



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:14 PM UTC

PDB ID : 5WG1 / pdb_00005wg1
Title : Kelch domain of human Keap1 bound to mutant Nrf2 EAGE peptide
Authors : Carolan, J.P.; Lynch, A.J.; Allen, K.N.
Deposited on : 2017-07-13
Resolution : 2.02 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

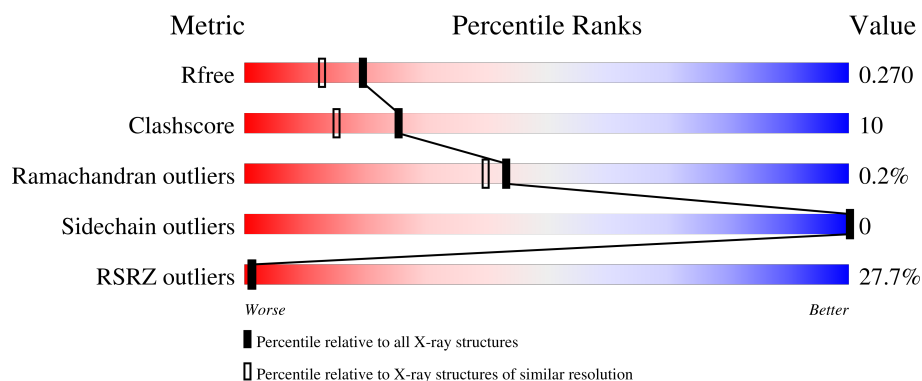
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.02 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}	180053	13299 (2.04-2.00)
Clashscore	190562	1022 (2.02-2.02)
Ramachandran outliers	187476	1014 (2.02-2.02)
Sidechain outliers	187428	1014 (2.02-2.02)
RSRZ outliers	180081	13314 (2.04-2.00)

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	336	43% 57% 26% 17%
1	B	336	4% 77% 9% 14%
2	P	9	44% 56% 44%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4502 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 Kelch-like ECH-associated protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	280	Total	C	N	O	S	0	1	0
			2145	1332	389	408	16			
1	B	289	Total	C	N	O	S	0	1	0
			2220	1381	401	421	17			

There are 90 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	289	MET	-	initiating methionine	UNP Q14145
A	290	GLY	-	expression tag	UNP Q14145
A	291	SER	-	expression tag	UNP Q14145
A	292	SER	-	expression tag	UNP Q14145
A	293	HIS	-	expression tag	UNP Q14145
A	294	HIS	-	expression tag	UNP Q14145
A	295	HIS	-	expression tag	UNP Q14145
A	296	HIS	-	expression tag	UNP Q14145
A	297	HIS	-	expression tag	UNP Q14145
A	298	HIS	-	expression tag	UNP Q14145
A	299	SER	-	expression tag	UNP Q14145
A	300	SER	-	expression tag	UNP Q14145
A	301	GLY	-	expression tag	UNP Q14145
A	302	GLY	-	expression tag	UNP Q14145
A	303	GLU	-	expression tag	UNP Q14145
A	304	ASN	-	expression tag	UNP Q14145
A	305	LEU	-	expression tag	UNP Q14145
A	306	TYR	-	expression tag	UNP Q14145
A	307	PHE	-	expression tag	UNP Q14145
A	308	GLN	-	expression tag	UNP Q14145
A	309	GLY	-	expression tag	UNP Q14145
A	310	HIS	-	expression tag	UNP Q14145
A	311	MET	-	expression tag	UNP Q14145
A	312	LYS	-	expression tag	UNP Q14145
A	313	PRO	-	expression tag	UNP Q14145

