	ASP	2.4
1	C	391	MET	2.4
2	J	124	VAL	2.4
1	A	12	LEU	2.4
1	E	12	LEU	2.4
2	F	103	PHE	2.4
1	A	6	ARG	2.4
1	A	397	SER	2.4
2	L	123	ALA	2.4
1	K	34	VAL	2.4
1	K	44	LYS	2.4
2	L	337	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	E	213	ASP	2.4
1	G	70	VAL	2.3
2	J	335	ILE	2.3
1	C	4	MET	2.3
1	E	407	TYR	2.3
1	K	480	GLU	2.3
1	A	65	ALA	2.3
2	L	339	PRO	2.3
2	B	179	PHE	2.3
1	A	212	GLU	2.3
1	E	479	TRP	2.3
2	N	391	VAL	2.3
1	A	51	LYS	2.3
2	B	165	PHE	2.3
2	L	98	TYR	2.3
2	L	215	ASP	2.3
1	A	396	ASP	2.2
1	G	478	PRO	2.2
1	A	34	VAL	2.2
1	C	478	PRO	2.2
1	E	212	GLU	2.2
1	C	91	TYR	2.2
1	E	70	VAL	2.2
1	A	41	GLN	2.2
1	I	215	THR	2.2
1	I	70	VAL	2.2
2	H	522	VAL	2.2
1	G	476	GLN	2.2
1	I	479	TRP	2.2
1	E	91	TYR	2.1
1	M	8	GLU	2.1
1	E	88	CYS	2.1
1	A	169	VAL	2.1
1	K	217	ALA	2.1
2	B	121	ASP	2.1
2	J	98	TYR	2.1
1	C	7	GLU	2.1
1	A	17	LEU	2.1
1	K	175	SER	2.1
2	L	315	LYS	2.1
1	C	231	ILE	2.1
1	M	425	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	157	GLY	2.1
1	K	446	TYR	2.1
2	P	102	TYR	2.1
1	O	110	VAL	2.1
2	N	111	VAL	2.1
2	F	97	ALA	2.1
2	J	210	LEU	2.1
1	C	10	GLU	2.1
1	E	11	SER	2.1
1	A	407	TYR	2.1
1	C	216	PHE	2.1
1	C	479	TRP	2.1
2	B	123	ALA	2.1
2	L	76	VAL	2.1
2	L	342	ALA	2.1
2	B	55	LEU	2.1
1	K	45	CYS	2.1
1	K	5	SER	2.1
1	K	47	ILE	2.1
1	E	474	LYS	2.0
1	O	74	PRO	2.0
1	E	33	ALA	2.0
1	I	217	ALA	2.0
2	H	98	TYR	2.0
1	I	9	VAL	2.0
2	J	211	LYS	2.0
1	O	214	THR	2.0
1	O	231	ILE	2.0
1	C	41	GLN	2.0
1	I	392	LYS	2.0
1	O	41	GLN	2.0
1	E	18	GLU	2.0
2	B	89	VAL	2.0
1	C	109	PHE	2.0
1	E	420	LEU	2.0
1	G	215	THR	2.0
2	D	121	ASP	2.0

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

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
3	HCA	O	501	14/14	0.93	0.15	0.49	7,11,15,17	0
3	HCA	M	501	14/14	0.94	0.15	0.49	6,9,12,12	0
3	HCA	I	501	14/14	0.93	0.15	0.05	11,13,16,17	0
3	HCA	A	501	14/14	0.92	0.13	-0.08	10,12,18,18	0
3	HCA	K	501	14/14	0.95	0.14	-0.19	9,12,15,15	0
6	CA	N	601	1/1	0.98	0.11	-0.19	11,11,11,11	0
6	CA	P	601	1/1	0.99	0.13	-0.23	12,12,12,12	0
6	CA	F	601	1/1	0.98	0.11	-0.30	13,13,13,13	0
3	HCA	E	501	14/14	0.93	0.13	-0.40	11,14,17,17	0
3	HCA	G	501	14/14	0.94	0.12	-0.59	9,10,12,15	0
6	CA	B	601	1/1	0.99	0.10	-0.68	12,12,12,12	0
3	HCA	C	501	14/14	0.93	0.12	-0.88	9,12,14,16	0
6	CA	L	601	1/1	0.95	0.13	-1.07	14,14,14,14	0
5	CLF	K	503	15/15	0.99	0.07	-1.65	11,12,14,14	0
5	CLF	G	503	15/15	0.99	0.06	-1.72	10,11,13,13	0
5	CLF	E	503	15/15	0.99	0.06	-1.74	12,13,13,14	0
6	CA	H	601	1/1	0.97	0.08	-1.76	14,14,14,14	0
6	CA	J	601	1/1	0.99	0.08	-1.77	12,12,12,12	0
5	CLF	I	503	15/15	0.99	0.06	-1.80	11,12,15,16	0
5	CLF	O	503	15/15	0.99	0.07	-1.86	9,11,12,12	0
4	ICS	G	502	18/18	0.99	0.07	-1.87	8,11,12,12	0
5	CLF	M	503	15/15	0.99	0.07	-1.98	8,9,11,13	0
6	CA	D	601	1/1	0.98	0.10	-2.01	12,12,12,12	0
4	ICS	O	502	18/18	0.99	0.07	-2.10	8,11,14,14	0
4	ICS	K	502	18/18	0.99	0.07	-2.39	9,12,13,13	0
5	CLF	A	503	15/15	0.98	0.06	-2.43	11,12,14,15	0
4	ICS	C	502	18/18	0.99	0.06	-2.46	9,12,14,14	0
4	ICS	A	502	18/18	0.99	0.06	-2.59	10,12,15,15	0
4	ICS	M	502	18/18	0.99	0.08	-2.61	5,10,11,12	0
5	CLF	C	503	15/15	0.99	0.05	-2.66	10,11,13,14	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	ICS	E	502	18/18	0.98	0.07	-2.93	11,14,17,18	0
4	ICS	I	502	18/18	0.99	0.08	-3.00	10,13,15,16	0

6.5 Other polymers [i](#)

There are no such residues in this entry.