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Chain	Residue	Modelled	Actual	Comment	Reference
A	314	THR	-	expression tag	UNP Q14145
A	315	GLN	-	expression tag	UNP Q14145
A	316	VAL	-	expression tag	UNP Q14145
A	317	MET	-	expression tag	UNP Q14145
A	318	PRO	-	expression tag	UNP Q14145
A	319	SER	-	expression tag	UNP Q14145
A	540	ALA	GLU	engineered mutation	UNP Q14145
A	542	ALA	GLU	engineered mutation	UNP Q14145
A	613	SER	-	expression tag	UNP Q14145
A	614	ARG	-	expression tag	UNP Q14145
A	615	LYS	-	expression tag	UNP Q14145
A	616	GLN	-	expression tag	UNP Q14145
A	617	ILE	-	expression tag	UNP Q14145
A	618	ASP	-	expression tag	UNP Q14145
A	619	GLN	-	expression tag	UNP Q14145
A	620	GLN	-	expression tag	UNP Q14145
A	621	ASN	-	expression tag	UNP Q14145
A	622	SER	-	expression tag	UNP Q14145
A	623	THR	-	expression tag	UNP Q14145
A	624	SER	-	expression tag	UNP Q14145
B	289	MET	-	initiating methionine	UNP Q14145
B	290	GLY	-	expression tag	UNP Q14145
B	291	SER	-	expression tag	UNP Q14145
B	292	SER	-	expression tag	UNP Q14145
B	293	HIS	-	expression tag	UNP Q14145
B	294	HIS	-	expression tag	UNP Q14145
B	295	HIS	-	expression tag	UNP Q14145
B	296	HIS	-	expression tag	UNP Q14145
B	297	HIS	-	expression tag	UNP Q14145
B	298	HIS	-	expression tag	UNP Q14145
B	299	SER	-	expression tag	UNP Q14145
B	300	SER	-	expression tag	UNP Q14145
B	301	GLY	-	expression tag	UNP Q14145
B	302	GLY	-	expression tag	UNP Q14145
B	303	GLU	-	expression tag	UNP Q14145
B	304	ASN	-	expression tag	UNP Q14145
B	305	LEU	-	expression tag	UNP Q14145
B	306	TYR	-	expression tag	UNP Q14145
B	307	PHE	-	expression tag	UNP Q14145
B	308	GLN	-	expression tag	UNP Q14145
B	309	GLY	-	expression tag	UNP Q14145
B	310	HIS	-	expression tag	UNP Q14145

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Chain	Residue	Modelled	Actual	Comment	Reference
B	311	MET	-	expression tag	UNP Q14145
B	312	LYS	-	expression tag	UNP Q14145
B	313	PRO	-	expression tag	UNP Q14145
B	314	THR	-	expression tag	UNP Q14145
B	315	GLN	-	expression tag	UNP Q14145
B	316	VAL	-	expression tag	UNP Q14145
B	317	MET	-	expression tag	UNP Q14145
B	318	PRO	-	expression tag	UNP Q14145
B	319	SER	-	expression tag	UNP Q14145
B	540	ALA	GLU	engineered mutation	UNP Q14145
B	542	ALA	GLU	engineered mutation	UNP Q14145
B	613	SER	-	expression tag	UNP Q14145
B	614	ARG	-	expression tag	UNP Q14145
B	615	LYS	-	expression tag	UNP Q14145
B	616	GLN	-	expression tag	UNP Q14145
B	617	ILE	-	expression tag	UNP Q14145
B	618	ASP	-	expression tag	UNP Q14145
B	619	GLN	-	expression tag	UNP Q14145
B	620	GLN	-	expression tag	UNP Q14145
B	621	ASN	-	expression tag	UNP Q14145
B	622	SER	-	expression tag	UNP Q14145
B	623	THR	-	expression tag	UNP Q14145
B	624	SER	-	expression tag	UNP Q14145

- Molecule 2 is a protein called Nrf2 EAGE mutant peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	P	9	Total	C	N	O	0	0	0
			71	45	9	17			

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

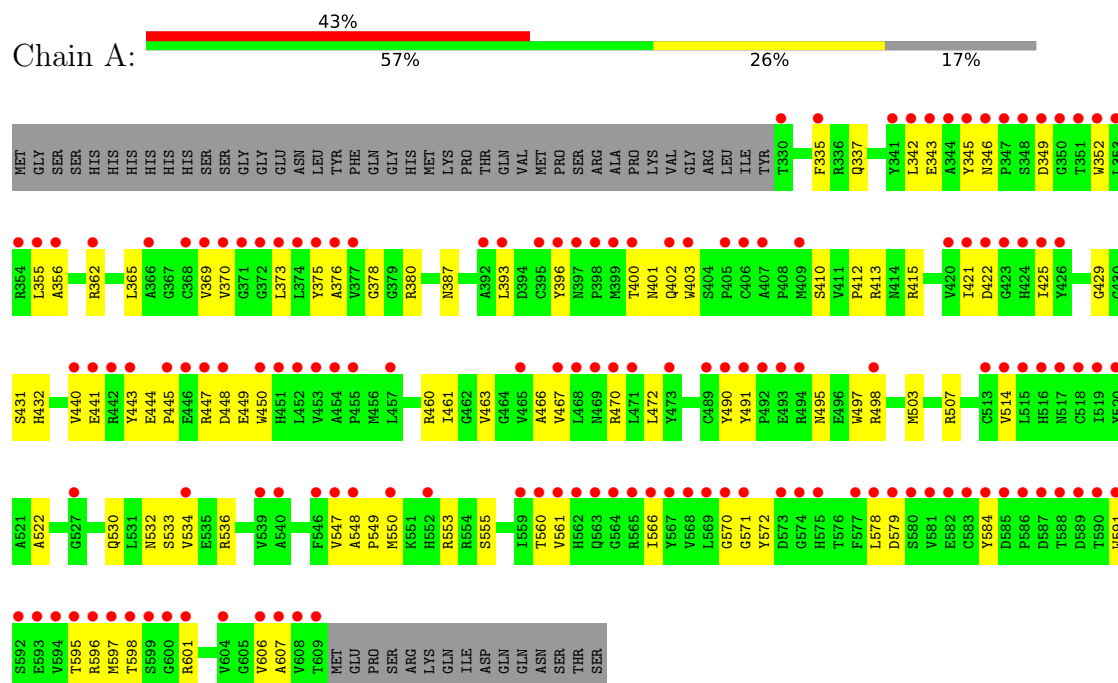
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	11	Total	O	0	0
			11	11		
4	B	45	Total	O	0	0
			45	45		

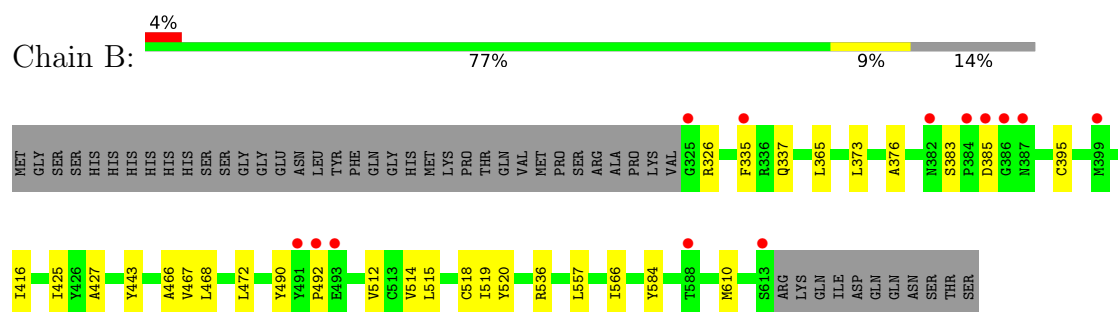
3 Residue-property plots

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.

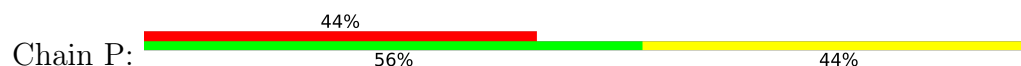
• Molecule 1: Kelch-like ECH-associated protein 1

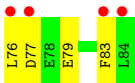


• Molecule 1: Kelch-like ECH-associated protein 1



• Molecule 2: Nrf2 EAGE mutant peptide





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	161.81Å 68.65Å 77.13Å 90.00° 117.54° 90.00°	Depositor
Resolution (Å)	34.33 – 2.02 34.33 – 2.02	Depositor EDS
% Data completeness (in resolution range)	94.6 (34.33-2.02) 91.9 (34.33-2.02)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 2.03Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.232 , 0.268 0.233 , 0.270	Depositor DCC
R_{free} test set	1994 reflections (4.28%)	wwPDB-VP
Wilson B-factor (Å ²)	33.8	Xtriage
Anisotropy	0.475	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.017 for -h-2*1,-k,l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4502	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.07% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 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: SO4

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	0.21	0/2200	0.43	0/2997
1	B	0.16	0/2277	0.39	0/3100
2	P	0.16	0/71	0.53	0/94
All	All	0.18	0/4548	0.42	0/6191

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2145	0	2040	64	0
1	B	2220	0	2118	18	0
2	P	71	0	60	3	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	11	0	0	1	0
4	B	45	0	0	0	0
All	All	4502	0	4218	83	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 10.

All (83) 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:422:ASP:H	1:A:470:ARG:NH2	1.65	0.94
1:A:370:VAL:HG11	1:A:445:PRO:HG2	1.64	0.78
1:A:597:MET:SD	1:A:598:THR:N	2.56	0.77
1:A:561:VAL:HG23	1:A:566:ILE:HD11	1.65	0.77
1:A:601:ARG:NH2	4:A:801:HOH:O	2.24	0.70
1:A:490:TYR:OH	1:A:495:ASN:OD1	2.10	0.69
1:B:466:ALA:HB1	1:B:514:VAL:HG23	1.75	0.68
1:A:422:ASP:H	1:A:470:ARG:HH21	1.41	0.68
1:A:356:ALA:HB2	1:A:401:ASN:OD1	1.94	0.68
1:A:597:MET:HE2	1:A:601:ARG:HH11	1.60	0.66
1:A:466:ALA:HB1	1:A:514:VAL:HG23	1.78	0.66
1:A:579:ASP:C	1:A:596:ARG:HD3	2.21	0.65
1:A:415:ARG:NH1	2:P:77:ASP:OD1	2.30	0.64
1:A:449:GLU:HG2	1:A:450:TRP:H	1.64	0.62
1:A:412:PRO:HG2	1:A:432:HIS:CG	2.36	0.61
1:A:447:ARG:CZ	1:A:449:GLU:HB2	2.31	0.60
1:A:447:ARG:O	1:A:447:ARG:NH2	2.35	0.60
1:B:472:LEU:HB3	1:B:490:TYR:HB3	1.84	0.59
1:A:425:ILE:HB	1:A:443:TYR:HB3	1.84	0.58
1:A:343:GLU:HA	1:A:355:LEU:HD12	1.85	0.57
1:A:345:TYR:HB2	1:A:352:TRP:CZ3	2.39	0.56
1:A:532:ASN:HD22	1:A:553:ARG:HG2	1.71	0.56
1:A:533:SER:HA	1:A:549:PRO:HB3	1.89	0.55
1:A:393:LEU:CD2	1:A:450:TRP:HZ2	2.20	0.55
1:A:345:TYR:CZ	1:A:595:THR:HG21	2.42	0.54
1:A:561:VAL:HA	1:A:566:ILE:CD1	2.39	0.53
1:A:547:VAL:HG12	1:A:548:ALA:H	1.74	0.53
1:A:444:GLU:HG3	1:A:447:ARG:HB3	1.89	0.53
1:A:342:LEU:HD22	1:A:403:TRP:CZ2	2.44	0.53
1:A:571:GLY:C	1:A:578:LEU:CD2	2.83	0.52
1:A:561:VAL:HA	1:A:566:ILE:HD12	1.93	0.51
1:A:447:ARG:NE	1:A:449:GLU:OE1	2.44	0.51
1:A:431:SER:HB3	1:A:461:ILE:HG21	1.93	0.50
1:A:579:ASP:CA	1:A:596:ARG:HD3	2.42	0.49
1:A:584:TYR:HB2	1:A:591:TRP:CE2	2.48	0.49
1:B:365:LEU:HD12	1:B:376:ALA:HB1	1.94	0.49
1:B:518:CYS:HB3	1:B:536:ARG:HG3	1.94	0.49
1:B:557:LEU:H	1:B:557:LEU:HD23	1.77	0.49
1:A:536:ARG:HG2	1:A:536:ARG:HH11	1.79	0.48
1:A:440:VAL:HG21	1:A:497:TRP:CZ2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:460:ARG:HB3	1:A:463:VAL:HB	1.95	0.48
1:A:503:MET:HE1	1:A:507:ARG:HB2	1.95	0.48
1:A:365:LEU:HD12	1:A:376:ALA:HB1	1.94	0.47
1:A:447:ARG:NH2	1:A:449:GLU:HB2	2.31	0.46
1:A:522:ALA:HA	1:A:534:VAL:HG22	1.97	0.46
1:A:547:VAL:HG12	1:A:548:ALA:N	2.29	0.46
1:A:369:VAL:HG13	1:A:607:ALA:HB1	1.97	0.46
1:A:365:LEU:HD23	1:A:365:LEU:H	1.79	0.46
1:A:555:SER:OG	2:P:79:GLU:O	2.31	0.46
2:P:76:LEU:HB3	2:P:83:PHE:HA	1.97	0.46
1:A:491:TYR:CE2	1:A:498:ARG:HG3	2.51	0.46
1:A:530:GLN:HG2	1:A:572:TYR:O	2.16	0.45
1:B:326:ARG:NH1	1:B:610:MET:HB3	2.30	0.45
1:B:335:PHE:C	1:B:337:GLN:H	2.24	0.45
1:B:515:LEU:HD22	1:B:566:ILE:HG13	1.97	0.45
1:B:520:TYR:CZ	1:B:536:ARG:HD3	2.52	0.45
1:A:373:LEU:HB2	1:A:375:TYR:CE2	2.52	0.45
1:A:421:ILE:HG12	1:A:467:VAL:HG11	1.99	0.45
1:A:570:GLY:C	1:A:578:LEU:HD21	2.42	0.45
1:A:362:ARG:HD2	1:A:378:GLY:O	2.17	0.45
1:B:383:SER:HB2	1:B:385:ASP:OD2	2.17	0.44
1:A:335:PHE:C	1:A:337:GLN:H	2.25	0.44
1:A:596:ARG:NE	1:A:597:MET:H	2.16	0.43
1:A:410:SER:OG	1:A:441:GLU:OE2	2.36	0.43
1:A:447:ARG:HH21	1:A:447:ARG:C	2.26	0.43
1:B:468:LEU:HD22	1:B:519:ILE:HG13	2.01	0.43
1:B:416:ILE:HD11	1:B:427:ALA:HB1	2.01	0.43
1:A:472:LEU:HB3	1:A:490:TYR:HB3	2.01	0.42
1:A:560:THR:O	1:A:566:ILE:HD12	2.19	0.42
1:B:425:ILE:HB	1:B:443:TYR:HB3	2.01	0.42
1:B:373:LEU:HB3	1:B:395:CYS:SG	2.60	0.42
1:B:467:VAL:O	1:B:514:VAL:HG21	2.20	0.41
1:B:512:VAL:HA	1:B:520:TYR:O	2.20	0.41
1:A:413:ARG:NH1	1:A:429:GLY:O	2.47	0.41
1:B:490:TYR:CE1	1:B:492:PRO:HA	2.55	0.41
1:A:396:TYR:HB2	1:A:403:TRP:CD2	2.55	0.41
1:A:400:THR:HG23	1:A:402:GLN:OE1	2.21	0.41
1:A:550:MET:HA	1:A:591:TRP:CG	2.56	0.41
1:A:560:THR:HB	1:A:606:VAL:HG12	2.03	0.41
1:A:380:ARG:HD2	1:A:387:ASN:ND2	2.36	0.40
1:A:346:ASN:HB3	1:A:349:ASP:HB2	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:566:ILE:HB	1:B:584:TYR:HB3	2.03	0.40
1:A:342:LEU:HB3	1:A:356:ALA:O	2.21	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	279/336 (83%)	262 (94%)	16 (6%)	1 (0%)	30	22
1	B	288/336 (86%)	281 (98%)	7 (2%)	0	100	100
2	P	7/9 (78%)	7 (100%)	0	0	100	100
All	All	574/681 (84%)	550 (96%)	23 (4%)	1 (0%)	43	40

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	448	ASP

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	226/275 (82%)	226 (100%)	0	100	100
1	B	234/275 (85%)	234 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	P	7/7 (100%)	7 (100%)	0	100	100
All	All	467/557 (84%)	467 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	387	ASN
1	A	451	HIS
1	B	402	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	A	701	-	4,4,4	0.24	0	6,6,6	0.06	0
3	SO4	B	701	-	4,4,4	0.25	0	6,6,6	0.06	0

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 ⓘ

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	280/336 (83%)	2.30	143 (51%) 0 0	30, 71, 135, 172	1 (0%)
1	B	289/336 (86%)	0.35	13 (4%) 38 37	19, 35, 60, 113	1 (0%)
2	P	9/9 (100%)	2.78	4 (44%) 0 0	49, 57, 78, 88	0
All	All	578/681 (84%)	1.33	160 (27%) 1 1	19, 46, 118, 172	2 (0%)

All (160) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	353	LEU	10.4
1	A	352	TRP	7.4
2	P	76	LEU	7.3
1	A	561	VAL	7.1
1	A	517	ASN	6.7
1	A	564	GLY	6.7
1	A	566	ILE	6.6
1	A	344	ALA	6.5
2	P	84	LEU	6.4
1	A	608	VAL	6.3
1	A	491	TYR	5.8
1	A	578	LEU	5.7
1	A	420	VAL	5.7
1	A	581	VAL	5.7
1	A	567	TYR	5.5
1	A	579	ASP	5.4
1	A	351	THR	5.3
1	A	594	VAL	5.3
1	A	516	HIS	5.3
1	A	393	LEU	5.2
1	A	403	TRP	5.1
1	A	518	CYS	5.1
1	A	425	ILE	5.1

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Mol	Chain	Res	Type	RSRZ
1	A	424	HIS	5.1
1	A	350	GLY	5.1
1	A	598	THR	5.0
1	A	568	VAL	5.0
1	A	569	LEU	4.9
1	A	560	THR	4.8
1	A	392	ALA	4.6
1	A	400	THR	4.5
1	A	355	LEU	4.5
1	A	570	GLY	4.4
1	A	374	LEU	4.4
1	A	423	GLY	4.4
1	A	589	ASP	4.3
1	A	590	THR	4.3
1	A	597	MET	4.3
1	A	356	ALA	4.2
1	A	583	CYS	4.2
1	A	369	VAL	4.2
1	A	609	THR	4.2
1	A	421	ILE	4.1
2	P	83	PHE	4.1
1	A	341	TYR	4.0
1	A	373	LEU	4.0
1	A	347	PRO	4.0
1	A	592	SER	3.9
1	A	596	ARG	3.9
1	A	580	SER	3.9
1	A	455	PRO	3.9
1	A	559	ILE	3.9
1	A	470	ARG	3.9
1	A	575	HIS	3.9
1	A	519	ILE	3.9
1	A	445	PRO	3.9
1	A	584	TYR	3.8
1	A	399	MET	3.8
1	A	493	GLU	3.8
1	A	468	LEU	3.7
1	A	565	ARG	3.7
1	A	591	TRP	3.7
1	A	375	TYR	3.7
1	A	443	TYR	3.7
1	A	452	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	396	TYR	3.6
1	A	492	PRO	3.6
1	A	515	LEU	3.6
1	A	586	PRO	3.6
1	B	384	PRO	3.6
1	A	562	HIS	3.6
1	B	613	SER	3.6
1	A	588	THR	3.5
1	A	587	ASP	3.5
1	A	370	VAL	3.5
1	A	405	PRO	3.3
1	A	450	TRP	3.2
1	A	571	GLY	3.2
1	A	426	TYR	3.2
1	A	398	PRO	3.2
1	A	377	VAL	3.2
1	A	397	ASN	3.2
1	A	346	ASN	3.2
2	P	77	ASP	3.2
1	A	330	THR	3.2
1	A	345	TYR	3.1
1	B	492	PRO	3.1
1	A	513	CYS	3.1
1	A	607	ALA	3.1
1	A	402	GLN	3.1
1	A	354	ARG	3.1
1	A	406	CYS	3.1
1	A	376	ALA	3.1
1	A	604	VAL	3.0
1	A	371	GLY	3.0
1	A	494	ARG	3.0
1	A	595	THR	3.0
1	A	606	VAL	3.0
1	A	573	ASP	2.9
1	B	385	ASP	2.8
1	A	489	CYS	2.8
1	A	446	GLU	2.8
1	A	552	HIS	2.8
1	A	540	ALA	2.8
1	A	342	LEU	2.8
1	A	442	ARG	2.8
1	A	563	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	593	GLU	2.8
1	A	395	CYS	2.8
1	A	467	VAL	2.8
1	A	577	PHE	2.7
1	A	548	ALA	2.7
1	A	453	VAL	2.7
1	B	382	ASN	2.7
1	A	546	PHE	2.7
1	A	335	PHE	2.6
1	A	547	VAL	2.6
1	A	457	LEU	2.6
1	A	599	SER	2.6
1	A	600	GLY	2.5
1	A	473	TYR	2.5
1	A	454	ALA	2.5
1	A	601	ARG	2.5
1	A	366	ALA	2.5
1	A	447	ARG	2.5
1	A	441	GLU	2.4
1	A	448	ASP	2.4
1	A	498	ARG	2.4
1	A	348	SER	2.4
1	A	490	TYR	2.4
1	B	386	GLY	2.4
1	B	588	THR	2.4
1	A	471	LEU	2.4
1	A	469	ASN	2.4
1	A	585	ASP	2.4
1	A	514	VAL	2.4
1	A	534	VAL	2.4
1	B	493	GLU	2.3
1	A	407	ALA	2.3
1	A	349	ASP	2.3
1	B	491	TYR	2.3
1	B	335	PHE	2.2
1	A	409	MET	2.2
1	A	343	GLU	2.2
1	A	520	TYR	2.2
1	A	550	MET	2.2
1	A	368	CYS	2.2
1	A	539	VAL	2.1
1	B	387	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	582	GLU	2.1
1	A	440	VAL	2.1
1	A	465	VAL	2.1
1	A	422	ASP	2.1
1	A	527	GLY	2.1
1	A	574	GLY	2.1
1	A	362	ARG	2.1
1	A	451	HIS	2.1
1	B	399	MET	2.0
1	A	372	GLY	2.0
1	B	325	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	B	701	5/5	0.73	0.17	78,82,84,86	0
3	SO4	A	701	5/5	0.74	0.15	90,92,93,94	0

6.5 Other polymers [i](#)

There are no such residues in this entry.